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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:31:51 ; Search time 20.3612 Seconds

(without alignments)  
2678.292 Million cell updates/sec

Title: US-09-830-972-32

Perfect score: 705

Sequence: 1 QASGEAGVCLRENFAVYV.....ESEVAISEELVQKYSNALG 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	680.5	96.5	522	3	AAY71312 Rat neuro
2	510	72.3	199	5	ABB81077 Rat neuro
3	503	71.3	118	5	ABB8192 Human pol
4	503	71.3	199	2	AAS53947 Human NSP
5	503	71.3	199	2	AAY78313 Fragment
6	503	71.3	199	2	AAY35903 Extended
7	503	71.3	199	3	AAB12805 Human NSP
8	503	71.3	199	4	AAB82348 Human NSP
9	503	71.3	199	5	ABG30939 Human Nog
10	503	71.3	199	5	ABB81080 Human neu
11	503	71.3	199	8	ADP19211 Human sec
12	503	71.3	199	8	ADP67236 Human Nog
13	499.5	70.9	199	3	AAY71559 Rat Nogo
14	496	70.4	199	7	ADK67504 Human RTN
15	448	63.5	1178	3	AAY71311 Human neu
16	447	63.4	403	3	AAY71563 Rat Nogo
17	447	63.4	893	3	AAY95012 Human sec
18	447	63.4	983	6	ABU11573 Human MDD
19	447	63.4	1162	3	AAY71557 Rat Nogo
20	447	63.4	1162	8	ADT89537 Mus muscu
21	447	63.4	1163	3	AAY71310 Rat neuro
22	447	63.4	1163	3	AAY71384 Alternati
23	447	63.4	1163	5	ABB81074 Rat neuro
24	447	63.4	1163	8	ADO26399 Rat trunc
25	447	63.4	1163	8	ADP45572 Rat NogoA

#### ALIGNMENTS

RESULT 1

AAY71312  
ID AAY71312 standard; protein; 522 AA.

XX AC AAY71312;

DT 02-NOV-2000 (first entry)

DE Rat neurite growth inhibitor Nogo C.

XX Rat; neurite growth inhibitor; Nogo C; neural cell; myelin; CNS;  
KW central nervous system; neoplastic disease; antiproliferative; glioma;  
KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
KW structural plasticity; screening.

XX Rattus sp.

XX Key Location/Qualifiers

FT Region 1..39 /note= "Sequence upstream to the N-terminus of Nogo C"

FT Misc-difference 3 /note= "Encoded by TAG"

FT Region 11..191 /note= "Region specifically described in claim 16"

FT Misc-difference 29 /note= "Encoded by TAA"

FT Protein 40..238 /label= Nogo\_C\_protein

FT Region 51..238 /note= "C-terminal common region found in Nogo A, B and C isoforms"

FT Region 239..522 /note= "Sequence downstream to the C-terminus of Nogo C protein"

FT Misc-difference 239 /note= "Encoded by TGA"

FT Misc-difference 263 /note= "Encoded by TGA"

FT Misc-difference 276 /note= "Encoded by TAG"

FT Misc-difference 281 /note= "Encoded by TGA"

FT Misc-difference 295 /note= "Encoded by TAA"





peptide, a nucleotide sequence the NS-specific antigen or its analogue or combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, where the injury is spinal cord injury, blunt trauma, penetrating trauma, hemorrhagic stroke, ischemic stroke or damages caused by surgery such as tumour excision. The disease is not an autoimmune disease or neoplasm. The disease results in a degenerative process occurring in either gray or white matter or both. The disease is diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's disease, facial nerve (Bell's) palsy, Glaucoma, Huntington's chorea, amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and vitamin deficiency, intervertebral disc herniation, prion diseases such as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral neuropathies associated with various diseases, including but not limited to uremia, porphyria, hypoglycemia, Sjogren Larsson syndrome, acute sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary amyloidosis, obstructive lung diseases, acromegaly, malabsorption syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-pathies, complications of various drugs (e.g., metronidazole) and toxins (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia telangiectasia, Friedreich's ataxia, amyloid polynuropathies, adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's disease, or lipoproteinemia. The present sequence represents the rat neurotransmitter receptor protein Nogo-C, an example of NS-specific antigen

XX SQ Sequence 199 AA;

Query Match 72.3%; Score 510; DB 5; Length 199;  
Best Local Similarity 99.0%; Pred. No. 1.4e-51;  
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 38 MDGQKHKKVVDLLYWRDIKKTGVVFGASLFLLSLTVPFSIVSVTAYIALALLSVTIS 97  
DB 1 MDGQKHKKVVDLLYWRDIKKTGVVFGASLFLLSLTVPFSIVSVTAYIALALLSVTIS 60

QY 98 PRIYKGVITQIAKSDGEGHPFRAYLESEVAISEELVQKYSNSALG 141  
DB 61 PRIYKGVITQIAKSDGEGHPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 3  
ID ABB89192 standard; protein; 118 AA.

XX AC ABB89192;

XX DT 24-MAY-2002 (first entry)

XX DE Human polypeptide SEQ ID NO 1568.

XX KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
KW antiallergic; hepatotropic; antidiabetic; antinflammatory; antitumor;  
KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;  
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; human; secreted protein.

XX OS Homo sapiens.

XX PN WO200190304-A2.

XX PD 29-NOV-2001.

XX PF 18-MAY-2001; 2001WO-US016450.

XX PR 19-MAY-2000; 2000US-0205515P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Birse CE, Rosen CA;

XX DR WPI; 2002-122018/16.

XX DR N-PSDB; ABL89601.

XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders.

XX PS Claim 11; SEQ ID NO 1568; 2081pp + Sequence Listing; English.

XX CC The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 118 AA;

Query Match 71.3%; Score 503; DB 5; Length 118;  
Best Local Similarity 98.1%; Pred. No. 4.7e-51;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 38 MDGQKHKKVVDLLYWRDIKKTGVVFGASLFLLSLTVPFSIVSVTAYIALALLSVTIS 97  
DB 1 MDGQKHKKVVDLLYWRDIKKTGVVFGASLFLLSLTVPFSIVSVTAYIALALLSVTIS 60

QY 98 PRIYKGVITQIAKSDGEGHPFRAYLESEVAISEELVQKYSNSALG 141  
DB 61 PRIYKGVITQIAKSDGEGHPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 4

AAW53947

ID AAW53947 standard; protein; 199 AA.

XX AC AAW53947;

XX DT 24-JUL-1998 (first entry)

XX DE Human NSPLP protein A.

XX KW NSPLP; neuroendocrine-specific protein-like protein; human; gene therapy;  
KW neurodegenerative disease; amyotrophic lateral sclerosis; cancer.

XX OS Homo sapiens.

XX PN WO9806841-A2.

XX PD 19-FEB-1998.

XX PF 24-JUL-1997; 97WO-US013469.

XX PR 12-AUG-1996; 96US-00700607.

XX PA (INCY-) INCYTE PHARM INC.

XX PI Bandman O, Au-Young J, Goli SK, Hillman J;

XX DR WPI; 1998-159533/14.

XX DR N-PSDB; AAV23695.

XX Human neuro-endocrine-specific protein-like proteins - useful for diagnosis, monitoring and treatment of cancer and neuro-degenerative

PT disease.

XX Claim 1; Page 38; 73pp; English.

XX This sequence is a human neuroendocrine-specific protein-like protein (NSPLP) of the invention. Recombinant cells transformed with the DNA are used to express the NSPLP proteins, which are used to treat cancer and neurodegenerative diseases such as amyotrophic lateral sclerosis. Also antisense nucleic acids and antagonists of NSPLP can be used to inhibit activity of the NSPLP proteins. Antibodies specific for NSPLP are used for diagnosis and monitoring treatment of diseases associated with NSPLP expression, in usual immunoassays, and to isolate NSPLP from natural sources. The NSPLP proteins, or their fragments can also be used in drug screening to identify NSPLP antagonists. The nucleic acid can be used diagnostically and for monitoring treatment (in hybridisation or amplification assays); to isolate closely related sequences; in gene therapy for both sense and antisense applications (including use of ribozymes) and for mapping the natural genomic sequence

SQ Sequence 199 AA;

Query Match 71.3%; Score 503; DB 2; Length 199;  
Best Local Similarity 98.1%; Pred. No. 9.4e-51;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 38 MDGQKKWKDKVVDLLYWRDIKKTGVFGASLFLLSLTVPFSIVSVTAYIALALLSVTIS 97  
DB 1 MDGQKKWKDKVVDLLYWRDIKKTGVFGASLFLLSLTVPFSIVSVTAYIALALLSVTIS 60

QY 98 PRIYKGVIOAKSDEGHPPFRAYLESEVAISEELVQKYSNSALG 141  
DB 61 PRIYKGVIOAKSDEGHPPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 5  
ID AAW78313  
XX AAW78313 standard; protein; 199 AA.  
AC AAW78313;  
XX  
DT 13-APR-1999 (first entry)  
XX  
DE Fragment of human secreted protein encoded by gene 69.  
XX Human; secreted protein; fusion protein; gene therapy; protein therapy;  
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
KW developmental abnormality; foetal deficiency; blood; allergy; renal;  
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

OS Homo sapiens.  
XX  
XX WO9856804-A1.  
XX  
PD 17-DEC-1998.  
XX  
XX 11-JUN-1998; 98WO-US012125.  
XX  
PR 13-JUN-1997; 97US-0049547P.  
PR 13-JUN-1997; 97US-0049548P.  
PR 13-JUN-1997; 97US-0049549P.  
PR 13-JUN-1997; 97US-0049550P.  
PR 13-JUN-1997; 97US-0049556P.  
PR 13-JUN-1997; 97US-0049606P.  
PR 13-JUN-1997; 97US-0049607P.  
PR 13-JUN-1997; 97US-0049608P.  
PR 13-JUN-1997; 97US-0049609P.  
PR 13-JUN-1997; 97US-0049610P.  
PR 13-JUN-1997; 97US-0049611P.  
PR 13-JUN-1997; 97US-0050901P.

PR 13-JUN-1997; 97US-0052989P.  
PR 08-JUL-1997; 97US-0051919P.  
PR 18-AUG-1997; 97US-0055984P.  
PR 12-SEP-1997; 97US-0058665P.  
PR 12-SEP-1997; 97US-0058668P.  
PR 12-SEP-1997; 97US-0058669P.  
PR 12-SEP-1997; 97US-0058750P.  
PR 12-SEP-1997; 97US-0058971P.  
PR 12-SEP-1997; 97US-0058972P.  
PR 12-SEP-1997; 97US-0058975P.  
PR 02-OCT-1997; 97US-0060834P.  
PR 02-OCT-1997; 97US-0060841P.  
PR 02-OCT-1997; 97US-0060844P.  
PR 02-OCT-1997; 97US-0060865P.  
PR 02-OCT-1997; 97US-0061059P.  
PR 02-OCT-1997; 97US-0061060P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Moore PA, Shi Y, Rosen CA, Ruben SM, Lafleur DW, Olsen HS;  
PI Ebner R, Brewer LA, Young P, Greene JM, Ferrie AM, Yu G, Ni J;  
PI Feng P;  
XX  
XX WPI; 1999-080881/07.  
XX N-PSDB; AAX04379.  
XX  
XX New isolated human genes and the secreted polypeptides they encode -  
PT useful for diagnosis and treatment of e.g. cancers, neurological  
PT disorders, immune diseases, inflammation or blood disorders.  
XX  
XX Disclosure; Page 62; 380pp; English.  
XX  
XX This sequence represents a fragment of a secreted human protein encoded  
CC by the nucleic acid molecule detailed in the descriptor line. The gene  
CC can be used to generate fusion proteins by linking to the gene to a human  
CC immunoglobulin Fc portion (e.g. AAX04302) for increasing the stability of  
CC the fused protein as compared to the human protein only. The invention  
CC relates to 86 novel genes and their fragments (nucleic acid sequences:  
CC AAX04311-X04410; amino acid sequences AAW78126-W78225) which are useful  
CC for preventing, treating or ameliorating medical conditions e.g. by  
CC protein or gene therapy. Also, pathological conditions can be diagnosed  
CC by determining the amount of the new polypeptides in a sample or by  
CC determining the presence of mutations in the new polynucleotides.  
CC Specific uses are described for each of the 86 polynucleotides, based on  
CC which tissues they are most highly expressed in (see AAX04311 for  
CC described uses)  
XX  
XX Sequence 199 AA;

Query Match 71.3%; Score 503; DB 2; Length 199;  
Best Local Similarity 98.1%; Pred. No. 9.4e-51;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 38 MDGQKKWKDKVVDLLYWRDIKKTGVFGASLFLLSLTVPFSIVSVTAYIALALLSVTIS 97  
DB 1 MDGQKKWKDKVVDLLYWRDIKKTGVFGASLFLLSLTVPFSIVSVTAYIALALLSVTIS 60

QY 98 PRIYKGVIOAKSDEGHPPFRAYLESEVAISEELVQKYSNSALG 141  
DB 61 PRIYKGVIOAKSDEGHPPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 6  
AAY35903  
ID AAY35903 standard; protein; 199 AA.  
XX  
XX AAY35903;  
AC  
XX  
DT 13-SEP-1999 (first entry)  
XX  
XX Extended human secreted protein sequence, SEQ ID NO. 152.  
XX Secreted protein; human; cytokine; cellular proliferation; cell movement;

KW cellular differentiation; immune system regulator; anti-inflammatory;  
KW haematopoiesis regulator; tissue growth regulator; tumour inhibitor;  
KW reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;  
KW genetic disease.  
XX Homo sapiens.  
XX WO9931236-A2.  
XX 24-JUN-1999.  
XX 17-DEC-1998; 98WO-IB002122.  
XX 17-DEC-1997; 97US-0069957P.  
PR 09-FEB-1998; 98US-0074121P.  
PR 13-APR-1998; 98US-0081563P.  
PR 10-AUG-1998; 98US-0096116P.  
XX (GEST ) GENSET.  
XX Bougueleret L, Duclert A, Dumas Milne Edwards J;  
XX  
XX WPI; 1999-385906/32.  
DR N-PSDB; AAX97587.  
XX  
XX New isolated human secreted proteins.  
XX  
XX Claim 9; Page 185-186; 516pp; English.  
XX

This sequence is encoded by an extended human secreted protein coding sequence of the invention. The secreted proteins can be used in treating or controlling a variety of human conditions. The secreted proteins may act as cytokines or may affect cellular proliferation or differentiation or may act as immune system regulators, haematopoiesis regulators, tissue growth regulators, regulators of reproductive hormones or cell movement or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or tumour inhibition activity. The DNAs can be used in forensic procedures to identify individuals or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal expression of the genes corresponding to the extended cDNAs. They are also useful for constructing a high resolution map of the human chromosomes. They can also be used for gene therapy to control or treat genetic diseases

XX Sequence 199 AA;

Query Match 71.3%; Score 503; DB 2; Length 199;  
Best Local Similarity 98.1%; Pred. No. 9.4e-51;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 38 MDGQKXHWKDVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 97  
Db 1 MDGQKXHWKDVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 60  
QY 98 FRIYKGVIOAIKSDGHPFRAYLSEVAISELVQKYSNSALG 141  
Db 61 FRIYKGVIOAIKSDGHPFRAYLSEVAISELVQKYSNSALG 104

RESULT 7  
AAB12805

ID AAB12805 standard; protein; 199 AA.

AC AAB12805;

XX 24-NOV-2000 (first entry)

DT Human NSPH protein sequence SEQ ID NO:4.

DE Human; neuroendocrine-specific protein; NSPH; NSPA; NSPB; NSPC.

KW Homo sapiens.

OS CN1253180-A.

PN

XX 17-MAY-2000.  
PD 30-OCT-1998; 98CN-00121473.  
PF 30-OCT-1998; 98CN-00121473.  
XX 30-OCT-1998; 98CN-00121473.  
PR (UYFU-) UNIV FUDAN.  
XX Yu L, Zhao Y, Zhang H;  
XX WPI; 2000-466537/41.  
DR N-PSDB; AAA72981.  
XX Specific protein of human neuroendocrine, coding sequence and its  
PT preparing process and application.  
XX Claim 4; Page 14-15; 21pp; Chinese.  
PS The present invention relates to a new member of the human neuroendocrine  
CC specific protein family, designated NSPH. The present sequence represents  
CC the human NSPH protein  
XX Sequence 199 AA;

Query Match 71.3%; Score 503; DB 3; Length 199;  
Best Local Similarity 98.1%; Pred. No. 9.4e-51;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 38 MDGQKXHWKDVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 97  
Db 1 MDGQKXHWKDVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 60  
QY 98 FRIYKGVIOAIKSDGHPFRAYLSEVAISELVQKYSNSALG 141  
Db 61 FRIYKGVIOAIKSDGHPFRAYLSEVAISELVQKYSNSALG 104

RESULT 8  
AAB82348

ID AAB82348 standard; protein; 199 AA.

XX AAB82348;

XX 23-JUL-2001 (first entry)

DE Human NOGO-C protein.

XX NOGO-C; human; chromosome 2p21; neuropathy; spinal injury; brain injury;  
KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;  
KW neuromuscular disorder; psychiatric disorder; developmental disorder;  
KW neuroprotective; nootropic; neuroleptic; antiparkinsonian;  
KW cerebroprotective; neuroleptic; diagnosis; therapy.

XX Homo sapiens.

OS WO200136631-A1.

PN 25-MAY-2001.

PD 14-NOV-2000; 2000WO-GB004345.

PF 15-NOV-1999; 99GB-00026995.

PR 24-JAN-2000; 2000GB-00001550.

XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Michalovich D, Prinjha R;

XX WPI; 2001-343822/36.

DR N-PSDB; AAF90323.

XX New polypeptide designated NOGO-C is a splice variant of the human NOGO

PT Gene and may be useful in the treatment of neural disorders including  
 PT Alzheimer's and Parkinson's diseases.  
 XX Claim 3; Page 25; 25pp; English.  
 XX  
 CC The present sequence is that of human Nogo-C, encoded by a novel splice  
 CC variant of the human Nogo gene on chromosome 2p21. 2 Other splice  
 CC variants, Nogo-A and Nogo-B, have previously been identified. The  
 CC invention provides Nogo-C polypeptides and polynucleotides, and methods  
 CC for producing such polypeptides by recombinant techniques. Also disclosed  
 CC are methods for utilising Nogo-C polypeptides and polynucleotides in the  
 CC treatment of diseases including neuropathies, spinal injury, brain  
 CC injury, stroke, neuronal degeneration, for example Alzheimer's disease  
 CC and Parkinson's disease, neuromuscular disorders, psychiatric disorders  
 CC and developmental disorders. Also provided are methods for identifying  
 CC agonists and agonists for use in treating conditions associated with Nogo  
 CC -C imbalance, and diagnostic assays for detecting diseases associated  
 CC with inappropriate Nogo-C activity or levels  
 XX Sequence 199 AA;  
 SQ  
 Query Match 71.3%; Score 503; DB 4; Length 199;  
 Best Local Similarity 98.1%; Pred. No. 9.4e-51;  
 Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 38 MDGQKKHKKDQVLLYWRDIKKTGVFGASLFLLLSLTVFSIVSYVTAYIALALLSVTIS 97  
 DB 1 MDGQKKHKKDQVLLYWRDIKKTGVFGASLFLLLSLTVFSIVSYVTAYIALALLSVTIS 60  
 QY 98 PRIYKGVIOAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 141  
 DB 61 PRIYKGVIOAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 104  
 RESULT 9  
 ABG30939  
 ID ABG30939 standard; protein; 199 AA.  
 XX  
 AC ABG30939;  
 XX  
 DT 21-OCT-2002 (first entry)  
 DE Human NogoC protein.  
 XX  
 KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;  
 KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;  
 KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;  
 KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;  
 KW tissue hypertrophy; central nervous system; axon regeneration; NogoC;  
 KW Nogo-associated disease; metastasis.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200257483-A2.  
 XX  
 PD 25-JUL-2002.  
 XX  
 PF 18-JAN-2002; 2002WO-GB0000228.  
 XX  
 XX 18-JAN-2001; 2001GB-00001312.  
 XX  
 PA (GLAXO) GLAXO GROUP LTD.  
 PA (SMK) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Blackstock WP, Hale RS, Prinjha R, Rowley A;  
 XX  
 XX WPI; 2002-599722/64.  
 DR N-P8DB; ABK90135.  
 XX  
 XX Identifying modulators of Nogo or BACE activity for treating acute  
 PT neuronal injuries, neoplastic or dysproliferative disorders, comprises  
 PT providing and monitoring interaction between Nogo and BACE polypeptides.  
 XX

PS Disclosure; Page 64; 68pp; English.  
 XX  
 CC The present invention relates to a new method of identifying modulators  
 CC of Nogo function or BACE activity. The method involves providing Nogo and  
 CC BACE polypeptides capable of binding with each other, monitoring the  
 CC interaction between these polypeptides, and determining if the test agent  
 CC is a modulator of Nogo or BACE activity. The method is useful in treating  
 CC acute neuronal injuries, such as spinal or head injury, stroke,  
 CC peripheral nerve damage, and in neoplastic (e.g. glioblastomas,  
 CC neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.  
 CC cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue  
 CC hypertrophy) of the central nervous system. The BACE polypeptide is  
 CC useful in screening methods to identify agents that may act as modulators  
 CC of BACE activity and in particular agents that may be useful in treating  
 CC Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,  
 CC and the polynucleotide encoding the BACE polypeptide are useful in  
 CC manufacturing a medicament for the treatment or prevention of disorders  
 CC responsive to the modulation of Nogo activity, in alleviating the  
 CC symptoms or improving the condition of a patient suffering from this  
 CC disorder, in axon regeneration, or in preventing metastasis or spreading  
 CC of a cancer. The polynucleotide may also be an essential component in  
 CC assays, a probe, in recombinant protein synthesis, and in gene therapy  
 CC techniques. The present amino acid sequence represents the human NogoC  
 CC protein of the invention  
 XX Sequence 199 AA;  
 SQ  
 Query Match 71.3%; Score 503; DB 5; Length 199;  
 Best Local Similarity 98.1%; Pred. No. 9.4e-51;  
 Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 38 MDGQKKHKKDQVLLYWRDIKKTGVFGASLFLLLSLTVFSIVSYVTAYIALALLSVTIS 97  
 DB 1 MDGQKKHKKDQVLLYWRDIKKTGVFGASLFLLLSLTVFSIVSYVTAYIALALLSVTIS 60  
 QY 98 PRIYKGVIOAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 141  
 DB 61 PRIYKGVIOAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 104  
 RESULT 10  
 ABG81080  
 ID ABG81080 standard; protein; 199 AA.  
 XX  
 AC ABG81080;  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Human neurotransmitter receptor protein Nogo-C.  
 XX  
 KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;  
 KW central nervous system; peripheral nervous system; tranquilizer; Nogo;  
 KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;  
 KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;  
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;  
 KW neurotransmitter receptor; human; receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 FN US2002072493-A1.  
 XX  
 XX 13-JUN-2002.  
 XX  
 XX 28-JUN-2001; 2001US-00893348.  
 XX  
 XX 19-MAY-1998; 98IL-00124500.  
 PR 21-JUL-1998; 98WO-US014715.  
 PR 22-DEC-1998; 98US-00218277.  
 PR 19-MAY-1999; 99US-00314161.  
 XX  
 XX (YEDA) YEDA RES & DEV CO LTD.  
 PA  
 XX Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;  
 PI

PI Moalem G;  
 XX WPI: 2002-607255/65.  
 DR N-PSDB; ABN86601.  
 XX  
 XX Promoting nerve regeneration and preventing neuronal degeneration in the  
 PT central/peripheral nervous system from injury/disease, comprises  
 PT administering nervous system-specific activated T cells/antigen, or  
 XX analogs/peptides.  
 XX  
 PS Example; Page 57-58; 93pp; English.  
 XX  
 XX The invention relates to promoting nerve regeneration or conferring  
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the  
 CC central/peripheral nervous system (NS). The method involves administering  
 CC central/peripheral nervous system (NS). The method involves administering  
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its  
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or  
 CC combinations. The method is useful for promoting nerve regeneration and  
 CC preventing neuronal degeneration in central/peripheral nervous system  
 CC from injury/disease, where the injury is spinal cord injury, blunt  
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or  
 CC damages caused by surgery such as tumour excision. The disease is not an  
 CC autoimmune disease or neoplasm. The disease results in a degenerative  
 CC process occurring in either gray or white matter or both. The disease is  
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,  
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and  
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such  
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral  
 CC neuropathies associated with various diseases, including but not limited  
 CC to uremia, porphyria, hypoglycemia, Sjogren Larsson syndrome, acute  
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary  
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption  
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-  
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins  
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia  
 CC telangiectasia, Friedreich's ataxia, amyloid polyneuropathies,  
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's  
 CC disease, or lipoproteinemia. The present sequence represents the human  
 CC neurotransmitter receptor protein Nogo-C, an example of NS-specific  
 XX antigen  
 XX  
 SQ Sequence 199 AA;  
 Query Match 71.3%; Score 503; DB 5; Length 199;  
 Best Local Similarity 98.1%; Pred. No. 9.4e-51;  
 Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 38 MDGQKXHWKDVLDLYWRDIKKTGVVFGASLFLLSLTIVFSIVSVTAYIALALLSVTIS 97  
 Db 1 MDGQKNWKKDVLDLYWRDIKKTGVVFGASLFLLSLTIVFSIVSVTAYIALALLSVTIS 60  
 QY 98 FRIYKGVIOAIKSDGHPFRAYLSEVAISELVQKYSNALS 141  
 Db 61 FRIYKGVIOAIKSDGHPFRAYLSEVAISELVQKYSNALS 104  
 RESULT 12  
 ADP67236  
 ID ADP67236 standard; protein; 199 AA.  
 XX  
 AC ADP67236;  
 AC  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Human Nogo-C protein.  
 XX  
 XX human; Nogo-C; neurite outgrowth inhibitor; Nogo;  
 KW contactin-associated protein-1; Caspr; neuroprotective; gene therapy;  
 KW CNS; spinal cord injury; multiple sclerosis; epilepsy; stroke.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004110939-A1.  
 XX

PD 10-JUN-2004.  
 XX  
 XX 15-OCT-2001; 2001US-00978360.  
 XX  
 PR 17-DEC-1998; 98WO-IB002122.  
 PR 09-FEB-1999; 99WO-IB000282.  
 PR 21-JUN-2000; 2000WO-IB000951.  
 PR 15-SEP-2000; 2000US-00663600.  
 XX  
 PA (GEST ) GENSET SA.  
 XX  
 XX Dumas Milne Edwards J, Bougueleret L, Jobert S, Clusel C;  
 PI Duclert A;  
 XX  
 DR WPI: 2004-440404/41.  
 DR N-PSDB; ADP18806.  
 XX  
 XX New isolated polynucleotide encoding secreted polypeptide, useful for  
 PT gene therapy, or in diagnostic procedures to identify individuals having  
 PT genetic diseases resulting from abnormal expression of the genes.  
 XX  
 PS Claim 2; SEQ ID NO 467; 113pp; English.  
 XX  
 CC The invention relates to human cDNA sequences that encode human secreted  
 CC proteins. The invention also relates to an antibody that specifically  
 CC binds to a polypeptide of the invention and a method of binding the  
 CC polypeptide to an antibody. The polynucleotides are useful for expressing  
 CC the entire secreted proteins which they encode and for distinguishing  
 CC human tissues and cells from non-human tissues and cells, and for  
 CC distinguishing between human tissues and cells that do or do not express  
 CC the polynucleotides comprising the cDNAs. The polynucleotides and  
 CC polypeptides are useful in forensic procedures or diagnostic procedures  
 CC to identify individuals with genetic diseases resulting from abnormal  
 CC expression of the genes corresponding to the cDNAs. The sequences are  
 CC also useful in gene therapy to control or treat genetic diseases. This  
 CC sequence represents a human secreted polypeptide of the invention. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html.  
 XX  
 SQ Sequence 199 AA;  
 Query Match 71.3%; Score 503; DB 8; Length 199;  
 Best Local Similarity 98.1%; Pred. No. 9.4e-51;  
 Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 38 MDGQKXHWKDVLDLYWRDIKKTGVVFGASLFLLSLTIVFSIVSVTAYIALALLSVTIS 97  
 Db 1 MDGQKNWKKDVLDLYWRDIKKTGVVFGASLFLLSLTIVFSIVSVTAYIALALLSVTIS 60  
 QY 98 FRIYKGVIOAIKSDGHPFRAYLSEVAISELVQKYSNALS 141  
 Db 61 FRIYKGVIOAIKSDGHPFRAYLSEVAISELVQKYSNALS 104  
 RESULT 12  
 ADP67236  
 ID ADP67236 standard; protein; 199 AA.  
 XX  
 AC ADP67236;  
 AC  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Human Nogo-C protein.  
 XX  
 XX human; Nogo-C; neurite outgrowth inhibitor; Nogo;  
 KW contactin-associated protein-1; Caspr; neuroprotective; gene therapy;  
 KW CNS; spinal cord injury; multiple sclerosis; epilepsy; stroke.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004052389-A2.  
 XX



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XX Human RTN-4C protein.
DE
XX
DE
XX
KW neuroprotective; gene therapy; BACE1 activity; RTN4; RTN3; amyloidosis;
KW Alzheimer's disease.
XX
XX
OS Homo sapiens.
XX
XX WO2003088926-A2.
XX
XX 30-OCT-2003.
XX
XX 08-APR-2003; 2003WO-US008829.
XX
XX 17-APR-2002; 2002US-0373284P.
XX
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX Yan R, Lu Y;
XX
XX WPI; 2003-854033/79.
XX
XX New polypeptide having BACE1 activity, useful in preparing a composition
XX for treating amyloidosis or Alzheimer's disease.
XX
XX Claim 52; SEQ ID NO 9; 42pp; English.
XX
XX The invention relates to an isolated polypeptide having BACE1 activity.
XX The protein is RTN4 or RTN3 protein. The polypeptide is useful in
XX preparing a composition for treating amyloidosis or Alzheimer's disease.
XX This sequence corresponds to the RTN-4C protein.
XX
XX Sequence 199 AA;
XX
Query Match 70.4%; Score 496; DB 7; Length 199;
Best Local Similarity 97.1%; Pred. No. 6.3e-50;
Matches 101; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 38 MDGQKHWDKVDLLYWRDIKKTGVVFGASLFLLSLTVFISVTVYATIALALLSVTIS 97
Db 1 MDGQKHWDKVDLLYWRDIKKTGVVFGASLFLLSLTVFISVTVYATIALALLSVTIS 60
Qy 98 FRIYKGVIOAIKSDGHPFRAYLESEVAISELVQKYSNSALG 141
Db 61 FRIYKGVIOAIKSDGHPFRAYLESEVAISELVQKYSNSALG 104
RESULT 15
AAV71311
ID AAV71311 standard; protein; 1178 AA.
XX
XX AAV71311;
AC
XX
XX 02-NOV-2000 (first entry)
DT
XX
XX Human neurite growth inhibitor Nogo.
DE
XX
XX Human; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 187 /label= Unknown
FT Misc-difference 188 /label= Unknown
FT Misc-difference 189
FT
FT
FT
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Human RTN-4C protein.
Misc-difference 190 /label= Unknown
FT
FT Misc-difference 221 /label= Unknown
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FT Misc-difference 328 /label= Unknown
FT
FT Misc-difference 477 /label= Unknown
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FT Region 977..1012 /label= Unknown
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FT Region 994..1174
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FT /note= "Region specifically described in claim 16"
FT Region 1079..1114
FT
FT /note= "Region specifically described in claim 16"
XX
XX WO200031235-A2.
XX
XX 02-JUN-2000.
XX
XX 05-NOV-1999; 99WO-US026160.
XX
XX 06-NOV-1998; 98US-0107446P.
XX
XX (SCHW/) SCHWAB M E.
XX (CHEN/) CHEN M S.
XX
XX Schwab ME, Chen MS;
XX
XX WPI; 2000-400052/34.
XX
XX Nogo proteins and nucleic acids useful for treating neoplastic disorders
XX of the central nervous system and inducing regeneration of neurons.
XX
XX Claim 11; Fig 13; 122pp; English.
XX
XX The present sequence is a human Nogo protein which is a potent neural
XX cell growth inhibitor and is free of all central nervous system (CNS)
XX myelin material with which it is natively associated. The human Nogo
XX sequence was derived by aligning human expressed sequence tags (ESTs)
XX e.g. AA158636, AA333267, AA081783, AA167765, AA322918, AA092585, AA081525
XX and AA081840 with the rat Nogo sequence. Nogo proteins and fragments
XX displaying neurite growth inhibitory activity are used in the treatment
XX of neoplastic disease of the CNS e.g. glioma, glioblastoma,
XX medulloblastoma, craniopharyngioma, ependyoma, pinealoma,
XX haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma,
XX neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.
XX Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo
XX activity can be used to treat or prevent hyperproliferative or benign
XX dysproliferative disorders e.g. psoriasis and tissue hypertrophy.
XX Ribozymes or antisense Nogo nucleic acids can be used to inhibit
XX production of Nogo protein to induce regeneration of neurons or to
XX promote structural plasticity of the CNS in disorders where neurite
XX growth, regeneration or maintenance are deficient or desired. The animal
XX models can be used in diagnostic and screening methods for predisposition
XX to disorders and to screen for or test molecules which can treat or
XX prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are
XX referred in claim 32 and SEQ ID NO: 29 in disclosure of the
XX specification. However the specification does not include sequences for
XX these SEQ ID numbers
XX
XX Sequence 1178 AA;
Query Match 63.5%; Score 448; DB 3; Length 1178;
Best Local Similarity 74.6%; Pred. No. 3.2e-43;
Matches 97; Conservative 8; Mismatches 3; Indels 22; Gaps 1;
Qy 12 RENFAYSVSVGVHNLLEGRSQWMDGQKHWDKVDLLYWRDIKKTGVVFGASLFL 71
Db 976 RSPSAIFSDLG-----KTSVDLLYWRDIKKTGVVFGASLFL 1013
Qy 72 LLSLTVFSIVSVTVYATIALALLSVTISFRIYKGVIOAIKSDGHPFRAYLESEVAISEL 131
|||||

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Db 1014 LSLTVFSIVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISEEL 1073

Qy 132 VQKYSNSALG 141

Db 1074 VQKYSNSALG 1083

Search completed: June 16, 2005, 13:11:07  
Job time : 21.3612 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:19:00 ; Search time 5.32448 Seconds  
(without alignments)  
1976.818 Million cell updates/sec

Title: US-09-830-972-32  
Perfect score: 705  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

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- 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCFUS COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	513	72.8	201	4	US-09-949-016-9124
2	503	71.3	199	2	US-08-700-607-1
3	349	49.5	208	2	US-08-700-607-7
4	348	49.4	267	2	US-08-700-607-8
5	337	47.8	356	2	US-08-700-607-6
6	337	47.8	439	4	US-08-949-016-9180
7	337	47.8	776	2	US-08-700-607-5
8	337	47.8	776	4	US-09-949-016-6998
9	309	43.8	192	4	US-09-949-016-8859
10	305	43.3	241	2	US-08-700-607-3
11	262	37.2	114	4	US-08-513-999C-7861
12	250	35.5	219	4	US-08-270-767-45132
13	227	32.2	168	4	US-08-149-476-563
14	214	30.4	588	4	US-09-949-016-7290
15	99	14.0	80	3	US-08-905-223-411
16	75	10.6	593	4	US-08-328-352-4866
17	73	10.4	374	4	US-09-248-796A-16008
18	73	10.4	597	4	US-09-949-016-7719
19	72.5	10.3	208	4	US-09-248-796A-14596
20	72.5	10.3	598	2	US-08-853-659A-53
21	71.5	10.1	154	1	US-08-366-783-5
22	71	10.1	408	4	US-09-710-279-2286
23	70	9.9	518	3	US-08-134-001C-4744
24	70	9.9	563	4	US-09-422-936-79
25	70	9.9	619	3	US-08-262-220-6
26	70	9.9	619	3	US-08-471-733-6
27	70	9.9	619	3	US-08-468-878-6

28	70	9.9	619	3	US-08-750-494-6	Sequence 6, Appli
29	70	9.9	619	4	US-08-470-638-6	Sequence 6, Appli
30	70	9.9	844	4	US-09-422-936-47	Sequence 47, Appl
31	70	9.9	844	4	US-09-422-936-51	Sequence 51, Appl
32	70	9.9	886	4	US-09-422-936-77	Sequence 77, Appl
33	70	9.9	892	4	US-09-422-936-75	Sequence 75, Appl
34	70	9.9	899	4	US-09-422-936-71	Sequence 71, Appl
35	70	9.9	960	4	US-09-422-936-45	Sequence 45, Appl
36	70	9.9	961	4	US-09-422-936-49	Sequence 49, Appl
37	70	9.9	961	4	US-09-914-259-14	Sequence 14, Appl
38	69	9.8	621	3	US-08-262-220-8	Sequence 8, Appli
39	69	9.8	621	3	US-08-471-733-8	Sequence 8, Appli
40	69	9.8	621	3	US-08-468-878-8	Sequence 8, Appli
41	69	9.8	621	3	US-08-750-494-8	Sequence 8, Appli
42	69	9.8	621	4	US-08-470-638-8	Sequence 8, Appli
43	69	9.8	1621	4	US-09-949-016-8450	Sequence 8450, Ap
44	68.5	9.7	383	4	US-09-248-796A-14833	Sequence 14833, A
45	68	9.6	232	4	US-09-897-425-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1

US-09-949-016-9124  
; Sequence 9124, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9124  
; LENGTH: 201  
; TYPE: PRT  
; ORGANISM: Human  
; US-09-949-016-9124

Query Match	72.8%	Score 513;	DB 4;	Length 201;
Best Local Similarity	98.1%	Pred. No. 2.5e-53;		
Matches 104;	Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;
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RESULT 2

US-08-700-607-1  
; Sequence 1, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:

```
;
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
;
; US-08-700-607-1
;
; Query Match 71.3%; Score 503; DB 2; Length 199;
; Best Local Similarity 98.1%; Pred. No. 3.8e-52;
; Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
; Qy 38 MDGQKHWDKVVLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTYIALALLSVTIS 97
; Db 1 MDGQKHWDKVVLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTYIALALLSVTIS 60
;
; Qy 98 FRIYKGVIOAKSDGHPFRAYLSEVAISEELVQKYSNLSALG 141
; Db 61 FRIYKGVIOAKSDGHPFRAYLSEVAISEELVQKYSNLSALG 104
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; RESULT 3
; US-08-700-607-7
; Sequence 7, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
;
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
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; Best Local Similarity 63.4%; Pred. No. 1.2e-33;
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; Db 69 SFRIYKSVLQAVQKTDEGHPFKAYLELEITLSQEQIQKYTD 109
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; RESULT 4
; US-08-700-607-8
; Sequence 8, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
;
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
;
; US-08-700-607-7
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; CLONE: 281046
US-08-700-607-8
Query Match          49.4%; Score 348; DB 2; Length 267;
Best Local Similarity 64.0%; Pred. No. 2.2e-33;
Matches 64; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

Qy 38 MDGQKHWDKVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTYATIALALLSVTIS 97
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MDCWNSNWKSOADLLYWRDIKQTGIVFGSFLLLSLTQFSVSVVAYLALALSAIS 60

Qy 98 FRIYKGVQIAKSDGHPFRAYLSEVAISELVQKYSN 137
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 FRIYKSVLQAVQKTDGHPFRAYLEILTLSQEQIQKYTD 100

RESULT 5
US-08-700-607-6
; Sequence 6, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 356 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307309
; US-08-700-607-6

Query Match          47.8%; Score 337; DB 2; Length 356;
Best Local Similarity 67.4%; Pred. No. 6.7e-32;
Matches 62; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

Qy 46 KDKVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTYATIALALLSVTISFRIYKGI 105
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Db 166 KQKADLLYWRDIKQTGIVFGSFLLLSLTQFSVSVVAYLALALSAISFRIYKSVL 225

Qy 106 QATAKSDGHPFRAYLSEVAISELVQKYSN 137
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 226 QAVQKTDGHPFRAYLEILTLSQEQIQKYTD 257

; CLONE: 281046
US-09-949-016-9180
; Sequence 9180, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9180
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-9180

Query Match          47.8%; Score 337; DB 4; Length 439;
Best Local Similarity 67.4%; Pred. No. 8.9e-32;
Matches 62; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

Qy 46 KQKVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTYATIALALLSVTISFRIYKGI 105
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 249 KQKADLLYWRDIKQTGIVFGSFLLLSLTQFSVSVVAYLALALSAISFRIYKSVL 308

Qy 106 QATAKSDGHPFRAYLSEVAISELVQKYSN 137
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Db 309 QAVQKTDGHPFRAYLEILTLSQEQIQKYTD 340

RESULT 7
US-08-700-607-5
; Sequence 5, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 356 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307309
; US-08-700-607-5
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 776 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307307
US-08-700-607-5

Query Match          47.8%; Score 337; DB 2; Length 776;
Best Local Similarity 67.4%; Pred. No. 2e-31;
Matches 62; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 46 KDKVDDLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 105
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Db 586 KQKAIIDLWYRDIKQTGIVFGSFLLLSLTQFSVVSVVAYIALAALSATISFRIYKSVL 645

QY 106 QAIKSDGHPFRAYLESEVAISELVOKYSN 137
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Db 646 QAVQKTDEGHPFKAYLEILTSQEQIQKYTD 677

RESULT 8
US-09-949-016-6998
; Sequence 6998, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6998
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6998

Query Match          47.8%; Score 337; DB 4; Length 776;
Best Local Similarity 67.4%; Pred. No. 2e-31;
Matches 62; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 46 KDKVDDLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 105
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Db 586 KQKAIIDLWYRDIKQTGIVFGSFLLLSLTQFSVVSVVAYIALAALSATISFRIYKSVL 645

QY 106 QAIKSDGHPFRAYLESEVAISELVOKYSN 137
   ||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 646 QAVQKTDEGHPFKAYLEILTSQEQIQKYTD 677

RESULT 9
US-09-949-016-8859
; Sequence 8859, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
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; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8859
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8859

Query Match          43.8%; Score 309; DB 4; Length 192;
Best Local Similarity 60.9%; Pred. No. 6.4e-29;
Matches 56; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

QY 49 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 108
   ||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 4 VHDLFWRDVKKTGTVFGTLLMLLSLAAFSVISVSYLLALLSVTISFRIYKSV 63

QY 109 AKSDGHPFRAYLESEVAISELVOKYSNSAL 140
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Db 64 QKSEGHPPFKAYLDVDTLSSEAFHNYNNA 95

RESULT 10
US-08-700-607-3
; Sequence 3, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: THPINOB01
; CLONE: 31870
US-08-700-607-3

Query Match          43.3%; Score 305; DB 2; Length 241;
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; SEQ_ID NO 45132
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45132

Query Match      35.5%; Score 250; DB 4; Length 219;
Best Local Similarity 50.6%; Pred. No. 9.1e-22;
Matches 45; Conservative 22; Mismatches 22; Indels 0; Gaps 0;

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Db      26  LITWRDVKSGIVFGAGLITLAAISSEFVSWPAYLSLLTFLGTVAFRYYKSVTQAVQKT  85
QY      112 DEGHPFRAYLSEVAJSEELVKQYSNSAL  140
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Db      86  NEGHPFKDYLELDLDTLSHEKVQNIAGVAV  114

RESULT 13
US-09-149-476-563
: Sequence 563, Application US/09149476

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; Patent No. 6420526
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; GENERAL INFORMATION:
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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23

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; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23

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/ EARLIER APPLICATION NUMBER: 60/047,503
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,592
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,581
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,584
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,500
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,587
/ EARLIER FILING DATE: 1997-05-23

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; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match      32.2%; Score 227; DB 4; Length 168;
Best Local Similarity 60.0%; Pred. No. 3.6e-19;
Matches 42; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

Qy 71 LLASLTVFISVTVAYIALLSVTISFRIYKGVIOAKSDGHPFRAYLESEVAISEE 130
Db 1 MLLSLAASFVSVVSYLLALLSVTISFRIYKSVIOAQKSEGHPPKAYLDVDITLSE 60

Qy 131 LVOKYSNSAL 140
Db 61 AFHNYNNAAM 70

RESULT 14
US-09-949-016-7290
; Sequence 7290, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7290
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7290

Query Match      30.4%; Score 214; DB 4; Length 588;
Best Local Similarity 46.7%; Pred. No. 7.4e-17;
Matches 42; Conservative 21; Mismatches 27; Indels 0; Gaps 0;

Qy 48 KVDLLYWRDIKKTGVVFGASLFLLSLTVFISVTVAYIALLSVTISFRIYKGVIOA 107
Db 387 KVADLLYWKDTRTSGVVFVFTGLMVSLCLLHFISVVAHLALLLGLCGTISLRVYRKVLOA 446

Qy 108 IAKSDGHPFRAYLESEVAISEELVQKYSN 137
Db 447 VHRGDGANPFQAYLDVDLTLTREQTERLSH 476

RESULT 15
US-08-905-223-411
; Sequence 411, Application US/08905223
; Patent No. 622029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duclert, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,223
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 411:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; TISSUE TYPE: Brain
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: -78..-1
; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: score 6.3
; OTHER INFORMATION: seq TLIMLLSWQLSVS/SV
US-08-905-223-411

Query Match      14.0%; Score 99; DB 3; Length 80;
Best Local Similarity 58.8%; Pred. No. 0.00028;
Matches 20; Conservative 7; Mismatches 5; Indels 2; Gaps 1;

Qy 49 VVDLLYWRDIKKTGVVFGASLFLLS--LTVFSI 80
Db 47 VHDLIWRDVKTGFVGTTLIMLLSWQLSVSV 80

Search completed: June 16, 2005, 12:33:41
Job time : 6.32448 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

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2960.058 Million cell updates/sec

Title: US-09-830-972-32

Perfect score: 705

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Total number of hits satisfying chosen parameters: 1714042

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Published Applications AA:\*

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3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*

4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*

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17: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep.\*

18: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*

19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep.\*

20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*

21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	510	72.3	199	16	US-10-810-653-21
3	503	71.3	118	15	US-10-264-237-1568
4	503	71.3	199	9	US-09-893-348-25
5	503	71.3	199	11	US-09-978-360A-467
6	503	71.3	199	15	US-10-660-946-1
7	503	71.3	199	16	US-10-466-258-11
8	503	71.3	199	16	US-10-810-653-25
9	496	70.4	199	15	US-10-408-967-9
10	447	63.4	1162	16	US-10-633-423-10
11	447	63.4	1162	16	US-10-427-741-10

12	447	63.4	1163	9	US-09-893-348-18	Sequence 18, Appl
13	447	63.4	1163	16	US-10-810-653-18	Sequence 18, Appl
14	447	63.4	1192	9	US-09-789-386-2	Sequence 2, Appli
15	447	63.4	1192	9	US-09-758-140-6	Sequence 6, Appli
16	447	63.4	1192	9	US-09-893-348-23	Sequence 23, Appli
17	447	63.4	1192	9	US-09-972-599A-6	Sequence 6, Appli
18	447	63.4	1192	14	US-10-060-036-71	Sequence 71, Appl
19	447	63.4	1192	15	US-10-267-502-429	Sequence 429, App
20	447	63.4	1192	16	US-10-327-213-9	Sequence 9, Appli
21	447	63.4	1192	16	US-10-466-258-9	Sequence 9, Appli
22	447	63.4	1192	16	US-10-810-653-23	Sequence 23, Appli
23	443	62.8	360	9	US-09-893-348-20	Sequence 20, Appl
24	443	62.8	360	16	US-10-810-653-20	Sequence 20, Appl
25	443	62.8	373	9	US-09-789-386-6	Sequence 6, Appli
26	443	62.8	373	9	US-09-765-205-6	Sequence 6, Appli
27	443	62.8	373	9	US-09-893-348-24	Sequence 24, Appl
28	443	62.8	373	14	US-10-060-036-72	Sequence 72, Appl
29	443	62.8	373	15	US-10-408-967-8	Sequence 8, Appli
30	443	62.8	373	16	US-10-466-258-4	Sequence 4, Appli
31	443	62.8	373	16	US-10-810-653-24	Sequence 24, Appl
32	443	62.8	373	17	US-10-347-669-6	Sequence 6, Appli
33	443	62.8	379	14	US-10-205-194-164	Sequence 164, App
34	440	62.4	1192	15	US-10-408-967-7	Sequence 7, Appli
35	436.5	61.9	1163	15	US-10-267-502-431	Sequence 431, App
36	349	49.5	208	15	US-10-660-946-7	Sequence 7, Appli
37	348	49.4	267	14	US-10-205-194-127	Sequence 127, App
38	348	49.4	267	15	US-10-660-946-8	Sequence 8, Appli
39	337	47.8	356	15	US-10-660-946-6	Sequence 6, Appli
40	337	47.8	776	15	US-10-660-946-5	Sequence 5, Appli
41	337	47.8	776	15	US-10-267-502-430	Sequence 430, App
42	337	47.8	776	16	US-10-723-860-1481	Sequence 1481, Ap
43	337	47.8	777	14	US-10-205-219-93	Sequence 93, Appl
44	337	47.8	780	15	US-10-267-502-432	Sequence 432, App
45	309	43.8	236	9	US-09-729-674-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1

US-09-893-348-21  
; Sequence 21, Application US/09893348  
; Patent No. US20020072493A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN, Irun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE:  
; FILE REFERENCE: EIS-SCHWARTZ=2A  
; CURRENT APPLICATION NUMBER: US/09/893,348  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,377  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 21  
; LENGTH: 199  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-09-893-348-21

Query Match 72.3%; Score 510; DB 9; Length 199;  
Best Local Similarity 99.0%; Pred. No. 2.4e-49;  
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 38 MDGQKHKWKVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97  
Db 1 MDGQKHKWKVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60  
Qy 98 PRIYKGVITQAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 141  
Db 61 PRIYKGVITQAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 2  
US-10-810-653-21  
; Sequence 21, Application US/10810653  
; Publication No. US20040253218A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN, Itun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SCHWARTZ-2A  
; CURRENT APPLICATION NUMBER: US/10/810,653  
; PRIOR FILING DATE: 2004-03-29  
; PRIOR APPLICATION NUMBER: US/09/893,348  
; PRIOR FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 21  
; LENGTH: 199  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-10-810-653-21

Query Match 72.3%; Score 510; DB 16; Length 199;  
Best Local Similarity 99.0%; Pred. No. 2.4e-49;  
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 38 MDGQKHKWKVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97  
Db 1 MDGQKHKWKVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60  
Qy 98 PRIYKGVITQAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 141  
Db 61 PRIYKGVITQAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 3  
US-10-264-237-1568  
; Sequence 1568, Application US/10264237  
; Publication No. US20040009491A1  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PA131P1  
; CURRENT APPLICATION NUMBER: US/10/264,237  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/16450  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: US 60/205,515  
; PRIOR FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 2876  
; SOFTWARE: PatentIn Ver. 3.1  
; SEQ ID NO 1568  
; LENGTH: 118  
; TYPE: PRT

; ORGANISM: Homo sapiens  
; FEATURE: MISC FEATURE  
; NAME/KEY: MISC FEATURE  
; LOCATION: (118)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
US-10-264-237-1568

Query Match 71.3%; Score 503; DB 15; Length 118;  
Best Local Similarity 98.1%; Pred. No. 7.5e-49;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 38 MDGQKHKWKVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97  
Db 1 MDGQKHKWKVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60  
Qy 98 PRIYKGVITQAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 141  
Db 61 PRIYKGVITQAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 4  
US-09-893-348-25  
; Sequence 25, Application US/09893348  
; Patent No. US20020072493A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN, Itun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SCHWARTZ-2A  
; CURRENT APPLICATION NUMBER: US/09/893,348  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 25  
; LENGTH: 199  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-893-348-25

Query Match 71.3%; Score 503; DB 9; Length 199;  
Best Local Similarity 98.1%; Pred. No. 1.5e-48;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 38 MDGQKHKWKVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97  
Db 1 MDGQKHKWKVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60  
Qy 98 PRIYKGVITQAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 141  
Db 61 PRIYKGVITQAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 5  
US-09-978-360A-467  
; Sequence 467, Application US/09978360A  
; Publication No. US20040110939A1  
; GENERAL INFORMATION:  
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bougueleret, Lydie  
; APPLICANT: Jobert, Severin  
; APPLICANT: Clusel, Catherine

;; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides  
;; FILE REFERENCE: 56.USA.CIP  
;; CURRENT APPLICATION NUMBER: US/09/978,360A  
;; PRIOR FILING DATE: 2001-10-15  
;; PRIOR APPLICATION NUMBER: US 60/066,677  
;; PRIOR FILING DATE: 1997-11-13  
;; PRIOR APPLICATION NUMBER: US 60/069,957  
;; PRIOR FILING DATE: 1997-12-17  
;; PRIOR APPLICATION NUMBER: US 60/074,121  
;; PRIOR FILING DATE: 1998-02-09  
;; PRIOR APPLICATION NUMBER: US 60/081,563  
;; PRIOR FILING DATE: 1998-04-13  
;; PRIOR APPLICATION NUMBER: US 60/096,116  
;; PRIOR FILING DATE: 1998-08-10  
;; PRIOR APPLICATION NUMBER: US 60/099,273  
;; PRIOR FILING DATE: -03-04  
;; PRIOR APPLICATION NUMBER: US 09/191,997  
;; PRIOR FILING DATE: 1998-11-13  
;; PRIOR APPLICATION NUMBER: US 09/215,435  
;; PRIOR FILING DATE: 1998-12-17  
;; PRIOR APPLICATION NUMBER: PCT/IB98/02122  
;; PRIOR FILING DATE: 1998-12-17  
;; PRIOR APPLICATION NUMBER: US 09/247,155  
;; PRIOR FILING DATE: 1999-02-09  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 810  
;; SOFTWARE: Patent.pm  
;; SEQ ID NO 467  
;; LENGTH: 199  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: SIGNAL  
;; LOCATION: -42...-1  
US-09-978-360A-467

Query Match 71.3%; Score 503; DB 11; Length 199;  
Best Local Similarity 98.1%; Pred. No. 1.5e-48;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 38 MDGQKHWDKVDLLYWRDIKKTGVVFGASFLFLLSLTVFSIVSVTAYIALALLSVTIS 97  
Db 1 MDGQKHWDKVDLLYWRDIKKTGVVFGASFLFLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy 98 FRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALG 141  
Db 61 FRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALG 104

RESULT 6  
US-10-660-946-1  
; Sequence 1, Application US/10660946  
; Publication No. US20040063131A1  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; Au-Young, Janice  
; Goli, Surya K.  
; Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/10/660,946  
;; FILING DATE: 12-Sep-2003  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/228,213A  
;; FILING DATE: <Unknown>  
;; APPLICATION NUMBER: 08/700,607  
;; FILING DATE: <Unknown>  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Billings, Lucy J.  
;; REGISTRATION NUMBER: 36,749  
;; REFERENCE/DOCKET NUMBER: PF-0114 US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-855-0555  
;; TELEFAX: 415-845-4166  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 199 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; IMMEDIATE SOURCE:  
;; LIBRARY: <Unknown>  
;; CLONE: Consensus  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-660-946-1

Query Match 71.3%; Score 503; DB 15; Length 199;  
Best Local Similarity 98.1%; Pred. No. 1.5e-48;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 38 MDGQKHWDKVDLLYWRDIKKTGVVFGASFLFLLSLTVFSIVSVTAYIALALLSVTIS 97  
Db 1 MDGQKHWDKVDLLYWRDIKKTGVVFGASFLFLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy 98 FRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALG 141  
Db 61 FRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALG 104

RESULT 7  
US-10-466-258-11  
; Sequence 11, Application US/10466258  
; Publication No. US20040132096A1  
; GENERAL INFORMATION:  
; APPLICANT: GLAXO GROUP LIMITED  
; TITLE OF INVENTION: ASSAY  
; FILE REFERENCE: P80966 GCW  
; CURRENT APPLICATION NUMBER: US/10/466,258  
; CURRENT FILING DATE: 2003-07-15  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 11  
; LENGTH: 199  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-466-258-11

Query Match 71.3%; Score 503; DB 16; Length 199;  
Best Local Similarity 98.1%; Pred. No. 1.5e-48;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 38 MDGQKHWDKVDLLYWRDIKKTGVVFGASFLFLLSLTVFSIVSVTAYIALALLSVTIS 97  
Db 1 MDGQKHWDKVDLLYWRDIKKTGVVFGASFLFLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy 98 FRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALG 141  
Db 61 FRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALG 104

RESULT 8  
US-10-810-653-25

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; Sequence 25, Application US/10810653
; Publication No. US20040253218A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
; FILE REFERENCE: EIS-SCHWARTZ-2A
; CURRENT APPLICATION NUMBER: US/10/810,653
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US/09/893,348
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US/09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US/09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-810-653-25

Query Match 71.3%; Score 503; DB 16; Length 199;
Best Local Similarity 98.1%; Pred. No. 1.5e-48;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 38 MDGQKHWKDKVVDLLYWRDIKKTGVFGASFLLLSLTVFSIVSVTYAIALLSVTIS 97
DB 1 MDGQKHWKDKVVDLLYWRDIKKTGVFGASFLLLSLTVFSIVSVTYAIALLSVTIS 60

QY 98 PRIYKGVIOAIKSDGHPFRAYLESEVAISELSELVOKYSNSALG 141
DB 61 PRIYKGVIOAIKSDGHPFRAYLESEVAISELSELVOKYSNSALG 104

RESULT 9
US-10-408-967-9
; Sequence 9, Application US/10408967
; Publication No. US20040063161A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn Company
; APPLICANT: Yan, Riqiang
; APPLICANT: Lu, Yifeng
; TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease
; FILE REFERENCE: 00925
; CURRENT APPLICATION NUMBER: US/10/408,967
; CURRENT FILING DATE: 2003-04-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-967-9

Query Match 70.4%; Score 496; DB 15; Length 199;
Best Local Similarity 97.1%; Pred. No. 9.2e-48;
Matches 101; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 38 MDGQKHWKDKVVDLLYWRDIKKTGVFGASFLLLSLTVFSIVSVTYAIALLSVTIS 97
DB 1 MDGQKHWKDKVVDLLYWRDIKKTGVFGASFLLLSLTVFSIVSVTYAIALLSVTIS 60

QY 98 PRIYKGVIOAIKSDGHPFRAYLESEVAISELSELVOKYSNSALG 141
DB 61 PRIYKGVIOAIKSDGHPFRAYLESEVAISELSELVOKYSNSALG 104
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DB 61 PRIYKGVIOAIKSDGHPFRAYLESEVAISELSELVOKYSNSALG 104

RESULT 10
US-10-633-423-10
; Sequence 10, Application US/10633423
; Publication No. US20040191240A1
; GENERAL INFORMATION:
; APPLICANT: Tohyama, Masaya
; APPLICANT: Yamashita, Toshihide
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION
; FILE REFERENCE: 59150-8023.US00
; CURRENT APPLICATION NUMBER: US/10/633,423
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: US 10/427,741
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: JP 2003-92923
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-633-423-10

Query Match 63.4%; Score 447; DB 16; Length 1162;
Best Local Similarity 96.9%; Pred. No. 3.3e-41;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 46 KDKVVDLLYWRDIKKTGVFGASFLLLSLTVFSIVSVTYAIALLSVTISFRIYKGV 105
DB 972 KTSVVDLLYWRDIKKTGVFGASFLLLSLTVFSIVSVTYAIALLSVTISFRIYKGV 1031

QY 106 QAIKSDGHPFRAYLESEVAISELSELVOKYSNSALG 141
DB 1032 QAIKSDGHPFRAYLESEVAISELSELVOKYSNSALG 1067

RESULT 11
US-10-427-741-10
; Sequence 10, Application US/10427741
; Publication No. US20040191291A1
; GENERAL INFORMATION:
; APPLICANT: Tohyama, Masaya
; APPLICANT: Yamashita, Toshihide
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION
; FILE REFERENCE: 59150-8023
; CURRENT APPLICATION NUMBER: US/10/427,741
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: JP 2003-92923
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-427-741-10

Query Match 63.4%; Score 447; DB 16; Length 1162;
Best Local Similarity 96.9%; Pred. No. 3.3e-41;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 46 KDKVVDLLYWRDIKKTGVFGASFLLLSLTVFSIVSVTYAIALLSVTISFRIYKGV 105
DB 972 KTSVVDLLYWRDIKKTGVFGASFLLLSLTVFSIVSVTYAIALLSVTISFRIYKGV 1031

QY 106 QAIKSDGHPFRAYLESEVAISELSELVOKYSNSALG 141
DB 1032 QAIKSDGHPFRAYLESEVAISELSELVOKYSNSALG 1067
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RESULT 12
US-09-893-348-18
; Sequence 18, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
; FILE REFERENCE: EIS-SCHWARTZ-2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 18
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-18

Query Match      63.4%; Score 447; DB 9; Length 1163;
Best Local Similarity 96.9%; Pred. No. 3.3e-41;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 46 KDKVDDLWYRDIKKTGWVFGASLFLLLSLTVFSIVSVTVAYIALALLSVTISFRIYKGV 105
Db 973 KTSVDDLWYRDIKKTGWVFGASLFLLLSLTVFSIVSVTVAYIALALLSVTISFRIYKGV 1032

Qy 106 QAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 141
Db 1033 QAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 1068

RESULT 13
US-10-810-653-18
; Sequence 18, Application US/10810653
; Publication No. US20040253218A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
; FILE REFERENCE: EIS-SCHWARTZ-2A
; CURRENT APPLICATION NUMBER: US/10/810,653
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US/09/893,348
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 18
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-18

Query Match      63.4%; Score 447; DB 9; Length 1163;
Best Local Similarity 96.9%; Pred. No. 3.3e-41;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 46 KDKVDDLWYRDIKKTGWVFGASLFLLLSLTVFSIVSVTVAYIALALLSVTISFRIYKGV 105
Db 973 KTSVDDLWYRDIKKTGWVFGASLFLLLSLTVFSIVSVTVAYIALALLSVTISFRIYKGV 1032

Qy 106 QAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 141
Db 1033 QAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 1068

RESULT 14
US-09-789-386-2
; Sequence 2, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: PRINJHA, RABINDER KUMAR
; APPLICANT: MICHALOVICH, DAVID
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-789-386-2

Query Match      63.4%; Score 447; DB 9; Length 1192;
Best Local Similarity 96.9%; Pred. No. 3.4e-41;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 46 KDKVDDLWYRDIKKTGWVFGASLFLLLSLTVFSIVSVTVAYIALALLSVTISFRIYKGV 105
Db 1002 KTSVDDLWYRDIKKTGWVFGASLFLLLSLTVFSIVSVTVAYIALALLSVTISFRIYKGV 1061

Qy 106 QAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 141
Db 1062 QAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 1097

RESULT 15
US-09-758-140-6
; Sequence 6, Application US/09758140
; Patent No. US20020012965A1
; GENERAL INFORMATION:
; APPLICANT: Strittmatter, Stephen M.
; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth
; FILE REFERENCE: 44574-5073-US
; CURRENT APPLICATION NUMBER: US/09/758,140
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/175,707
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,378
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1192
```

```
US-10-810-653-18

Query Match      63.4%; Score 447; DB 16; Length 1163;
Best Local Similarity 96.9%; Pred. No. 3.3e-41;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 46 KDKVDDLWYRDIKKTGWVFGASLFLLLSLTVFSIVSVTVAYIALALLSVTISFRIYKGV 105
Db 973 KTSVDDLWYRDIKKTGWVFGASLFLLLSLTVFSIVSVTVAYIALALLSVTISFRIYKGV 1032

Qy 106 QAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 141
Db 1033 QAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 1068

RESULT 14
US-09-789-386-2
; Sequence 2, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: PRINJHA, RABINDER KUMAR
; APPLICANT: MICHALOVICH, DAVID
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-789-386-2

Query Match      63.4%; Score 447; DB 9; Length 1192;
Best Local Similarity 96.9%; Pred. No. 3.4e-41;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 46 KDKVDDLWYRDIKKTGWVFGASLFLLLSLTVFSIVSVTVAYIALALLSVTISFRIYKGV 105
Db 1002 KTSVDDLWYRDIKKTGWVFGASLFLLLSLTVFSIVSVTVAYIALALLSVTISFRIYKGV 1061

Qy 106 QAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 141
Db 1062 QAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 1097

RESULT 15
US-09-758-140-6
; Sequence 6, Application US/09758140
; Patent No. US20020012965A1
; GENERAL INFORMATION:
; APPLICANT: Strittmatter, Stephen M.
; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth
; FILE REFERENCE: 44574-5073-US
; CURRENT APPLICATION NUMBER: US/09/758,140
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/175,707
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,378
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1192
```

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-140-6

Query Match      63.4%; Score 447; DB 9; Length 1192;
Best Local Similarity 96.9%; Pred. No. 3.4e-41;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 105
Db      1002 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 1061

QY      106 QAIKSDGHPPEAYLSEVAISELVQKYSNLSG 141
Db      1062 QAIKSDGHPPEAYLSEVAISELVQKYSNLSG 1097
```

Search completed: June 16, 2005, 13:04:05  
Job time : 19.2906 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 12:55:32 ; Search time 4.23986 Seconds  
(without alignments)  
3199.767 Million cell updates/sec

**Title:** US-09-830-972-32  
**Perfect score:** 705  
**Sequence:** 1 QASGEAGVSCLRNFAVYSV.....ESEVAISELVQKYSNSALG 141

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

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```
Database :      PIR_79:*
1:  pir1:*
2:  pir2:*
3:  pir3:*
4:  pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	349	49.5	208	2	I60904	neuroendocrine-spe	
2	348	49.4	287	2	A60021	tropomyosin-relate	
3	337	47.8	776	2	A46593	neuroendocrine-spe	
4	162	23.0	2484	2	T26216	hypothetical prote	
5	159	22.6	2607	2	T26215	hypothetical prote	
6	158	22.4	222	2	T26213	hypothetical prote	
7	83.5	11.8	295	2	S59439	probable membrane	
8	81.5	11.6	464	2	C88188	protein C18H9.5 [i	
9	79	11.2	618	2	T24228	hypothetical prote	
10	78.5	11.1	458	2	A72258	hypothetical prote	
11	77.5	11.0	261	2	F64924	probable thiosulfa	
12	77.5	11.0	583	2	T49359	hypothetical prote	
13	76.5	10.9	481	2	C95920	hypothetical membr	
14	75.5	10.7	545	2	F64665	glucose-6-phosphat	
15	74.5	10.6	545	2	E71851	glucose-6-phosphat	
16	74	10.5	268	2	F64024	hypothetical prote	
17	73	10.4	393	2	S67763	probable membrane	
18	73	10.4	888	2	T01081	hypothetical prote	
19	72.5	10.3	278	2	AD0147	probable ABC trans	
20	72.5	10.3	302	2	AE2863	conserved hypothet	
21	72.5	10.3	302	2	D97640	hypothetical prote	
22	72.5	10.3	417	2	B96977	probable Mn transp	
23	72.5	10.3	598	2	T14886	leukotoxin express	
24	72	10.2	271	2	T13013	hypothetical prote	
25	72	10.2	299	2	B69155	hypothetical prote	
26	72	10.2	1783	2	T42386	unconventional myo	
27	72	10.2	3511	2	A59295	hypothetical prote	
28	71.5	10.1	255	2	B84999	hypothetical prote	
29	71.5	10.1	537	2	G82873	conserved hypothet	

## ALIGNMENTS

## RESULT 1

I60904  
neuroendocrine-specific protein C - human  
C|Species: Homo sapiens (man)  
C|Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 09-Jul-2004  
C|Accession: I60904  
R|Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramae  
J. Biol. Chem. 268, 13439-13447, 1993  
A|Title: Cloning and expression of alternative transcripts of a novel neuro  
A|Reference number: A46583; MUID:93293865; PMID:7685762  
A|Accession: I60904  
A|Status: preliminary; translated from GB/EMBL/DDBJ

```

Query Match      49.5%; Score 349; DB 2; Length 208;
Best Local Similarity 63.4%; Pred. No. 6.7e-28;
Matches        64; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

Qy   37 EMDGQKHKKDKVDVLLYWRDIKKTGVVFCSLFLLSLVFVSIVSYAIALLSVTI 96
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db    9 KPDVCWNKNSOAIIDLYWEDIKOTGVFGFSFLFLPSLFDSWSWYALAAALSATI 68

```

## RESULT 2

A60021  
tropomyosin-related protein, neuronal - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 05-Nov-1999  
C:Accession: A60021  
R:Wieczorek, D.F.; Hughes, S.R.  
Brain Res. Mol. Brain Res. 10, 33-41, 1991  
A:Title: Developmentally regulated cDNA expressed exclusively in neural tissue.  
A:Reference number: A60021; MUID:91278684; PMID:1647480  
A:Accession: A60021  
A:Molecule type: mRNA  
A:Residues: 1-267 <IE>  
A:Cross-references: EMBL:X52817; NID:g456549; PIDN:CAA37001.1; PID:g456550  
C:Comment: This neuronal-specific mRNA was identified by hybridization to an al

Query Match	49.4%	Score 348;	DB 2;	Length 267;
Best Local Similarity	64.0%;	Pred. No. 1.1e-27;		
Matches 64;	Conservative	18;	Mismatches 18;	Indels 0;
				Gaps 0;





Db 156 GTISEWSWPINEIGTFVAFLSAFOIS 182

RESULT 9

T24228

hypothetical protein R166.2 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T24228

R;Matthews, P.

submitted to the EMBL Data Library, August 1995

A;Reference number: Z19859

A;Accession: T24228

A;Molecule type: DNA

A;Residues: 1-618 <WIL>

A;Cross-references: UNIPROT:Q22003; EMBL:Z50795; PIDN:CAA90663.1; GSPDB:GN00020; CESP:RL1

A;Experimental source: clone R166

C;Genetics:

A;Gene: CESP:R166.2

A;Map position: 2

A;Introns: 41/3; 86/3; 118/3; 164/3; 207/3; 554/3

Query Match 11.2%; Score 79; DB 2; Length 618;

Best Local Similarity 29.1%; Pred. No. 4.8;

Matches 32; Conservative 22; Mismatches 32; Indels 24; Gaps 6;

Qy 51 DLLYWRDIKK-TGVVFGASLFL-LLSLTVF-----SIVSVTAIALAL----- 91

Db 353 DIQFWNRKDLVGLSVRSFNIPQSLIVELYICDNETNTMVKTGVIGLLIECKWIKPKV 412

Qy 92 LSVTISFR-IYKGVIOAIKSDGHPFRAYLESEVAISELVOKYSNSAL 140

Db 413 MNVSIDWQNKWFGVIRLVISDKG----SYVESETKIYDQMAFKYLQWAL 458

RESULT 10

A72258

hypothetical protein - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004

C;Accession: A72258

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: A72258

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-458 <ARN>

A;Cross-references: UNIPROT:Q9X1C8; GB:AE001793; GB:AE000512; NID:G4981963; PIDN:AAD3647

A;Experimental source: strain MSB8

C;Genetics:

A;Gene: TM1408

Query Match 11.1%; Score 78.5; DB 2; Length 458;

Best Local Similarity 26.6%; Pred. No. 3.9;

Matches 42; Conservative 17; Mismatches 34; Indels 65; Gaps 9;

Qy 14 NEAVY-----SVSGVMHNLLEGRSQWQMDGKKH-----WKD 47

Db 196 NFILSLRSSIRIGDFDLLLL-----TRKIPQLLFGFYFYLSTWIDNFIAWKV 244

Qy 48 KVVDDL-----YWRDIKKTGVVFGASLFLSLTVFSIVSVTAIALALLSVTISFR 99

Db 245 KGIEIAPGPFMSPEY--DIPK----FMASLFFPISLVFEN-----LSMETVQR 287

Qy 100 IYKGVIOAIKSDGHPFRAYLESEVAISELVOKYSN 137

Db 288 NYKGLMQSIV-SDK--PMRVIENKKLKLSLRHAFSN 322

Db 106 QAIKAS-----DEGHPFRAYLESEVAIS 128

RESULT 7

S59439

probable membrane protein YDR233c - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein YD934.17c

C;Species: Saccharomyces cerevisiae

C;Date: 30-Nov-1995 #sequence\_revision 16-Feb-1996 #text\_change 09-Jul-2004

C;Accession: S59439

R;Murphy, L.; Harris, D.

submitted to the EMBL Data Library, March 1995

A;Reference number: S59423

A;Accession: S59439

A;Molecule type: DNA

A;Residues: 1-295 <MUR>

A;Cross-references: UNIPROT:Q04947; EMBL:Z48612; PID:G728671; PID:G728688; GSPDB:GN00004

A;Experimental source: strain AB972

C;Genetics:

A;Gene: MIPS:YDR233c

A;Cross-references: SGD:S0002641

A;Map position: 4R

C;Keywords: transmembrane protein

F;40-56/Domain: transmembrane #status predicted <TM1>

F;146-162/Domain: transmembrane #status predicted <TM2>

Query Match 11.8%; Score 83.5; DB 2; Length 295;

Best Local Similarity 26.3%; Pred. No. 0.76;

Matches 25; Conservative 17; Mismatches 32; Indels 21; Gaps 2;

Qy 41 QKHKKDKVVDLLYWRDIKKTGVVFGASLFLSLTVFSIVSVTAIALALLSVTISFRI 100

Db 12 QQQQKSCNCDLLWRNPVQTKYFGGSLALLILKKNLITFLKVAITLFT----- 66

Qy 101 YKGVIOAIKSDGHPFRAYLESEVAISELVOKY 135

Db 67 --GSIEFVSK-----LFLGQGLITKY 85

RESULT 8

C88188

protein C18H9.5 [imported] - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004

C;Accession: C88188

R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog

A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.ele

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A;Accession: C88188

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-464 <STO>

A;Cross-references: UNIPROT:Q09484; GB:chr\_II; PID:G722384; GSPDB:GN00020; CESP:C18H9.5

A;Genetics:

A;Gene: C18H9.5

A;Map position: 2

Query Match 11.6%; Score 81.5; DB 2; Length 464;

Best Local Similarity 25.9%; Pred. No. 2;

Matches 38; Conservative 28; Mismatches 50; Indels 31; Gaps 8;

Qy 8 VSLRENFAVYSVGMHNLLEGRSQWQMDGKKWKKVDLLYWRDIKKTGVVFG- 66

Db 41 ITCTNANMLNFTVICNDVITIQKSF-----SNQTHLEKSSDISLTFSAAAAGAIFGT 96

Qy 67 ASPLLLS-----LTVPSTVSV--TAYIALA-----LLSVTISFRYIKGV-----I 105

Db 97 VPATLISKYIKRVLTIVGLLSAGGTLLPLAVNYGLIPLVLA-RLFOGVGASILYSSI 155

Qy 106 QAIKAS-----DEGHPFRAYLESEVAIS 128

Db 156 GTISEWSWPINEIGTFVAFLSAFOIS 182

RESULT 9

T24228

hypothetical protein R166.2 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T24228

R;Matthews, P.

submitted to the EMBL Data Library, August 1995

A;Reference number: Z19859

A;Accession: T24228

A;Molecule type: DNA

A;Residues: 1-618 <WIL>

A;Cross-references: UNIPROT:Q22003; EMBL:Z50795; PIDN:CAA90663.1; GSPDB:GN00020; CESP:RL1

A;Experimental source: clone R166

C;Genetics:

A;Gene: CESP:R166.2

A;Map position: 2

A;Introns: 41/3; 86/3; 118/3; 164/3; 207/3; 554/3

Query Match 11.2%; Score 79; DB 2; Length 618;

Best Local Similarity 29.1%; Pred. No. 4.8;

Matches 32; Conservative 22; Mismatches 32; Indels 24; Gaps 6;

Qy 51 DLLYWRDIKK-TGVVFGASLFL-LLSLTVF-----SIVSVTAIALAL----- 91

Db 353 DIQFWNRKDLVGLSVRSFNIPQSLIVELYICDNETNTMVKTGVIGLLIECKWIKPKV 412

Qy 92 LSVTISFR-IYKGVIOAIKSDGHPFRAYLESEVAISELVOKYSNSAL 140

Db 413 MNVSIDWQNKWFGVIRLVISDKG----SYVESETKIYDQMAFKYLQWAL 458

RESULT 10

A72258

hypothetical protein - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004

C;Accession: A72258

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: A72258

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-458 <ARN>

A;Cross-references: UNIPROT:Q9X1C8; GB:AE001793; GB:AE000512; NID:G4981963; PIDN:AAD3647

A;Experimental source: strain MSB8

C;Genetics:

A;Gene: TM1408

Query Match 11.1%; Score 78.5; DB 2; Length 458;

Best Local Similarity 26.6%; Pred. No. 3.9;

Matches 42; Conservative 17; Mismatches 34; Indels 65; Gaps 9;

Qy 14 NEAVY-----SVSGVMHNLLEGRSQWQMDGKKH-----WKD 47

Db 196 NFILSLRSSIRIGDFDLLLL-----TRKIPQLLFGFYFYLSTWIDNFIAWKV 244

Qy 48 KVVDDL-----YWRDIKKTGVVFGASLFLSLTVFSIVSVTAIALALLSVTISFR 99

Db 245 KGIEIAPGPFMSPEY--DIPK----FMASLFFPISLVFEN-----LSMETVQR 287

Qy 100 IYKGVIOAIKSDGHPFRAYLESEVAISELVOKYSN 137

Db 288 NYKGLMQSIV-SDK--PMRVIENKKLKLSLRHAFSN 322

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RESULT 11
F64924
C:Species: thiosulfate-dithiol sulfurtransferase (EC 2.8.1.5) - Escherichia coli (strain K12)
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: F64924
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: F64924
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-261 <BLAT>
A:Cross-references: UNIPROT:P77409; GB:AE000262; GB:U00096; NID:gi787955; PIDN:AAC74740.
A:Experimental source: strain K-12, substrain MGI655
A:Superfamily: hycA protein
C:Keywords: sulfurtransferase; transmembrane protein
F:30-46/Domain: transmembrane #status predicted <TM01>
F:83-99/Domain: transmembrane #status predicted <TM02>
F:112-128/Domain: transmembrane #status predicted <TM03>
F:187-203/Domain: transmembrane #status predicted <TM04>
F:224-240/Domain: transmembrane #status predicted <TM05>

Query Match 11.0%; Score 77.5; DB 2; Length 261;
Best Local Similarity 27.6%; Pred. No. 2.7;
Matches 29; Conservative 16; Mismatches 43; Indels 17; Gaps 4;

Qy 22 VGMHNLLEGRSQEMD-GQKHWKDKVVDLLYWRDIKKTGVVFGASLFLLL---SLT 76
Db 44 LGLHALLRARGVKKSATDHGSKIYLYSKAVRLHWSN-----ALLFVLLLASGLIN 94

Qy 77 VFSIVSVTAYIALALLSVTISFRI---YKGVQIAKSDGHPFR 118
Db 95 HFAMVGATVKSIVAVHEVCGFLLLACWLGFLVINA VGDNGHHYR 139

RESULT 12
T49359
hypothetical protein BId1.130 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C:Accession: T49359
R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A:Reference number: Z25022
A:Accession: T49359
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-583 <SCH>
A:Cross-references: UNIPROT:Q9P6A7; EMBL:AL355927; GSPDB:GN00116; NCSP:BId1.130
A:Experimental source: BAC clone BId1, strain OR74A
C:Genetics:
A:Gene: NCSP:BId1.130
A:Map position: 6
A:Introns: 44/1

Query Match 11.0%; Score 77.5; DB 2; Length 583;
Best Local Similarity 27.5%; Pred. No. 6.4;
Matches 28; Conservative 13; Mismatches 28; Indels 33; Gaps 4;

Qy 52 LLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQIAKSD 111
Db 67 LCYV-PLRRLVLVHALLLLLSLEHYS-----AVTRVLLHLHITSSILNL----- 109

Qy 112 DECHPFRAYLSEVAIS-----BELVKYSNSALG 141
Db 110 ----PLRVLVDDEVRAKAIAMAKDINPELIQRIEBCAG 147

RESULT 13
T49359
hypothetical protein BId1.130 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C:Accession: T49359
R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A:Reference number: Z25022
A:Accession: T49359
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-583 <SCH>
A:Cross-references: UNIPROT:Q9P6A7; EMBL:AL355927; GSPDB:GN00116; NCSP:BId1.130
A:Experimental source: BAC clone BId1, strain OR74A
C:Genetics:
A:Gene: NCSP:BId1.130
A:Map position: 6
A:Introns: 44/1

Query Match 11.0%; Score 77.5; DB 2; Length 583;
Best Local Similarity 27.5%; Pred. No. 6.4;
Matches 28; Conservative 13; Mismatches 28; Indels 33; Gaps 4;

Qy 52 LLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQIAKSD 111
Db 67 LCYV-PLRRLVLVHALLLLLSLEHYS-----AVTRVLLHLHITSSILNL----- 109

Qy 112 DECHPFRAYLSEVAIS-----BELVKYSNSALG 141
Db 110 ----PLRVLVDDEVRAKAIAMAKDINPELIQRIEBCAG 147
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C95920
hypothetical membrane protein [imported] - Sinorhizobium meliloti (strain 1021) magaplas
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: C95920
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: C95920
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-481 <KUR>
A:Cross-references: UNIPROT:Q92VS2; GB:AL591985; PIDN:CAC49027.1; PID:gi5140512; GSPDB:G
A:Experimental source: strain 1021, megaplasmid pSymB
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wellis, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: SMB21048
A:Genome: plasmid

Query Match 10.9%; Score 76.5; DB 2; Length 481;
Best Local Similarity 37.7%; Pred. No. 6.6;
Matches 23; Conservative 8; Mismatches 27; Indels 3; Gaps 2;

Qy 53 LYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQIAKSD 112
Db 238 VYWRKTSR--VAQALAFLLVLLLSSTSSV-AYVGLAVLSIPVALSISWSFLSGRMDKD 294

Qy 113 E 113
Db 295 E 295

RESULT 14
F64665
glucose-6-phosphate isomerase (EC 5.3.1.9) - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: F64665
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: F64665
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-545 <TOM>
A:Cross-references: UNIPROT:O25781; GB:AE000622; GB:AE000511; NID:g2314317; PIDN:AAD0821
A:Superfamily: glucose-6-phosphate isomerase
C:Keywords: intramolecular oxidoreductase; isomerase

Query Match 10.7%; Score 75.5; DB 2; Length 545;
Best Local Similarity 25.3%; Pred. No. 9.5;
Matches 37; Conservative 20; Mismatches 44; Indels 45; Gaps 6;

Qy 23 GHNHLL-----LLEGRSQEMDQO---KKHWKDKVVDLLYWRDIKKTGVVFGASL 69
Db 411 GHHEILFSNVLAQAQAFMKGSYEALGELLFKGLDKDQDLAHR-----VFFGNRP 464

Qy 70 FLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQIAKSD----- 112
Db 465 SNILLEKISPSNIGALVALYEHKVFV-----QGVINDINSFDQGWVGLKELAVPIIQE 519
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Qy 113 -EGHPFRAYLESEVAISEELVQKYSN 137
Db 520 LEGHKNAYFDSS---TKHLIELYKN 542

RESULT 15
E71851
glucose-6-phosphate isomerase - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: Strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: E71851
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: E71851
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-545 <ARN>
A:Cross-references: UNIPROT:Q9ZK49; GB:AE001536; GB:AE001439; NID:g4155675; PIDN:AA066666
A:Experimental source: strain J99
C:Genetics:
A:Gene: psi
C:Superfamily: glucose-6-phosphate isomerase

Query Match 10.6%; Score 74.5; DB 2; Length 545;
Best Local Similarity 25.3%; Pred. No. 12;
Matches 37; Conservative 19; Mismatches 45; Indels 45; Gaps 6;

Qy 23 GMMNLI-----LLEGRSQWMDGQ---KHHWKVVDLLLYWRDIKKTGVVFGASL 69
Db 411 GHHEILLFSNVLAQAQAFMKGKSYEEALGELLKGLDKDEAKDLAHR-----VFFGNRP 464
Qy 70 FLILLSLTVSIVSVTAYIALALLSVTISPRIYKGVITQAIKSD----- 112
Db 465 SNTLLLEKISPSNIGALVALYEHKVFV-----QGVWINDISPDQWVGELGKELAVILOE 519
Qy 113 -EGHPFRAYLESEVAISEELVQKYSN 137
Db 520 LEGHKNAYFDSS---TRHLIELYKN 542

Search completed: June 16, 2005, 13:32:02
Job time : 5.23986 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 12:33:51 ; Search time 19.1287 Seconds  
(without alignments)  
3774.604 Million cell updates/sec

Title: US-09-830-972-32

Perfect score: 705

Sequence: 1 QASGEAGVCLRENFAVYSV.....ESEVAISELVQKYSNLSALG 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	503	71.3	199	2	Q6IM70 sus scrofa
2	503	71.3	199	2	Q7YRW9 bos taurus
3	497	70.5	199	2	Q7PCJ7 macaca fasc
4	495	70.2	199	1	RTN4 MOUSE
5	490	69.5	170	2	Q6IG20 mus musculus
6	460	65.2	199	2	Q7T224 gallus gall
7	447	63.4	578	2	Q8OW95 mus musculus
8	447	63.4	639	2	Q8K290 mus musculus
9	447	63.4	986	2	Q8IU44 homo sapien
10	447	63.4	1046	2	Q8BGK7 mus musculus
11	447	63.4	1162	2	Q8BGW9 mus musculus
12	447	63.4	1163	1	RTN4 RAT
13	447	63.4	1192	1	RTN4 HUMAN
14	443	62.8	343	2	Q6IPN0 homo sapien
15	443	62.8	356	2	Q8BH78 mus musculus
16	443	62.8	375	2	Q8BH75 mus musculus
17	443	62.8	392	2	Q8BH16 mus musculus
18	439	62.3	187	2	Q6IG15 sus scrofa
19	436.5	61.9	1163	2	Q8K3G8 mus musculus
20	432.5	61.3	357	2	Q8K3G7 mus musculus
21	423	60.0	658	2	Q6RSS8 gallus gall
22	389	55.2	199	2	Q6PB23 xenopus lae
23	386	54.8	179	2	Q9GMJ3 macaca fasc
24	384	54.5	214	2	Q7T222 carassius a
25	381	54.0	199	2	Q6JRW3 xenopus lae
26	369.5	52.4	1024	2	Q6JRW2 xenopus lae
27	369.5	52.4	1043	2	Q6JRW0 xenopus lae
28	369.5	52.4	1055	2	Q6JRW1 xenopus lae
29	368	52.2	193	2	Q6IFV5 xenopus tro
30	368	52.2	315	2	Q6IFV4 xenopus tro
31	366	51.9	193	2	Q6JRW6 xenopus lae

32 366 51.9 311 2 Q6JRV3 xenopus lae  
33 366 51.9 330 2 Q6JRV4 xenopus lae  
34 363 51.5 197 2 Q6JH23 brachydanio  
35 362 51.3 1013 2 Q6JRV9 xenopus lae  
36 362 51.3 1032 2 Q6JRV7 xenopus lae  
37 362 51.3 1044 2 Q6JRV8 xenopus lae  
38 360.5 51.1 209 2 Q6IEJ1 oncorhynchus  
39 360 51.1 316 2 Q6JRW2 xenopus lae  
40 358 50.8 193 2 Q6JRW4 xenopus lae  
41 358 50.8 304 2 Q6JRW0 xenopus lae  
42 358 50.8 323 2 Q6JRW1 xenopus lae  
43 354 50.2 196 2 Q6IEI6 cyprinus ca  
44 349 49.5 172 2 Q6IGI4 bos taurus  
45 349 49.5 208 2 Q6IAX4 homo sapien

#### ALIGNMENTS

##### RESULT 1

Q6IM70 PRELIMINARY; PRT; 199 AA.  
AC Q6IM70; 2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE RTN4-C.  
GN Name=RTN4;  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22715887; PubMed=12832288;  
RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;  
RT "A reticular rhapsody: phylogenetic evolution and nomenclature of the  
RTN/Nogo gene family.";  
RL FASEB J. 17:1238-1247(2003).  
CC -I- MISCELLANEOUS: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.  
DR EMBL; BK001795; DAA01967.1; -  
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS0845; RETICULON; 1.  
SQ SEQUENCE 199 AA; 22425 MW; C61D11DF3FB34D80 CRC64;

Query Match 71.3%; Score 503; DB 2; Length 199;  
Best Local Similarity 98.1%; Pred. No. 5.8e-41;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 38 MDQCKKHKDKVVDLLYWRDIKKTGVFGASLFLLSLTVPFSIVSVTAYTALALLSVTIS 97  
DB 1 MDGQKKNKDKVVDLLYWRDIKKTGVFGASLFLLSLTVPFSIVSVTAYTALALLSVTIS 60  
QY 98 FRIYKGVIOIAKSDGHPFRAYLSEVAISELVQKYSNLSALG 141  
DB 61 FRIYKGVIOIAKSDGHPFRAYLSEVAISELVQKYSNLSALG 104

##### RESULT 2

Q7YRW9 PRELIMINARY; PRT; 199 AA.  
AC Q7YRW9; 2003 (Tremblrel. 25, Created)  
DT 01-OCT-2003 (Tremblrel. 26, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE RTN4-C.  
GN Name=RTN4;  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

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OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22715887; PubMed=12832288;
RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT "A reticular rhapsody: phylogenetic evolution and nomenclature of the
RTN/Nogo gene family.";
RL FASEB J. 17:1238-1247(2003).
DR EMBL; AY164744; A047319.2; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 199 AA; 22395 MW; C60161DF3FB34D80 CRC64;

Query Match          71.3%; Score 503; DB 2; Length 199;
Best Local Similarity 98.1%; Pred. No. 5.8e-41;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 38 MDGQKKHKDKVVDLLYRDIKKTGVFGASFLLLSLTVFSIVSVTAYIALALLSVTIS 97
DB 1 MDGQKKHKDKVVDLLYRDIKKTGVFGASFLLLSLTVFSIVSVTAYIALALLSVTIS 60

QY 98 PRIYKGVQIAKSGDEGHPFRAYLSEVAISELQKYSNSALG 141
DB 61 PRIYKGVQIAKSGDEGHPFRAYLSEVAISELQKYSNSALG 104

RESULT 3
Q7PCU7 PRELIMINARY; PRT; 199 AA.
ID Q7PCU7
AC Q7PCU7
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE RTN4-C.
GN Name=RTN4;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22715887; PubMed=12832288;
RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT "A reticular rhapsody: phylogenetic evolution and nomenclature of the
RTN/Nogo gene family.";
RL FASEB J. 17:1238-1247(2003).
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 199 AA; 22469 MW; 761A5FDB6C1DEC3C CRC64;

Query Match          70.5%; Score 497; DB 2; Length 199;
Best Local Similarity 96.2%; Pred. No. 2.3e-40;
Matches 100; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 38 MDGQKKHKDKVVDLLYRDIKKTGVFGASFLLLSLTVFSIVSVTAYIALALLSVTIS 97
DB 1 MDGQKKHKDKVVDLLYRDIKKTGVFGASFLLLSLTVFSIVSVTAYIALALLSVTIS 60

QY 98 PRIYKGVQIAKSGDEGHPFRAYLSEVAISELQKYSNSALG 141
DB 61 PRIYKGVQIAKSGDEGHPFRAYLSEVAISELQKYSNSALG 104

RESULT 4

```

```

RTN4_MOUSE
ID RTN4_MOUSE STANDARD; PRT; 199 AA.
AC Q99F72; Q9CTE3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein).
GN Name=Rtn4; Synonyms=Nogo;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=3T3-L1; TISSUE=Adipocyte;
RA Coulson A.C., Craggs P.D., Morris N.J.;
RL "Mouse vp20/RTN4C cDNA.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 170-199 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia K., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Giasi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
CC block the regeneration of the nervous central system in adults (By
CC similarity).
CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-x1 and Bcl-2 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the
CC membrane of the endoplasmic reticulum through 2 putative
CC transmembrane domains (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms may be produced;
CC Name=1;
CC IsoId=Q99F72-1; Sequence=Displayed;
CC -!- SIMILARITY: Contains 1 reticulon domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

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Qy	98	FRIYKGVIOAIKSDGHPFRAYLSEVAISELVOKYSNSALG	141
Db	61	FRIYKGVIOAIKSDGHPFRAYLSEVAISELVOKYSNSALG	104
RESULT 6			
Qy	7T224	PRELIMINARY;	PRT; 199 AA.
ID	Q7T224		
AC	Q7T224;		
DT	01-OCT-2003 (TtEMBLrel. 25, Created)		
DT	01-OCT-2003 (TtEMBLrel. 25, Last sequence update)		
DT	01-MAR-2004 (TtEMBLrel. 26, Last annotation update)		
DE	RTN4-C.		
GN	Name=RTN4;		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus		
OX	NCBI_TaxID=9031;		
OX	[1]		
RN	SEQUENCE FROM N.A.		
RP	MEDLINE=22715887; PubMed=12832288;		
RX	Cartle T., Klinger M., Stuewer C.A., Schwab M.E.;		
RT	"A reticular rhapsody: phylogenetic evolution and nomenclature of the		
RT	RTN/Nogo gene family.";		
RL	FASEB J. 17:1238-1247 (2003).		
DR	EMBL; AY164737; AAP47312.1; -.		
DR	GO; GO:0005783; C:endoplasmic reticulum; IEA.		
DR	InterPro; IPR003388; Reticulon.		
DR	Pfam; PF02453; Reticulon.1.		
DR	PROSITE; PS50845; RETICULON; 1.		
SQ	SEQUENCE 199 AA; 22293 MW; 07CF4E4EF2723251 CRC64;		
Query Match 65.2%; Score 460; DB 2; Length 199;			
Best Local Similarity 88.5%; Pred.No.9.2e-37;			
Matches 92; Conservative 5; Mismatches 7; Indels 0; Gaps			
Qy	38	MDQKQHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAIALALLSVTIS	
Db	1	MDSQPSGWDKVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAIALALLSVTIS	
Qy	98	FRIYKGVIOAIKSDGHPFRAYLSEVAISELVOKYSNSALG	141
Db	61	FRIYKGVIOAIKSDGHPFRAYLSEVAISELVOKYSNSALG	104
RESULT 7			
Qy	8Q0W95	PRELIMINARY;	PRT; 578 AA.
ID	Q8QW95		
AC	Q8QW95;		
DT	01-JUN-2003 (TtEMBLrel. 24, Created)		
DT	01-JUN-2003 (TtEMBLrel. 24, Last sequence update)		
DT	01-OCT-2003 (TtEMBLrel. 25, Last annotation update)		
DE	Nogo-A (Fragment).		
GN	Name=Nogo-A;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
OX	[1]		
RN	SEQUENCE FROM N.A.		
RP	Tozaki H., Hirata T.;		
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB073672; BAC75974.1; -.		
DR	GO; GO:0005783; C:endoplasmic reticulum; IEA.		
DR	InterPro; IPR003388; Reticulon.		
DR	Pfam; PF02453; Reticulon.1.		
DR	PROSITE; PS50845; RETICULON; 1.		
FT	NON_TER 1 1		
SQ	SEQUENCE 578 AA; 63696 MW; 832670C171E4AC61 CRC64;		
Query Match 63.4%; Score 447; DB 2; Length 578;			

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Best Local Similarity 96.9%; Pred. No. 5.1e-35;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 46 KDKVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 105
DB 388 KTSVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 447

QY 106 QAIKSDGHPFRAYLESEVAISELVQKYSNLSG 141
DB 448 QAIKSDGHPFRAYLESEVAISELVQKYSNLSG 483

RESULT 8
Q8K290 PRELIMINARY; PRT; 639 AA.
ID Q8K290;
AC Q8K290;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Rtn4 protein.
GN Name=Rtn4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska J., Smaluk J., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032192; AAH32192.1; -
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:cytoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 639 AA, 70312 MW, 309A19DA37603F11 CRC64;

Query Match 63.4%; Score 447; DB 2; Length 639;
Best Local Similarity 96.9%; Pred. No. 5.1e-35;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 46 KDKVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 105
DB 449 KTSVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 508

QY 106 QAIKSDGHPFRAYLESEVAISELVQKYSNLSG 141
DB 509 QAIKSDGHPFRAYLESEVAISELVQKYSNLSG 544
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RESULT 9
Q8IUUA PRELIMINARY; PRT; 986 AA.
ID Q8IUUA;
AC Q8IUUA;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE RNT4 (RTN4 isoform Ab) (RTN4 isoform D) (RTN4 isoform E) (RTN4 isoform F) (RTN4 isoform G) (RTN4 isoform Aa).
GN Name=RTN4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT "Genomic structure and functional characterisation of the promoters of
human and mouse nogo/rtn4."
RL J. Mol. Biol. 325:299-323(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Oertle T., Schwab M.E.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102285; AAM64244.1; -
DR EMBL; AY123246; AAM64250.1; -
DR EMBL; AY123247; AAM64251.1; -
DR EMBL; AY123248; AAM64252.1; -
DR EMBL; AY123249; AAM64253.1; -
DR EMBL; AY123250; AAM64254.1; -
DR EMBL; AY123245; AAM64249.1; -
DR GO; GO:0005783; C:cytoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 986 AA, 108449 MW, 0CDEBF647036415A CRC64;

Query Match 63.4%; Score 447; DB 2; Length 986;
Best Local Similarity 96.9%; Pred. No. 8.8e-35;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 46 KDKVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 105
DB 796 KTSVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 855

QY 106 QAIKSDGHPFRAYLESEVAISELVQKYSNLSG 141
DB 856 QAIKSDGHPFRAYLESEVAISELVQKYSNLSG 891

RESULT 10
Q8BGK7 PRELIMINARY; PRT; 1046 AA.
ID Q8BGK7;
AC Q8BGK7;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Rtn4.
GN Name=Rtn4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

RL EMBL; AY102284; AAM73506.1; -;  
DR EMBL; AY102286; AAM73511.1; -;  
DR MGD; MGI:1915835; Rtn4.  
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0001525; P:angiogenesis; IMP.  
DR GO; GO:0007399; P:neurogenesis; IDA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
DR SQ SEQUENCE 1162 AA; 126612 MW; 855697FBE11781F CRC64;

Query Match 63.4%; Score 447; DB 2; Length 1162;  
Best Local Similarity 96.9%; Pred. No. 1e-34;  
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 46 KDKVVDLLYRDIKKTGWFGASFLILLSLTVFSIVSYATYIALLSVTISPRIYKGV 105  
DB 972 KTSVVDLLYRDIKKTGWFGASFLILLSLTVFSIVSYATYIALLSVTISPRIYKGV 1031

QY 106 QAIKSDGHPFRAYLSEVAISEELVQKYSNALS 141  
DB 1032 QAIKSDGHPFRAYLSEVAISEELVQKYSNALS 1067

RESULT 12

RTN4\_RAT STANDARD; PRT; 1163 AA.  
ID Q9UKL1; Q9UK10; Q9ROD9; Q9WUE9; Q9WUF0;  
AC 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
OS -JUL-2004 (Rel. 44, Last annotation update)  
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)  
DE (Glut4 vesicle 20 kDa protein).  
GN Name=Rtn4; Synonyms=Nogo;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.  
RC STRAIN=Sprague-Dawley; TISSUE=Adipocyte;  
RX MEDLINE=9249816; PubMed10231557; DOI=10.1016/S0167-4889(99)00033-6;  
RA Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lienhard G.E.;  
RT "Cloning and characterization of a 22 kDa protein from rat adipocytes;  
a new member of the reticulon family.";  
RL Biochim. Biophys. Acta 1450:68-76(1999).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RX MEDLINE=20129258; PubMed10667796; DOI=10.1038/35000219;  
RA Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,  
RA Spillmann A.A., Christ F., Schwab M.E.;  
RT "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an  
RT antigen for monoclonal antibody IN-1.";  
RL Nature 403:434-439(2000).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).  
RC STRAIN=Wistar Kyoto; TISSUE=vascular smooth muscle;  
RA Ito T., Schwartz S.M.;  
RT "Cloning of a member of the reticulon gene family in rat: one of two  
RT minor splice variants.";  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP FUNCTION.  
RX MEDLINE=22033691; PubMed12037567; DOI=10.1038/417547a;  
RA GrandPre T., Li S., Strittmatter S.M.;  
RT "Nogo-66 receptor antagonist peptide promotes axonal regeneration.";  
RL Nature 417:547-551(2002).  
CC -1- FUNCTION: Potent neurite outgrowth inhibitor which may also help  
CC block the regeneration of the nervous central system in adults (by  
CC similarity).  
CC -1- SUBUNIT: Binds to RTN4R. Interacts with Bcl-x1 and Bcl-2 (By



RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,  
RT Yu J., Han L.H.;  
RT "Novel human cDNA clones with function of inhibiting cancer cell  
RT growth.";  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
RN [9]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Brain;  
RX MEDLINE=99156230; PubMed=10048485;  
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hiroseawa M.,  
RA Miyajima N., Tanaka A., Kohani H., Nomura N., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. XII.  
RT The complete sequences of 100 new cDNA clones from brain which code  
RT for large proteins in vitro.";  
RL DNA Res. 5:355-364(1998).  
RN [10]  
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).  
RC TISSUE=Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S.E., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Whiting J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,  
RA Wahing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [11]  
RP SEQUENCE FROM N.A. (ISOFORM 3).  
RC TISSUE=Umbilical cord blood;  
RX MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200;  
RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,  
RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,  
RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;  
RT "Cloning and functional analysis of cDNAs with open reading frames for  
RT 300 previously undefined genes expressed in CD34+ hematopoietic  
RT stem/progenitor cells.";  
RL Genome Res. 10:1546-1560(2000).  
RN [12]  
RP SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).  
RC TISSUE=Brain;  
RX MEDLINE=20129259; PubMed=10667797; DOI=10.1038/35000226;  
RA Grandpre T., Nakamura F., Varcantian T., Strittmatter S.M.;  
RT "Identification of the Nogo inhibitor of axon regeneration as a  
RT Reticulon protein.";  
RL Nature 403:439-444(2000).  
RN [15]  
RP FUNCTION.  
RC TISSUE=Brain;  
RX MEDLINE=21069055; PubMed=11201742; DOI=10.1038/35053072;  
RA Fournier A.E., Grandpre T., Strittmatter S.M.;

RT "Identification of a receptor mediating Nogo-66 inhibition of axonal  
RT regeneration.";  
RL Nature 409:341-346(2001).  
RN [16]  
RP REVIEW.  
RX MEDLINE=21889956; PubMed=11891768; DOI=10.1002/jnr.10134;  
RA Ng C.E.L., Tang B.L.;  
RT "Nogog and the Nogo-66 receptor: factors inhibiting CNS neuron  
RT regeneration.";  
RL J. Neurosci. Res. 67:559-565(2002).  
CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help  
CC block the regeneration of the nervous central system in adults.  
CC Isoform 2 reduces the anti-apoptotic activity of Bcl-x1 and Bcl-2.  
CC This is likely consecutive to their change in subcellular  
CC location, from the mitochondria to the endoplasmic reticulum,  
CC after binding and sequestration.  
CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-x1 and Bcl-2.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic  
CC reticulum. Anchored to the membrane of the endoplasmic reticulum  
CC through 2 putative transmembrane domains.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=4;  
CC Name=1; Synonyms=RTN 4A, Nogo-A, RTN-XL;  
CC IsoId=Q9NQC3-1; Sequence=Displayed;  
CC Name=2; Synonyms=RTN 4B, Nogo-B, RTN-XS, Foccen-M;  
CC IsoId=Q9NQC3-2; Sequence=VSP\_005655;  
CC Name=3; Synonyms=RTN 4C, Nogo-C, Foccen-S;  
CC IsoId=Q9NQC3-3; Sequence=VSP\_005652, VSP\_005653;  
CC Name=4;  
CC IsoId=Q9NQC3-4; Sequence=VSP\_005654;  
CC -!- TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain  
CC and testis and weakly in heart and skeletal muscle. Isoform 2 is  
CC widely expressed excepted for the liver. Isoform 3 is expressed in  
CC brain, skeletal muscle and adipocytes. Isoform 4 is testis-  
CC specific.  
CC -!- SIMILARITY: Contains 1 reticulon domain.  
CC -!- CAUTION: Ref.11 sequence differs from that shown due to  
CC frameshifts in positions 1149 and 1156.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AJ251383; CAB99248.1; -  
DR EMBL; AJ251384; CAB99249.1; -  
DR EMBL; AJ251385; CAB99250.1; -  
DR EMBL; AB040462; BAB18927.1; -  
DR EMBL; AB040463; BAB18928.1; -  
DR EMBL; AF148537; AAG12176.1; -  
DR EMBL; AF148538; AAG12177.1; -  
DR EMBL; AF087901; AAG12205.1; -  
DR EMBL; AF320999; AAG40878.1; -  
DR EMBL; AF132047; AAD31021.1; -  
DR EMBL; AF132048; AAD31022.1; -  
DR EMBL; AB015639; BAA83712.1; -  
DR EMBL; AF077050; AAD27783.1; -  
DR EMBL; AF177332; AAG17976.1; -  
DR EMBL; AB020693; BAA74909.2; ALT\_INIT.  
DR EMBL; BC001035; AAH01035.1; -  
DR EMBL; BC007109; AAH07109.1; -

Query Match 63.4%; Score 447; DB 1; Length 1192;  
Best Local Similarity 96.9%; Pred. No. 1.1e-34;  
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 46 KDKVDLLYWRDIKKTGVFGASFLILLSTVFSIVSVYATYIALALLSVTISFRIYKGI 105  
Db 1002 KTSVDLLYWRDIKKTGVFGASFLILLSTVFSIVSVYATYIALALLSVTISFRIYKGI 1061

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QY 106 QAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 141
Db 1062 QAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 1097

RESULT 14
Q6IPNO PRELIMINARY; PRT; 343 AA.
AC Q6IPNO;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE RTN4 protein.
GN Name=RTN4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boesak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grigunov J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC071848; AAH71848.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 343 AA; 36918 MW; 813207C29AB15BA4 CRC64;

Query Match 62.8%; Score 443; DB 2; Length 343;
Best Local Similarity 98.9%; Pred. No. 7.3e-35;
Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTVAYIALALLSVTISFRIYKGVIOAI 108
Db 156 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTVAYIALALLSVTISFRIYKGVIOAI 215

QY 109 AKSDGHPFRAYLESEVAISEELVQKYSNSALG 141
Db 216 QKSDGHPFRAYLESEVAISEELVQKYSNSALG 248

RESULT 15
Q8BH78 PRELIMINARY; PRT; 356 AA.
AC Q8BH78;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
```

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DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE RTN4.
GN Name=RTN4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7; and 129SVCJ7;
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT "Genomic structure and functional characterisation of the promoters of
human and mouse nogo/rtn4."
RL J. Mol. Biol. 325:299-323(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7;
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129SVCJ7;
RA Van der Putten H., Mir A.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102281; AAM73503.1; -.
DR EMBL; AY102286; AAM73508.1; -.
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0005515; P:protein binding; IPI.
DR GO; GO:0001525; P:angiogenesis; IMP.
DR GO; GO:0007399; P:neurogenesis; IDA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 356 AA; 38403 MW; 4366C03BA9630B56 CRC64;

Query Match 62.8%; Score 443; DB 2; Length 356;
Best Local Similarity 98.9%; Pred. No. 7.6e-35;
Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTVAYIALALLSVTISFRIYKGVIOAI 108
Db 169 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTVAYIALALLSVTISFRIYKGVIOAI 228

QY 109 AKSDGHPFRAYLESEVAISEELVQKYSNSALG 141
Db 229 QKSDGHPFRAYLESEVAISEELVQKYSNSALG 261

Search completed: June 16, 2005, 13:17:44
Job time : 20.1287 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 12:31:51 ; Search time 167.944 Seconds  
(without alignments)  
2678.292 Million cell updates/sec

Title: US-09-830-972-2

Perfect score: 5848

Sequence: 1 MEDIDQSLVSSSTDSPPR.....VKDAMAKIQAKIPGLKRRAD 1163

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5848	100.0	1163	5	ABB81074
2	5848	100.0	1163	8	ADO26399
3	5848	100.0	1163	8	ADP45572
4	5846	100.0	1163	3	AAV71310
5	5840	99.9	1162	3	AAV71557
6	5823	99.6	1163	3	AAV71384
7	5312.5	90.8	1162	8	ADT89537
8	5307	90.7	1163	8	ADO08105
9	4921	84.1	974	3	AAV71560
10	4403.5	75.3	1192	4	AAU04591
11	4403.5	75.3	1192	5	APB68600
12	4403.5	75.3	1192	6	ABR59667
13	4403.5	75.3	1192	8	ADP45551
14	4398.5	75.2	1192	3	AAV56967
15	4398.5	75.2	1192	4	AAAB2349
16	4398.5	75.2	1192	5	ABG30938
17	4398.5	75.2	1192	5	ABH1078
18	4398.5	75.2	1192	8	ADO08103
19	4398.5	75.2	1192	8	ADP67234
20	4398.5	75.2	1192	8	ADR13966
21	4389.5	75.1	1192	7	ADK67502
22	4358.5	74.5	1192	8	ADO26400
23	4276.5	73.1	1178	3	AAV71311
24	4116	70.4	1246	4	AAU33228
25	4023	68.8	803	3	AAV71562

ALIGNMENTS

RESULT 1

ABB81074  
ID ABB81074 standard; protein; 1163 AA.

XX AC ABB81074;

XX DT 05-NOV-2002 (first entry)

XX DE Rat neurotransmitter receptor protein Nogo-A.

XX KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;  
central nervous system; peripheral nervous system; tranquilizer; Nogo;  
vulnerable; cerebroprotective; anti-tumor; antidiabetic; anticonvulsant;  
nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;  
osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;  
neurotransmitter receptor; rat; receptor.

XX OS Rattus norvegicus.

XX PN US2002072493-A1.

XX FD 13-JUN-2002.

XX PF 28-JUN-2001; 2001US-00893348.

XX PR 19-MAY-1998; 98IL-00124500.

XX PR 21-JUL-1998; 98MO-US014715.

XX PR 22-DEC-1998; 98US-00218277.

XX PR 19-MAY-1999; 99US-00314161.

XX PA (YEDA ) YEDA RES & DEV CO LTD.

XX PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;

XX FI Moalem G;

XX DR WPI; 2002-607255/65.

XX DR N-PSDB; ABN86600.

XX PT Promoting nerve regeneration and preventing neuronal degeneration in the  
central/peripheral nervous system from injury/disease, comprises  
administering nervous system-specific activated T cells/antigen, or  
analogs/peptides.

XX PS Example 5; Page 44-47; 93pp; English.

XX CC The invention relates to promoting nerve regeneration or conferring  
neuroprotection and preventing or inhibiting neuronal degeneration in the  
central/peripheral nervous system (NS). The method involves administering





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Db 481 QIIITEKTSKTNPFVLAVQDSEADIVTTDTLSKVTEAAVSNMPEGLTDLVQECESL 540
QY 541 NEATGTKIAYETKVDLVQTSQAQESLYPTAQCPSEFEAEATPSPVLDPDIYMEAPLNSL 600
Db 541 NEATGTKIAYETKVDLVQTSQAQESLYPTAQCPSEFEAEATPSPVLDPDIYMEAPLNSL 600
QY 601 LPSAGASVQVPSPLAEAPPVSYDSIKLEPENPPPYEAMNVALKALGTGKIGIKEPESF 660
Db 601 LPSAGASVQVPSPLAEAPPVSYDSIKLEPENPPPYEAMNVALKALGTGKIGIKEPESF 660
QY 661 NAAVQETAPYISACDLTKETKLSPEPSPDPSNTSEIAKFKSVPEHAELVEDSSPSE 720
Db 661 NAAVQETAPYISACDLTKETKLSPEPSPDPSNTSEIAKFKSVPEHAELVEDSSPSE 720
QY 721 PVDLFSDDSIPEVPTQOEAVMLMKESLTVESVETVAQHKERLSASQBELGKPYLESFOP 780
Db 721 PVDLFSDDSIPEVPTQOEAVMLMKESLTVESVETVAQHKERLSASQBELGKPYLESFOP 780
QY 781 NLHSTKDAASNDIPTLTKEKISLQMEERENTAIYSNDDLLSKEDKIKESETFSDSPIE 840
Db 781 NLHSTKDAASNDIPTLTKEKISLQMEERENTAIYSNDDLLSKEDKIKESETFSDSPIE 840
QY 841 IIDEPTFVSADKDSPLAKAYETDLEVSQKSIANIQSGADSLPCLLEPCDLSPKNIYPK 900
Db 841 IIDEPTFVSADKDSPLAKAYETDLEVSQKSIANIQSGADSLPCLLEPCDLSPKNIYPK 900
QY 901 DEVHVSDEFSENRSVSKASISPSNVSALEPQTEMGSIYKSKSLTKEAKKLPSDTEKED 960
Db 901 DEVHVSDEFSENRSVSKASISPSNVSALEPQTEMGSIYKSKSLTKEAKKLPSDTEKED 960
QY 961 RLSAVLSAELSKTSVVDLLYRDIKKTGVGASLFLLLSLTIVSVIYVTAIALALIS 1020
Db 961 RLSAVLSAELSKTSVVDLLYRDIKKTGVGASLFLLLSLTIVSVIYVTAIALALIS 1020
QY 1021 VTISFRIYKGVQIAQKSDGHPFRAYLESEVAISEELVQKYSNAGLGHVNSTIKELRRL 1080
Db 1021 VTISFRIYKGVQIAQKSDGHPFRAYLESEVAISEELVQKYSNAGLGHVNSTIKELRRL 1080
QY 1081 FLVDDLVDLSKFAVLMMWFTYVVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGIA 1140
Db 1081 FLVDDLVDLSKFAVLMMWFTYVVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGIA 1140
QY 1141 NKSVDAMAKIOAKTIGLKRKAD 1163
Db 1141 NKSVDAMAKIOAKTIGLKRKAD 1163

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## RESULT 5

AAY71557

ID AAY71557 standard; protein; 1162 AA.

XX AAY71557;

XX 02-NOV-2000 (first entry)

XX Rat Nogo A truncated protein used in the construction of mutant Nogo-A.

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XX 06-NOV-1998; 98US-0107446P.
XX (SCHW/) SCHWAB M E.
XX (CHEN/) CHEN M S.
XX Schwab ME, Chen MS;
XX WPI; 2000-400052/34.

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Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons.

Example; Page; 122pp; English.

The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is natively associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. The present sequence is a truncated form of rat Nogo A protein shown in AAY71310, which is tagged with vector/Nogo-A sequence aa 1-1162. Nogo-A is composed of His-tag/T7-tag/vector/Nogo-A sequence aa 1-1162. Nogo A deletion mutants were used for mapping the inhibitory sites of Nogo protein. Major inhibitory region was identified in the Nogo A sequence from amino acids 172-974, particularly amino acids 542-722. In addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: the present sequence is not given in the specification but is derived from rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However, the specification does not include sequences for these SEQ ID numbers

XX Sequence 1162 AA;

Query Match 99.9%; Score 5840; DB 3; Length 1162;

Best Local Similarity 99.9%; Pred. No. 9.8e-298;

Matches 1161; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MEDIDQSSILVSSSTDSPPRPAPFKYQVTFPEDEDEDEDEDEDEDEDEDEDELEELVERK 60
Db 1 MEDIDQSSILVSSSTDSPPRPAPFKYQVTFPEDEDEDEDEDEDEDEDEDEDELEELVERK 60
QY 61 PAAGLSAAVPAAPAAAPLLDFSSDVPPAPRGPLPAAPAPROPSPWERSPAAAPSLP 120
Db 61 PAAGLSAAVPAAPAAAPLLDFSSDVPPAPRGPLPAAPAPROPSPWERSPAAAPSLP 120
QY 121 PAAAVLPKLPEDDEPPAPPPPPPPAGASPLAEAPAPSTPAAPKRGSGSVDETLFALP 180
Db 121 PAAAVLPKLPEDDEPPAPPPPPPPAGASPLAEAPAPSTPAAPKRGSGSVDETLFALP 180
QY 181 AASEPVIIPSSAEKIMDLMEQGNVTSSQGEPPSVLLLETAASLPSLSTVSPFKEHGYL 240
Db 181 AASEPVIIPSSAEKIMDLMEQGNVTSSQGEPPSVLLLETAASLPSLSTVSPFKEHGYL 240
QY 241 GNLSAVSSSEGTIETLNASKELPERATNPVNDLAEFSELEYSEMGSSFKGSPKGES 300
Db 241 GNLSAVSSSEGTIETLNASKELPERATNPVNDLAEFSELEYSEMGSSFKGSPKGES 300
QY 301 AILVENTKEVIVRSKOKEDLVCSAALHSPOESPVGKEDRVVSPKTMDFINEMQMSVVA 360

```

Db 301 AILVENTKEEIVIRSKDKEDLVCSAALHSPQESPVGKEDRVVSPKTMDFIENQMVSVA 360  
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Db 361 PVREYADPKPEQAWKVDYVGRDVLAAANVESKVDKCLDSLEQSLGKDSGR 420  
Qy 421 NEDASFPSTPEPVKDSRAYITCASFTSATSTTANTPFLLEDHTSENKTDKIEERKA 480  
Db 421 NEDASFPSTPEPVKDSRAYITCASFTSATSTTANTPFLLEDHTSENKTDKIEERKA 480  
Qy 481 QIITEKTSKTSNPLVAVQSEADYVTTDLTSKVTEAAVSNMPEGLTPDLVQACSESL 540  
Db 481 QIITEKTSKTSNPLVAVQSEADYVTTDLTSKVTEAAVSNMPEGLTPDLVQACSESL 540  
Qy 541 NEATGKTIAYTKVDLVOTSAIQESLYPTAQPCSPPEEAATSPVLPDVMAPLNSL 600  
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Db 601 LPSAGASVQPSVSPLEAPPVVSVDISKLEPENPPPYEEANMVALKGTKEGKEPESF 660  
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Db 661 NAAVQETAPYISACDLIKETKLTSTSPSPFSNYSEIAKPEKSVPEHAELVEDSSPESE 720  
Qy 721 PVDLFSDDSIPEVPOTQEEAVMLKESLTVSETVAQKHEERLSASPOELGKPYLESFQP 780  
Db 721 PVDLFSDDSIPEVPOTQEEAVMLKESLTVSETVAQKHEERLSASPOELGKPYLESFQP 780  
Qy 781 NLHSTKOAASNDIPTLTKEKISIQMEEFNFTAIYSNDDLLSSKEDKIKESFTFSDSSPIE 840  
Db 781 NLHSTKOAASNDIPTLTKEKISIQMEEFNFTAIYSNDDLLSSKEDKIKESFTFSDSSPIE 840  
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Db 841 IIDFPPTVSAKDSPLAKAYTDLVSDKSEIANIQSGADSLPCLDLSPKNIYPK 900  
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Db 901 DEVHSDSFNSRNSVSKASISPSNVSALEPQTEMGSIKVSLSITKEAKKLPSDTKEB 960  
Qy 961 RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLS 1020  
Db 961 RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLS 1020  
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Db 1021 VTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISELVQKYSNLSALGHVNSTIKELRRL 1080  
Qy 1081 FLVDDLVDSLAFVLMVFTVVGALFNLGLTLLILALISLFSIPVIYERHQQVIDHYLGLA 1140  
Db 1081 FLVDDLVDSLAFVLMVFTVVGALFNLGLTLLILALISLFSIPVIYERHQQVIDHYLGLA 1140  
Qy 1141 NKSVDAMAKIQAIPGLKKA 1162  
Db 1141 NKSVDAMAKIQAIPGLKKA 1162

## RESULT 6

AAV71384

ID AAV71384 standard; protein; 1163 AA.

XX AC AAV71384;

XX DT 02-NOV-2000 (first entry)

XX DE Alternative version of rat neurite growth inhibitor Nogo A.

XX KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;

XX KW central nervous system; neoplastic disease; antiproliferative; glioma;

XX KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;

XX KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;

KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
XX structural plasticity; screening.

Rattus sp.

Key Location/Qualifiers

FT Inhibitory-site 1..171  
/note= "Inhibits NIH 3T3 fibroblast spreading"

FT Modified-site 30  
/note= "Casein kinase II site"

FT Region 31..58  
/note= "Acidic region"

FT Region 172..259  
/note= "This region is not essential for inhibitory activity"

FT Misc-difference 223  
/label= Unknown

FT /note= "There is Leu at this position in the sequence shown in AAY71310"

FT Modified-site 233  
/note= "Protein kinase C (PKC) site"

FT Modified-site 242..244  
/note= "Asn is N-glycosylated"

FT Modified-site 291  
/note= "Protein kinase C (PKC) site"

FT Modified-site 295  
/note= "Protein kinase C (PKC) site"

FT Misc-difference 404  
/note= "There is Ile at this position in the sequence shown in AAY71310"

FT Modified-site 436  
/note= "Protein kinase C (PKC) site"

FT Modified-site 468..470  
/note= "Asn is N-glycosylated"

FT Misc-difference 469  
/label= Unknown

FT /note= "There is Lys at this position in the sequence shown in AAY71310"

FT Modified-site 484  
/note= "Protein kinase C (PKC) site"

FT Modified-site 488  
/note= "Protein kinase C (PKC) site"

FT Modified-site 502  
/note= "Casein kinase II site"

FT Inhibitory-site 542..722

FT Modified-site 576  
/note= "Casein kinase II site"

FT Peptide 623..640  
/note= "used as immunogen to generate antibody AS 472"

FT Modified-site 626  
/note= "Protein kinase C (PKC) site"

FT Misc-difference 661  
/note= "There is Asn at this position in the sequence shown in AAY71310"

FT Modified-site 694..696  
/note= "Asn is N-glycosylated"

FT Modified-site 715  
/note= "Casein kinase II site"

FT Peptide 762..1163  
/note= "used as immunogen to generate antibody AS Bruna"

FT Modified-site 784  
/note= "Protein kinase C (PKC) site"

FT Misc-difference 820  
/note= "There is Leu at this position in the sequence shown in AAY71310"

FT Modified-site 821  
/note= "Protein kinase C (PKC) site"

FT Modified-site 850  
/note= "Protein kinase C (PKC) site"

FT Modified-site 855  
/note= "Protein kinase C (PKC) site"

FT Modified-site 863

FT Modified-site /note= "Casein kinase II site"

FT 868 /note= "Protein kinase C (PKC) site"

FT 893 /note= "Protein kinase C (PKC) site"

FT 912. .914 /note= "Asn is N-glycosylated"

FT 925. .927 /note= "Asn is N-glycosylated"

FT 954 /note= "PKC and casein kinase II sites"

FT 956 /note= "PKC and casein kinase II sites"

FT 975. .1162 /note= "This region is not essential for inhibitory activity"

FT 976. .1163 /note= "C-terminal common region found in Nogo A, B and C isoforms"

FT 988. .1023 /label= Transmembrane domain

FT /note= "C-terminal hydrophobic region"

FT 1024 /note= "Protein kinase C (PKC) site"

FT 1071. .1073 /note= "Asn is N-glycosylated"

FT 1073 /note= "Protein kinase C (PKC) site"

FT 1089 /note= "Protein kinase C (PKC) site"

FT 1090. .1125 /label= Transmembrane domain

FT /note= "C-terminal hydrophobic region"

FT 1141. .1143 /note= "Asn is N-glycosylated"

FT 1143 /note= "Protein kinase C (PKC) site"

XX WO200031235-A2.

XX 02-JUN-2000.

XX 05-NOV-1999; 99WO-US026160.

XX 06-NOV-1998; 98US-0107446P.

XX (SCHW/) SCHWAB M E.

XX (CHEN/) CHEN M S.

XX Schwab ME, Chen MS;

XX WPI; 2000-400052/34.

XX Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons.

XX Claim 3; Fig 13; 122pp; English.

XX The present sequence is an alternative version of rat Nogo A protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) myelin material with which it is natively associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The

CC animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. Note: The present sequence is an alternative version of the Nogo A sequence shown in Fig. 2A (see AAY71310). SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However the specification does not include sequences for these SEQ ID numbers

XX Sequence 1163 AA;

Query Match 99.6%; Score 5823; DB 3; Length 1163;  
Best Local Similarity 99.7%; Pred. No. 7.6e-297;  
Matches 1159; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEDIDQSSLVSSSTDSPPRPAPAFKYQVTEPDEDEDEDEDEDEDEDELEELVLERK 60

DB 1 MEDIDQSSLVSSSTDSPPRPAPAFKYQVTEPDEDEDEDEDEDEDELEELVLERK 60

QY 61 PAAGLSAAAVPAAAPAAALLDFSSDVPPAPRGPLPAAAPPAEROPSPERSPAAPAPSLP 120

DB 61 PAAGLSAAAVPAAAPAAALLDFSSDVPPAPRGPLPAAAPPAEROPSPERSPAAPAPSLP 120

QY 121 PAAAVLPKLPEDDEPPARPPPPPPAGASPLAEPAPPTDPAAPKRGSGSVDETLFALP 180

DB 121 PAAAVLPKLPEDDEPPARPPPPPPAGASPLAEPAPPTDPAAPKRGSGSVDETLFALP 180

QY 181 AASEVPIPSAFAKIMDLMEQPGNTVSSQEDFPSPVLLLETAASLPSPSTVTFKEHGYL 240

DB 181 AASEVPIPSAFAKIMDLMEQPGNTVSSQEDFPSPVLLLETAASLPSPSTVTFKEHGYL 240

QY 241 GNLSAVSSSEGTIEETLNEASKELPERATNPVNDLAEFSELEYSEMGSSFGKSPKGES 300

DB 241 GNLSAVSSSEGTIEETLNEASKELPERATNPVNDLAEFSELEYSEMGSSFGKSPKGES 300

QY 301 ALLVENTKEEIVIRSKDKEDLVCSAALHSPQESPVGKEDRVVSPKTTMDIFNEMQMSVVA 360

DB 301 ALLVENTKEEIVIRSKDKEDLVCSAALHSPQESPVGKEDRVVSPKTTMDIFNEMQMSVVA 360

QY 361 PVREYADFKPFEQAWKVDYEGSRDVLAAANVESKVDKCLDSLEQSLGKDSGR 420

DB 361 PVREYADFKPFEQAWKVDYEGSRDVLAAANVESKVDKCLDSLEQSLGKDSGR 420

QY 421 NEDASFPSTPVPKDSRAYITCASFTSATSTTANTPFLLEDHTSENKTEKKIERKA 480

DB 421 NEDASFPSTPVPKDSRAYITCASFTSATSTTANTPFLLEDHTSENKTEKKIERKA 480

QY 481 QIITEKTSPTSNPFLVAVQDSEADYVTTDLTKVTEAAVSNMPESGLTPDLVQEAACESL 540

DB 481 QIITEKTSPTSNPFLVAVQDSEADYVTTDLTKVTEAAVSNMPESGLTPDLVQEAACESL 540

QY 541 NEATGKIAYETKVQDLVOTSEAIQESLYPTAQLCPSPFEAEATPSVLPDIWMAPLNSL 600

DB 541 NEATGKIAYETKVQDLVOTSEAIQESLYPTAQLCPSPFEAEATPSVLPDIWMAPLNSL 600

QY 601 LPSAGASVVQSVSPLEAPPVSVYSIKLEPENPPPYEAMNVALKGTKEGKEPSP 660

DB 601 LPSAGASVVQSVSPLEAPPVSVYSIKLEPENPPPYEAMNVALKGTKEGKEPSP 660

QY 661 NAAVQTEAPYISACDLIKETKLTSTEPSDFNSYSEIAKFEKSVPEHAELVEDSSPSE 720

DB 661 NAAVQTEAPYISACDLIKETKLTSTEPSDFNSYSEIAKFEKSVPEHAELVEDSSPSE 720

QY 721 PVDLFSDSDSIPEVPQTEAEVWLMKESLTVSETVAQHKERLSASPOELGKPYLESQP 780

DB 721 PVDLFSDSDSIPEVPQTEAEVWLMKESLTVSETVAQHKERLSASPOELGKPYLESQP 780

QY 781 NLHSTKDAASNDIPTLTKEKISIQMEEFNTAIVSNDLLSSKEDIKESFSDSSPTE 840

DB 781 NLHSTKDAASNDIPTLTKEKISIQMEEFNTAIVSNDLLSSKEDIKESFSDSSPTE 840

QY 841 IIDEPTFTVSAKDDSPKLAKEYTDLVSDKSEIANIQSGADSLPCLLPCLSPFNVPK 900

DB 841 IIDEPTFTVSAKDDSPKLAKEYTDLVSDKSEIANIQSGADSLPCLLPCLSPFNVPK 900





QY 1014 IALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNST 1073  
 Db |||||  
 QY 1014 IALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNST 1073  
 Db |||||  
 QY 1074 IKELRRFLVDLVDLSKFAVLMMVFTTVGALFNGLTLLILALSLSPVPIYERHQVQI 1133  
 Db |||||  
 QY 1074 IKELRRFLVDLVDLSKFAVLMMVFTTVGALFNGLTLLILALSLSPVPIYERHQVQI 1133  
 Db |||||  
 QY 1134 DHYLGANKSVKDAWAKIQAKIPGLKRAK 1163  
 Db |||||  
 QY 1134 DHYLGANKSVKDAWAKIQAKIPGLKRAE 1163  
 Db |||||

## RESULT 9

AAV71560 standard; protein; 974 AA.

XX AAV71560;

AC AAV71560;

XX 02-NOV-2000 (first entry)

XX Rat Nogo A protein fragment used in the construction of mutant N1aext.

XX Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
 KW central nervous system; neoplastic disease; antiproliferative; glioma;  
 KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
 KW structural plasticity; screening; mutant; mutein.

XX Rattus sp.

XX WO200031235-A2.

XX 02-JUN-2000.

XX 05-NOV-1999; 99WO-US026160.

XX 06-NOV-1998; 98US-0107446P.

XX (SCHW/) SCHWAB M E.

PA (CHEN/) CHEN M S.

XX Schwab ME, Chen MS;

XX WPI; 2000-400052/34.

XX Nogo proteins and nucleic acids useful for treating neoplastic disorders  
 PT of the central nervous system and inducing regeneration of neurons.

XX Example; Page; 122pp; English.

XX The patent relates to neurite growth inhibitor Nogo which is free of all  
 CC central nervous system (CNS) myelin material with which it is natively  
 CC associated. Nogo proteins and fragments displaying neurite growth  
 CC inhibitory activity are used in the treatment of neoplastic disease of  
 CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,  
 CC ependymoma, pinealoma, haemangioblastoma, acoustic neuroma,  
 CC oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and  
 CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.  
 CC Therapeutics which promote Nogo activity can be used to treat or prevent  
 CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis  
 CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be  
 CC used to inhibit production of Nogo protein to induce regeneration of  
 CC neurons or to promote structural plasticity of the CNS in disorders where  
 CC neurite growth, regeneration or maintenance are deficient or desired. The  
 CC animal models can be used in diagnostic and screening methods for  
 CC predisposition to disorders and to screen for or test molecules which can  
 CC treat or prevent disorders or diseases of the CNS. The present sequence  
 CC is a fragment of rat Nogo A protein shown in AAV71310, which is used in  
 CC the construction of mutant N1aext. The mutant is composed of His-tag/T7-  
 CC tag/vector/Nogo-A sequence aa 1-974/T7-tag. Nogo A deletion mutants were

CC used for mapping the inhibitory sites of Nogo protein. Major inhibitory  
 CC region was identified in the Nogo A sequence from amino acids 172-974,  
 CC particularly amino acids 542-722. In addition, N-terminal region 1-171  
 CC was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The  
 CC present sequence is not given in the specification but is derived from  
 CC rat Nogo A sequence shown in AAV71310. SEQ ID numbers 35-42 are referred  
 CC in claim 32 and SEQ ID NO: 29 in disclosure of the specification.  
 CC However, the specification does not include sequences for these SEQ ID  
 CC numbers

XX Sequence 974 AA;

Query Match 84.1%; Score 4921; DB 3; Length 974;

Best Local Similarity 99.9%; Pred. No. 1.3e-249;

Matches 973; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEDIDQSLVSSSTDSPPRPAPAFKYQVTEPEDEDEDEDEDEDEDEDEDEDEDELEVLRLK 60  
 Db |||||  
 QY 1 MEDIDQSLVSSSTDSPPRPAPAFKYQVTEPEDEDEDEDEDEDEDEDEDEDELEVLRLK 60  
 Db |||||  
 QY 61 PAAGLSAAVPPAAAPLLDFSSDVPAPRGPLPAPPAAPQPPQSWERSPAPAPSLP 120  
 Db |||||  
 QY 61 PAAGLSAAVPPAAAPLLDFSSDVPAPRGPLPAPPAAPQPPQSWERSPAPAPSLP 120  
 Db |||||  
 QY 121 PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAPSTPAAKRRGGSGVDLTFALP 180  
 Db |||||  
 QY 121 PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAPSTPAAKRRGGSGVDLTFALP 180  
 Db |||||  
 QY 181 AASEPVIPTSSAEKIMDLMEQPGNTVSSGQDFPVSLLTAASLPSLSTVSPKEHGYL 240  
 Db |||||  
 QY 181 AASEPVIPTSSAEKIMDLMEQPGNTVSSGQDFPVSLLTAASLPSLSTVSPKEHGYL 240  
 Db |||||  
 QY 241 GNLSAVSSSEGTTEETLINEASKELPERATNPFVNRDLAEFSELYSEMGSPKSGPAGES 300  
 Db |||||  
 QY 241 GNLSAVSSSEGTTEETLINEASKELPERATNPFVNRDLAEFSELYSEMGSPKSGPAGES 300  
 Db |||||  
 QY 301 ALLVENTKBEYIVRSKDKEDLVCSAALHSPQESVPGKEDRVVSPKTMDFINEMQMSVVA 360  
 Db |||||  
 QY 301 ALLVENTKBEYIVRSKDKEDLVCSAALHSPQESVPGKEDRVVSPKTMDFINEMQMSVVA 360  
 Db |||||  
 QY 361 PVREYADFPFQAEVKEVOTYEGSRDVLAAARAVESKVDKCKLESLEQKSLGKDSGR 420  
 Db |||||  
 QY 361 PVREYADFPFQAEVKEVOTYEGSRDVLAAARAVESKVDKCKLESLEQKSLGKDSGR 420  
 Db |||||  
 QY 421 NEDASFPSTPEPVKDSRAYITCASFTSATESITANTFPLEDHTSENKTKIEERKA 480  
 Db |||||  
 QY 421 NEDASFPSTPEPVKDSRAYITCASFTSATESITANTFPLEDHTSENKTKIEERKA 480  
 Db |||||  
 QY 481 QIITEKTSPTKSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQACESEL 540  
 Db |||||  
 QY 481 QIITEKTSPTKSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQACESEL 540  
 Db |||||  
 QY 541 NEATGKIATYETKVDLVQTSSEATQESLYPTAQLCPSFEAEATPSVLPDIMEAPLNSL 600  
 Db |||||  
 QY 541 NEATGKIATYETKVDLVQTSSEATQESLYPTAQLCPSFEAEATPSVLPDIMEAPLNSL 600  
 Db |||||  
 QY 601 LPSAGASVWQPSVPLREAPPVSDTKLSPENPPPYEEAMNVALKALGTKEGKPESEF 660  
 Db |||||  
 QY 601 LPSAGASVWQPSVPLREAPPVSDTKLSPENPPPYEEAMNVALKALGTKEGKPESEF 660  
 Db |||||  
 QY 661 NAAVQETEAQYIETACDLIKETKLTSTPSPDFNSYSEIAKFEKSVPEHAELVEDSSPESE 720  
 Db |||||  
 QY 661 NAAVQETEAQYIETACDLIKETKLTSTPSPDFNSYSEIAKFEKSVPEHAELVEDSSPESE 720  
 Db |||||  
 QY 721 PVDLFSDSDSIPVPTQOEAAVLMKESLTVSETVAQHKERLSASQELGKPYLESFQP 780  
 Db |||||  
 QY 721 PVDLFSDSDSIPVPTQOEAAVLMKESLTVSETVAQHKERLSASQELGKPYLESFQP 780  
 Db |||||  
 QY 781 NLHSTKDAASNDIPTLTKEKISIQMEEFNATLYSNDLLSKEDKIKESSTSDSSPIE 840  
 Db |||||  
 QY 781 NLHSTKDAASNDIPTLTKEKISIQMEEFNATLYSNDLLSKEDKIKESSTSDSSPIE 840  
 Db |||||  
 QY 841 IIDEFPFTFVSAKODSPKLAKEYTDLVSDKSEIANIQSGADSLPCLPLCDLSPKNYYPK 900  
 Db |||||







634 PPPEAMNVALKAL-GTKGKIKPESFNAVQETAPYISACDLIKETKLTSPSPDF 692  
 656 PPPPEAMSVSLKVGKIKKEIPENINAALQETAPYISACDLIKETKLSAEPAPDF 715  
 693 SNYSEIAKESVPHAEALVESSPSEBPVDLFSDDSIPEVQTOEEAVMLKESLTVS 752  
 716 SYSEMAKVEQVPDHSSELVEDSSPSEBPVDLFSDDSIPEVQTOEEAVMLKESLTVS 775  
 753 -ETVAQHK-EERLSASPQELGPKYLESFQNLHSTKDA-ASNDIPTLTKEKISIQMEEF 809  
 776 FPMIEYENKEKLSALPPGGKPYLESFKSLDNTKOTLLPDEVSTLSKEKIPLOMEEL 835  
 810 NTAYISNDLLSKEDKIKESFTSDSPPIEIIDEPPTFVSADDS-PKLAKEYTDLEVS 868  
 836 STAVYSNDOLFISKEAQIRETETFSDDSPPIEIIDEPPTLISKTDSFKLAREYTDLEVS 895  
 869 DKSETANIOSGADSLPCLPCLDLPKNIYK--DEVHVSDFSENRSSVSKASISPSNV 926  
 896 HKSEIANAPDGAGSLPCTELPHDLNLKNIQPKVEEKISFSDDFSRNGSATSKVLLLPDV 955  
 927 SALEPOTEMGSIVKSKLTKAEKLPSTDEKEDRSLSAVLSAELSKTSVVDLLYWRDIK 986  
 956 SALATQAEIESIVKPKVYKAEKLPSTDEKEDRSLSAELSKTSVVDLLYWRDIK 1015  
 987 KTGWFVAGSLFLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVITQAIQKSDGHPFRA 1046  
 1016 KTGWFVAGSLFLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVITQAIQKSDGHPFRA 1075  
 1047 YLESEVAISEELVQKYSNLSALGHVNSTIKELRLFLVDLVDLSLKFVILMWFTYVYVGLF 1106  
 1076 YLESEVAISEELVQKYSNLSALGHVNSTIKELRLFLVDLVDLSLKFVILMWFTYVYVGLF 1135  
 1107 NGTLTLLILALISFSPVYIYERHQVQIDHYLGLANKSVKDMAKIOAKIPGLKRRKAD 1163  
 1136 NGTLTLLILALISFSPVYIYERHQVQIDHYLGLANKSVKDMAKIOAKIPGLKRRKAE 1192  
 RESULT 12  
 ABR59667  
 ID ABR59667 standard; protein; 1192 AA.  
 AC ABR59667;  
 XX  
 XX  
 22-JUL-2003 (first entry)  
 DT  
 DE Human NogoA protein.  
 XX  
 XX Human; Nogo receptor; Ngr; CTS domain; neuroprotective; gene therapy;  
 KW axonal growth; central nervous system; CNS; Nogo; spinal cord injury;  
 KW cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;  
 KW demyelinating disease; multiple sclerosis; monophasic demyelination;  
 KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2003031462-A2.  
 PN  
 XX  
 17-APR-2003.  
 XX  
 XX 04-OCT-2002; 2002WO-US032007.  
 PF  
 XX  
 06-OCT-2001; 2001US-00972599.  
 PR  
 XX  
 PA (UYUA ) UNIV YALE.  
 XX  
 XX Strittmatter SM;  
 PI  
 XX  
 XX WPI; 2003-393433/37.  
 DR N-PSDB; ACC81048.  
 XX  
 XX New human Nogo receptor polypeptides and nucleic acids, useful for  
 PT decreasing inhibition of axonal growth by a central nervous system

neuron, or in treating central nervous system disease, disorder or  
 injury, e.g. spinal cord injury.  
 PT  
 PT  
 XX  
 XX Disclosure; Page 131-135; 148pp; English.

The invention relates to a novel nucleic acid encoding a polypeptide  
 comprising amino acid residues 27-309 of a 473 amino acid sequence (P1,  
 human Nogo receptor (Ngr) NTLRRCT domain), or residues 27-309 of P1 with  
 1-20 conservative amino acid substitutions, and less than a complete CTS  
 domain, provided that a partial CTS domain, if present, consists of no  
 more than the first 39 consecutive residues. The nucleic acid of the  
 invention has neuroprotective activity. The polynucleotide may have a use  
 in gene therapy. The nucleic acid is useful for decreasing inhibition of  
 axonal growth by a central nervous system (CNS) neuron. The Ngr  
 polypeptide or an agent inhibits the binding of Nogo to Ngr or Ngr-  
 dependent signal transduction in the central nervous system neuron may be  
 used in treating central nervous system disease, disorder or injury, e.g.  
 spinal cord injury. Expression of an Ngr protein may be associated with  
 inhibition of axonal regeneration following cranial, cerebellar or spinal  
 trauma, stroke or a demyelinating disease, such as multiple sclerosis,  
 monophasic demyelination, encephalomyelitis, multifocal  
 leukoencephalopathy, panencephalitis, or Krabbe's disease. The present  
 sequence is used in the exemplification of the invention

Sequence 1192 AA;

Query Match 75.3%; Score 4403.5; DB 6; Length 1192;  
 Best Local Similarity 75.9%; Pred. No. 2.3e-222;  
 Matches 909; Conservative 104; Mismatches 145; Indels 39; Gaps 20;

QY 1 MEDIDSSIVSSSTDPSPRPAPFKYQVTEPEDEDEDEDEDEDEDEDEDEDEDELELEVLK 60  
 DB 1 MEDDQSPVLVSS--DSPRPAPFKYQVREPEDEE-EEEEEEDEDEDEDEDELELEVLK 58  
 QY 61 PAAGLSAAAVP--PAAAPLPLDFSDSVPPAPGRPLPAAPPAAPRQSPWSPAA---P 115  
 DB 59 PAAGLSAAVPTAPAGAPLMDFGNDFVPPAPGRPLPAAPPVAPRQSPWSPVSSVTP 118  
 QY 116 APSLPPAAAVLPSKLPEDDEPPAPPPPPAGASPLAE-----PAAPSTPAAPK 166  
 DB 119 APSPLSAAAVSPSKLPEDDEPPAPPPPPASVQAPSPVMPVTPPAPAPAPAPSTPAAPK 178  
 QY 167 RG-SGSVDETLPAAPAAEPVTPSSAEKIMDLMEOPGNTVSSGQDFPSVLLETAASLPS 225  
 DB 179 RGSVGSVDETLPAAPAAEPVTPSSAEKIMDLMEOPGNTVSSGQDFPSVLLETAASLPS 237  
 QY 226 LSPSLTVSPKHEGYLGNLSAVSSSEGTIETLNEASKELPERATNPFVNRDLAEFSELY 285  
 DB 238 LSPSLSAAAFKHEGYLGNLSTVLPTEGLQENVSEASKEVSEKAKTLLIDRLDTFSELY 297  
 QY 286 SEMGSSFKGSPKGSAILVENTKEVIVRSKDKED-LVCSAALHSPQESPVG-----KED 339  
 DB 298 SEMGSSFSVSPKASAVIANPREIIVKNKDEEEKLSNNILHNQOQLPTALTCLKVKED 357  
 QY 340 RVVSPKTMIDIFENQMSVVAVRREYADFKPEQAWKVDYEGSRDVLAA----RANV 395  
 DB 358 EVVSEKAKDSFNERRVAEAPREYADFKFERVWEVKDSKEDS-DMLAAGGKTESNL 416  
 QY 396 ESKVDRKCLLEDSLEQKSLGKDESEGNEDASFPSTPEPVKDSRAVITCASFT-SATESTT 454  
 DB 417 ESKVDKCKFADSLQETNHEKDESSNDTSPSTPEGIDKDRSGAVITCAPFNPATATESIA 476  
 QY 455 ANTFFLLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPLVAVQDEADYVTTDL 513  
 DB 477 TNIFPLLDGPTSENKTDEKKIEERKAQIVTEKNTKTSNPNFLVAAQDSEYTVTTDLT 536  
 QY 514 KYTEAAVSNMPEGLTPDLVQEAECESLNEATGKTAYETKVDLVOTSEAIQESLYPTAQL 573  
 DB 537 KYTEEVVANNMPEGLTPDLVQEAECESLNEVGTGKTAYETKMDLVQTSFVWQSLYPAAQL 596  
 QY 574 CFSFEAEATPSPVLPDIIVMEAPLNSLPSAGASVQVSPVSPLEAPPVPSYISIKLEPEN 633  
 DB 597 CFSFESEATPSPVLPDIIVMEAPLNSVPSAGASVIQPSSPLEA-SSVNYESIKHEPEN 655



Qy	693	SNTYSEIAKFKSPVPEHAELVEDDSDSPSEPVDLFSDDSIPVPTQOEAVMLMKESLTFS	752
Db	716	SDYSEMAKVQEPVHDHSELVEDDSDSPSEPVDLFSDDSIPVPOKQDETVMVLVKESLTFS	775
Qy	753	-ETVAQHK-BERLSASPOELGKPVLESFQPNLHSTKDA-ASNDIPTLTTKKEKSLQWEEF	809
Db	776	FESMIEYENKEKUSALPPEGGKPVLESFKLSLWNTKDTLPDDEVSTLUSKKEKPLQWEE	835
Qy	810	NTAIYSNDDLLSSKEDIKESETFSDSSPIEIIDEPFTFVSADKDS-PLKAKEYTDLVS	868
Db	836	STAVYSNDDLLFISKEAQIRETETFSDSSPIEIIDEPFTLISSTKTDSPKLAREYTDLVS	895
Qy	869	DKESEIANIQSAGNSLPCLELPDCLSFKNIYPK--DEVHVHSDSESENESSVYSKASISPNV	926
Db	896	HKSEIANAPDAGSLPCTELPHDLSLKNIOQKVEEKISFSDDFSKNGSATSKVLLLPD	955
Qy	927	SALPEPTQMGSIYVKSKSILTKEAEKLPDSTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK	986
Db	956	SALATQAEIESIVKPKVLVKEAEKLPDSTEKEDRSPSAIFSAELSKTSVVDLLYWRDIK	1015
Qy	987	KTGVVFGASIFLLLSLTVFSIVSVTAIALALISVTFISPRIYKGVIQAIOKSDEGHPFRA	1046
Db	1016	KTGVVFGASIFLLLSLTVFSIVSVTAIALALISVTFISPRIYKGVIQAIOKSDEGHPFRA	1075
Qy	1047	YLESEVAISELVOKYSNSALGHWNSTIKELRRLFLVDDLDVSLKPAVLMMWFTYVGALF	1106
Db	1076	YLESEVAISELVOKYSNSALGHWNCTIKELRRLFLVDDLDVSLKPAVLMMWFTYVGALF	1135
Qy	1107	NGUTLLILALISFSPVPIYERHQVQIDHYGLANKSVKDMAKIOAKIOPGLKRRAD	1163
Db	1136	NGUTLLILALISFSPVPIYERHQVQIDHYGLANKSVKDMAKIOAKIOPGLKRRKE	1192

RESUIT, T 14

RESULI I  
ADV56967

AA156967  
ID AAY56967 standard: protein: 1192 AA.

XX  
XX  
/ 095057W DTAA  
AC  
AAAY56967.AC  
XX  
AA150967;

25-APR-2000

DI  
YY  
25-APR-2000

XX  
DE  
Human MACT 20DE  
HUMAN MAGI po  
VVXX  
MAGT proteins.

KW MAGI protein;  
KW anti- $\beta$ -tubulin

spinal injury

psychiatric d

KW stroke; cytos

XX

OS Homo sapiens.

XX

PN WO200005364-A

XX

PD 03-FEB-2000.

XX

21-JUL-1999;

XX

PR 22-JUL-1998;

PR 19-JUL-1999;

CC neuroendocrine-specific protein. The MAGI protein can be expressed by  
CC standard recombinant methodology. The MAGI polypeptides, polynucleotides  
CC and antibodies are useful for treating diseases, including neuropathies  
CC spinal injury, neuronal degeneration, neuromuscular disorders,  
CC psychiatric disorders and developmental disorders, cancer, stroke and  
CC inflammatory disorders. The polynucleotide is also useful for chromosome  
CC localization and for tissue expression studies. The present sequence  
XX represents the human MAGI protein  
SQ Sequence 1192 AA;

75.28:	Score	4398.5:	DB	3:	Length	1192:
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Very Match	75.2%	Score 4398:3, DB 3, Length 1132,
at Local Similarity	75.9%	pred No 4 3e-222:

Local Similarity 73.3%; Fied: NO: 4.3E-222;  
 Conservative 104: Mismatches 146: Indels 39:

Qy	1	MEDIDOSIIVSSSTDSPPRPPAPKYOFVTEPEDEEDEDDEEDEDLEBEVLERK	60
Db	1	MEDLDQSPLVVSS--DSPRPQPAPKYOFVREPEDEE--EEEEEEDEDEDLBEVLERK	58
Qy	61	PAAGLSAAAVP--PAAAAPLLDFSGSDVPAPRGPFAAPAAPAQPSWERSPAA---P	115
Db	59	PAAGLSAAPPVTATAAGAFLMDFGNDFFVPAPRGPFAAPPVAPERQPSWDSPVSSTVP	118
Qy	116	ABSLPAAAAVPSKLPEDEDPAPPPPPPACASPLAE-----PAAPSTPAAPKR	166
Db	119	ABSPLSAAAVSPSKLPEDEDPAPPPPPPASVSPAEPVMTPPAPAPAAPPSTPAAPKR	178
Qy	167	RG-SCGSVDETLFALPAASEPVIPSSAEKIIMDLMEPGNTVSSGOEDFPSSLTAAASLPS	225
Db	179	RSSSGSVDETLFALPAASEPVIRSAEN-MDLKEQPGNTISAGOEDFPSVLTAASLPS	237
Qy	226	LSPLTVSFGKHGYIGNLSAVSSSEGTIEETLNASKELPERATNFVNRLAPESELEY	285
Db	238	LSPLSAASFKEHYELGNLSTVPTGETLOENVSEAKESVKARTLLIRDLTFRSELEY	297
Qy	286	SMWGSSFSGSPKGBSAILVENTKEVTVRSKXED-LVCSAAHLSPOESPVG----	339
Db	298	SEMGSSFVSFKAESAIVANPREIIIVKNKDBEEKLVSNLIHQOELPTALTCLVKED	357
Qy	340	RVVSPEKTMDIFNEMQMSVVAPEEYVADPKPEQAWEVKDTVEGGRDVLA-----	395
Db	358	EYVSEKAKDSFNKRVAVEAMREEYADPKFERVWEVKDSKEDS-DMLAAGKGKTESNL	416
Qy	396	ESKVDRKCLEDSLQKSILGKDSGRNDDASFPSTPEPVKDSSRAYITCASFT-SATESITT	454
Db	417	ESKVDKKCFADSLGOTNHKXDSSENDDTSFPSTPEGIKDRPGAYITCAPNPAAETISA	476
Qy	455	ANTFPLEBHTSENKTDKKIIEERKAQIITEK-TSPKTSNPFPLVAVODSEADVTTDTJUS	513
Db	477	TNIIFLLGDPTSENKTDKKIIEERKAQIVTEKNTSTKTSNPFVAAQSDSTDVVTVDNLT	536
Qy	514	KYTEAAVNMPEGLTPDLVQACSELNEATGTKIAYETKVDLVQTSSEAIQBSLYPTAOL	573
Db	537	KYTEEVNAMPEGLTPDLVQACSELNEVTGTKIAYETKMDLVQISEVMQESLYPAAQL	596
Qy	574	CPSFEAEATPSVLPDIIMEAPLNSLLPSAGASVVOQPSVSPLEAPPVSYDSIKULEPEN	633
Db	597	CPSFESEATPSVLPDIIMEAPLNSAVPSAGASVIQSSSPLEA--SSVNYESIKEHPEN	655
Qy	634	PPPYEAMNVALKAL-GTKEGIKEPESFNAAQETEAPYLISIACDLIKETKLSTEPSPDF	692
Db	656	PPPYEAMSVLUKVGSIKEBIKEPENINALQETEAPYLISIACDLIKETKLSAGEPADP	715
Qy	693	SNNYSIAKFESVPEHAELVDSSPEPDVDFSDDSIPEVPQTQBEAVLMKESLTYEVS	752
Db	716	SDYSEMAKVEQVPDHSSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLKESLTETS	775
Qy	753	-ETVAQH-K-ERELNSPOSLEGKPYLESFQPNILSHTKDA-ASNIDIPTLTKEKISLOWEFP	809
Db	776	FESMIYEYNKGIKALSALPEGGKPYLESFKULSONTKDLLPDEVSTLSKKKEKPIQMEEL	835
Qy	810	NTAIYNSDDLSSKEDIKETSETSDSSPTETIDEFFTFFVSARKDS--PKLKEYETDLEVS	868

Db 836 STAVYNSNDLFLSKAQIRETETFTSDSSPIIIDEFTPLTSSKTDTSFSLKAREYTDLEVS 895  
 QY 869 DKSEIANQSGADSLPCLPCLDSFKNIYK--DEVHVSDEFSENRSSVSKASISPNV 926  
 Db 896 HKSEIANAPDAGSLPCTELPHDLISLKNIOQKVEKISFSDDFSKNGSATSKVLLPPDV 955  
 QY 927 SALEPQTEMGISVKSLSKTBKAEKKLPSTDEKRSLSAVLSAELSKTSVVDLLYWRDIK 986  
 Db 956 SALATQABIESIVKPKVLVKEAEKKLPSTDEKRSLSAIFSAELSKTSVVDLLYWRDIK 1015  
 QY 987 KTGUVFGASLFLLSLTVFSIVSTAYIALALLSVTISFRIYKGVIOAIQKSDGHPRA 1046  
 Db 1016 KTGUVFGASLFLLSLTVFSIVSTAYIALALLSVTISFRIYKGVIOAIQKSDGHPRA 1075  
 QY 1047 YLESEVALSEELVOKYSNSALGHVNSTIKELRRFLVDLVDLSLKFAVLMMVFTVVGALF 1106  
 Db 1076 YLESEVALSEELVOKYSNSALGHVNSTIKELRRFLVDLVDLSLKFAVLMMVFTVVGALF 1135  
 QY 1107 NGLTLLIALLSLFSIPVIYERHQVQIDHYILGLANKSVKDMAKIOAKIPGLKRAK 1163  
 Db 1136 NGLTLLIALLSLFSIPVIYERHQVQIDHYILGLANKSVKDMAKIOAKIPGLKRAE 1192

## RESULT 15

AAB82349  
 ID AAB82349 standard; protein; 1192 AA.

XX AAB82349;

XX 23-JUL-2001 (first entry)

DT Human NOGO-A protein.

DE NOGO-A; human; chromosome 2p21; neuropathy; spinal injury; brain injury;  
 KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;  
 KW neuromuscular disorder; psychiatric disorder; developmental disorder;  
 KW neuroprotective; nontropic; neuroleptic; antiparkinsonian;  
 KW cerebroprotective; neuroleptic; diagnosis; therapy.

XX Homo sapiens.

XX WO200136631-Al.

XX 25-MAY-2001.

XX 14-NOV-2000; 2000WO-GB004345.

XX 15-NOV-1999; 99GB-00026995.

XX 24-JAN-2000; 2000GB-00001550.

XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Michalovich D, Prinjha R;

XX WPI; 2001-343822/36.

XX N-PSDB; AAF90324.

PT New polypeptide designated NOGO-C is a splice variant of the human NOGO  
 gene and may be useful in the treatment of neural disorders including

PT Alzheimer's and Parkinson's diseases.

PS Disclosure; Page 26-27; 25pp; English.

CC The present sequence is that of human NOGO-A. NOGO-A is a previously  
 known splice variant of the human NOGO gene on chromosome 2p21. The  
 CC invention relates to a novel splice variant, NOGO-C (see AAB82348). It  
 CC provides NOGO-C polypeptides and polynucleotides, and methods for  
 CC producing such polypeptides by recombinant techniques. Also disclosed are  
 CC methods for utilising NOGO-C polypeptides and polynucleotides in the  
 CC treatment of diseases including neuropathies, spinal injury, brain  
 CC injury, stroke, neuronal degeneration, for example Alzheimer's disease  
 CC and Parkinson's disease, neuromuscular disorders, psychiatric disorders  
 CC and developmental disorders. Also provided are methods for identifying

CC agonists and agonists for use in treating conditions associated with NOGO  
 CC -C imbalance, and diagnostic assays for detecting diseases associated  
 CC with inappropriate NOGO-C activity or levels  
 XX Sequence 1192 AA;

Query Match 75.2%; Score 4398.5; DB 4; Length 1192;  
 Best Local Similarity 75.9%; Pred. No. 4.3e-222;  
 Matches 908; Conservative 104; Mismatches 146; Indels 39; Gaps 20;

QY 1 MEDIDQSSLSVSSSTDSPPRPAPKQYQVTEPEDEDEDEDEDEDEDEDEDEDEDELEVLK 60  
 Db 1 MEDIDQSLPLVSS--DSPRPQPAKQYQVREPEDEE--EEEEDEDEDEDELEVLK 58  
 QY 61 PAAGLSAAAVP--PAAAPLIDFSSDVPPAPRGLPAAPAPAPAPAPAPAPAPAPAPAPAP 115  
 Db 59 PAAGLSAAVPTAPAGAPLMDFGNDFVPPAPRGLPAAPVAPERQSWDPSPVSTVP 118  
 QY 116 APSLPPAAAVLPSKLPEDDEPPAPPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166  
 Db 119 APSPLSAAAVSPSKLPEDDEPPAPPPPPPPASVSPQAEVWVTPPAPAPAPAPSTPAAPKR 178  
 QY 167 RG-SGSVDLTFALPAASEPVIPSSAEKIMDLMEQPGNTVSSQGDPPSVLLETAASLPS 225  
 Db 179 RGSSGSVDLTFALPAASEPVIRSSAEN-MDLKEQPGNTISAGQDPPSVLLETAASLPS 237  
 QY 226 LSPLSVTSFKHEGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLASFSELEY 285  
 Db 238 LSPLSAASFKEHEGYLGNLSVLPTEGLQENVSASKEVSEKAKTLIDRLDTFSELEY 297  
 QY 286 SEMGSSFKGSPKGESAILVENTKEEVIVRSKOKED-LVCSAALHSPOESPVG-----KED 339  
 Db 298 SEMGSSFSVSPKAEASAVIVANPREEIIYKVKDEEKLVSNNILANQOELPTALTKLVKED 357  
 QY 340 RVVSPKTMIDFNEMQMSVAVPVEEYADFPKQAEVVDKTYGSDVLA-----RANV 395  
 Db 358 EVVSEKAKDSFNEKRVAVAPRREYADFPKPERVWEVSKEDS-DMLAAGKIKISNL 416  
 QY 396 ESKVDRKCLDSLEOKSLGKDSGRNEDASFPSTPEPVKDSRAYITCASFT-SATESTT 454  
 Db 417 ESKVDKCFADSLQETHKDSSESSNDTTFSTPEGIKORPGAYITCAPNPARTSIA 476  
 QY 455 ANTFFLLEDHTSENKTKDEKIEERKAIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLS 513  
 Db 477 TNIFPLLGDPSTENKTKDEKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSEADYVTTDTLT 536  
 QY 514 KVTEAAVSNMPEGLTPDLVQACESELNATGKIAYETKVDLVQTSQAQESLYPTAQL 573  
 Db 537 KVTEEVVANNMPEGLTPDLVQACESELNATGKIAYETKMDLVQTSQESLYPTAQL 596  
 QY 574 CPSFERAEATPSVLPDIVMEAPLNSLLPSAGASVWQSPVSPLEAPPVSDSIKLRPEN 633  
 Db 597 CPSFEESEATPSVLPDIVMEAPLNSAVPSAGASVIOFSSSPLA-SSVYVESIKHREPEN 655  
 QY 634 PPPYEAMNVALKAL-GTKEGIKEPESFNAVQTEAPYISACDLIKETKLSLTPSPDF 692  
 Db 656 PPPYEAMSVLSKVGSKKEIKPENINAALQTEAPYISACDLIKETKLSAEPADF 715  
 QY 693 SNTYSEIAKFKSVPEHAELVEDSSPESEPVLDSDSDSIPEVPQTEAEAVMLKESLTVS 752  
 Db 716 SDYSEMAKVEQVPDHSSELVEDSSPDSEPVLDSDSDSIPEVPQKQDETVMVLKESLTETS 775  
 QY 753 -ETVAQHK-EERLSASPOELGKPVLESFQPNLHSTKDA-ASNDIPTLTKEKISLOWEEF 809  
 Db 776 FESMIEYENKLSALPPEGKPVLESFKLSLONTKDTLLPDEVSTLSKKEKIPLOWEEL 835  
 QY 810 NTAIYNSNDLLSSKEDKIKESFTSDSSPIEIDEFTFVSADKDS--PKLAKETDLEVS 868  
 Db 836 STAVYNSNDLFLSKAQIRETETFTSDSSPIEIDEFTPLTSSKTDTSFSLKAREYTDLEVS 895  
 QY 869 DKSEIANQSGADSLPCLPCLDSFKNIYK--DEVHVSDEFSENRSSVSKASISPNV 926  
 Db 896 HKSEIANAPDAGSLPCTELPHDLISLKNIOQKVEKISFSDDFSKNGSATSKVLLPPDV 955

Qy	927	SALEPQTEMGSIVKSKSLTKAEKKLP	SDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK	986
Db	956	SALATQAEIESIVKPKVLKAEKKLP	SDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIK	1015
Qy	987	KTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDEGHPRA	1046	
Db	1016	KTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDEGHPRA	1075	
Qy	1047	YLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGALF	1106	
Db	1076	YLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGALF	1135	
Qy	1107	NGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAKIQAKIPGLKRAKAD	1163	
Db	1136	NGLTLLILALISLFSVPVIYERHQVQIDHYLGLANKSVKDAKIQAKIPGLKRAE	1192	

Search completed: June 16, 2005, 13:10:59  
Job time : 174.944 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:19:00 ; Search time 43.9175 Seconds  
(without alignments)  
1976.818 Million cell updates/sec

Title: US-09-830-972-2  
Perfect score: 5848  
Sequence: 1 MEDIDQSLVSSSTDSPRP.....VKDAMAKIQAKIPGLKRRAD 1163

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	908	15.5	199	2	US-08-700-607-1
2	908	15.5	201	4	US-09-949-016-9124
3	789.5	13.5	776	2	US-08-700-607-5
4	789.5	13.5	776	4	US-09-949-016-6998
5	724.5	12.4	439	4	US-09-949-016-9180
6	716.5	12.3	356	2	US-08-700-607-6
7	685	11.7	208	2	US-08-700-607-7
8	671	11.5	267	2	US-08-700-607-8
9	625.5	10.7	192	4	US-09-949-016-8859
10	539.5	9.2	168	4	US-09-149-476-563
11	522.5	8.9	219	4	US-09-270-767-45132
12	519	8.9	241	2	US-08-700-607-3
13	490	8.4	588	4	US-09-949-016-7290
14	387.5	6.6	127	4	US-09-513-999C-5000
15	302.5	5.2	8991	4	US-08-714-741-32
16	288	4.9	2468	4	US-09-976-594-726
17	288	4.9	2468	4	US-09-538-092-1135
18	288	4.9	2522	4	US-09-949-016-10237
19	286	4.9	68	4	US-09-513-999C-6304
20	286	4.9	92	4	US-09-149-476-411
21	282.5	4.8	1219	4	US-09-344-624-4
22	279.5	4.8	1786	3	US-08-973-462-8
23	275.5	4.7	2753	4	US-09-949-016-7659
24	275.5	4.7	2753	4	US-09-949-016-7660
25	275.5	4.7	3924	4	US-09-538-092-1246
26	267	4.6	1781	4	US-09-961-403-13
27	265.5	4.5	1780	1	US-08-769-309A-5

28	265.5	4.5	1780	3	US-08-994-570-5	Sequence 5, Appli
29	265	4.5	2137	3	US-09-134-001C-4463	Sequence 4463, Ap
30	259.5	4.4	1020	4	US-09-538-092-911	Sequence 911, App
31	256.5	4.4	75	4	US-09-621-976-4600	Sequence 4600, Ap
32	256.5	4.4	75	4	US-09-621-976-4601	Sequence 4601, Ap
33	255.5	4.4	1140	4	US-09-538-092-647	Sequence 647, App
34	254.5	4.4	1596	4	US-08-978-277A-4	Sequence 4, Appli
35	252	4.3	114	4	US-09-513-999C-7861	Sequence 7861, Ap
36	251.5	4.3	3913	4	US-09-949-016-10933	Sequence 10933, A
37	250.5	4.3	4377	4	US-09-949-016-6978	Sequence 6978, Ap
38	239.5	4.1	1344	4	US-09-949-016-10925	Sequence 10925, A
39	238.5	4.1	1341	4	US-09-949-016-6890	Sequence 6890, Ap
40	238	4.1	1306	4	US-09-538-092-330	Sequence 330, App
41	237	4.1	1878	4	US-09-949-016-8902	Sequence 8902, Ap
42	237	4.1	1878	4	US-09-949-016-8903	Sequence 8903, Ap
43	233	4.0	1142	2	US-08-993-118-7	Sequence 7, Appli
44	233	4.0	1142	3	US-08-845-528C-7	Sequence 7, Appli
45	233	4.0	1142	4	US-09-066-281B-7	Sequence 7, Appli

## ALIGNMENTS

RESULT 1  
US-08-700-607-1  
; Sequence 1, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/700,607  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0114 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 199 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: Consensus  
; CLONE: US-08-700-607-1

Query Match 15.5% Score 908; DB 2; Length 199;  
Best Local Similarity 96.3%; Pred No. 1.5e-50;  
Matches 184; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
Qy 973 KTSYVDLLYWRDKKTVGFQASFLLLSLTVFSIVSYATIALALLSVTISFRIYKGV 1032

Db 9 KDKVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGYI 68  
QY 1033 QAIQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKF 1092  
Db 69 QAIQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKF 128  
QY 1093 AVLMMVFTVVGALFNGLLTLLIALISLFSIPVYERHQVQIDHYLGLANKSVKDMAKIQ 1152  
Db 129 AVLMMVFTVVGALFNGLLTLLIALISLFSIPVYERHQVQIDHYLGLANKSVKDMAKIQ 188  
QY 1153 AKIPGLKRAKAD 1163  
Db 189 AKIPGLKRAE 199

RESULT 2  
US-09-949-016-9124  
; Sequence 9124, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9124  
; LENGTH: 201  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-9124

Query Match 15.5%; Score 908; DB 4; Length 201;  
Best Local Similarity 96.3%; Pred. No. 1.5e-50;  
Matches 184; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 973 KTSVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGYI 1032  
Db 11 KDKVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGYI 70  
QY 1033 QAIQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKF 1092  
Db 71 QAIQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKF 130  
QY 1093 AVLMMVFTVVGALFNGLLTLLIALISLFSIPVYERHQVQIDHYLGLANKSVKDMAKIQ 1152  
Db 131 AVLMMVFTVVGALFNGLLTLLIALISLFSIPVYERHQVQIDHYLGLANKSVKDMAKIQ 190  
QY 1153 AKIPGLKRAKAD 1163  
Db 191 AKIPGLKRAE 201

RESULT 3  
US-08-700-607-5  
; Sequence 5, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/700,607  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PP-0114 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 776 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 307107  
US-08-700-607-5  
Query Match 13.5%; Score 789.5; DB 2; Length 776;  
Best Local Similarity 31.2%; Pred. No. 4.1e-42;  
Matches 243; Conservative 115; Mismatches 252; Indels 169; Gaps 28;  
QY 487 TSPKTSNPFVAVQDSEADYVTTDTLSKVTRAAVSNMPEGLTPDLVQACSELNEATGT 546  
Db 65 SGPARQSP--VAMETASTAGVAGVSAMDHTFTSTTKDGE-----SCVTSLI-----S 110  
QY 547 KIAYETKVDLVQTSIAIQ-ESLYPTAQLCPSEAEATPSPVLPDI--VMEAPLNS---- 599  
Db 111 DICVPPQEDSYFTGILQENGHVITSESP---BELGTPGSLPDVPGIERSGLFSSDSG 167  
QY 600 --LLPSAGASVQPSVSPLEAPPVSY-----DSIKLEPNPPYEEA-----M 641  
Db 168 IEMTPAESTEVNKILLADPLDQMKAEYKVIDITREEVKHQEQHHPELEDKDLDFKNKDT 227  
QY 642 NVALKALGTGKGIKEPE-----SFNAVQTEAPYISACDLIKETKLSTE-PSP 690  
Db 228 DISIK---PEGVREPPDKPAPVEGKIIKDHLLESTFAPYID---DLSEEQRRAPQITTP 280  
QY 691 DFSNYSYTAKEKSVPEHAELVEDSSPESEPVDLF--SDDSIPEV---POTQEEAVMLMK 745  
Db 281 VKITUTEIE-----PSVETTTQKTPKQDILCLPSPDTVFTVTVSEPDSDSPSITPP 334  
QY 746 ESLTEVSETVAQHK-----EERLSASQELGKPYLESFQ-----NLHSTKDAASND---- 792  
Db 335 SSGTEPSAAESQKGSISEDELIITAIKEAKGLSYETAENPRPVGQLADRPEVKARSGPPT 394  
QY 793 IPTLTKEKISLQMEEFNTAYISNDDLLSSKEDI----- 827  
Db 395 IPSPLDHEASSAEGSDSEIELVSEDPM--AAEDALPSGVSVSGHVGPPSPSPSPSIQVS 452  
QY 828 ---KESETFSDSSPIEIDEPFTFVSAXDDSPKLAKYETDLEVSQKSEI-----ANIQSG 879  
Db 453 ILREEREAELDS---ELIIESCDASSASEEPKRDQSDPPMKPSALDAIRETGTVAER 509  
QY 880 ADSLPCLELPCDLSFKNIYPKDEHVSDSEFSENRSVSKASISPSNSVALEPQETMGSTIV 939  
Db 510 APSRRGLAEPG--SFLD--YPSTEPQGPPEL-----PPGDGALEPETPM----- 549









1	EARLIER FILING DATE: 1997-04-11	
2	EARLIER APPLICATION NUMBER: 60/048,974	
3	EARLIER FILING DATE: 1997-06-06	
4	EARLIER APPLICATION NUMBER: 60/056,886	
5	EARLIER FILING DATE: 1997-08-22	
6	EARLIER APPLICATION NUMBER: 60/056,877	
7	EARLIER FILING DATE: 1997-08-22	
8	EARLIER APPLICATION NUMBER: 60/056,889	
9	EARLIER FILING DATE: 1997-08-22	
10	EARLIER APPLICATION NUMBER: 60/056,893	
11	EARLIER FILING DATE: 1997-08-22	
12	EARLIER APPLICATION NUMBER: 60/056,630	
13	EARLIER FILING DATE: 1997-08-22	
14	EARLIER APPLICATION NUMBER: 60/056,878	
15	EARLIER FILING DATE: 1997-08-22	
16	EARLIER APPLICATION NUMBER: 60/056,662	
17	EARLIER FILING DATE: 1997-08-22	
18	EARLIER APPLICATION NUMBER: 60/056,872	
19	EARLIER FILING DATE: 1997-08-22	
20	EARLIER APPLICATION NUMBER: 60/056,882	
21	EARLIER FILING DATE: 1997-08-22	
22	EARLIER APPLICATION NUMBER: 60/056,637	
23	EARLIER FILING DATE: 1997-08-22	
24	EARLIER APPLICATION NUMBER: 60/056,903	
25	EARLIER FILING DATE: 1997-08-22	
26	EARLIER APPLICATION NUMBER: 60/056,888	
27	EARLIER FILING DATE: 1997-08-22	
28	EARLIER APPLICATION NUMBER: 60/056,879	
29	EARLIER FILING DATE: 1997-08-22	
30	EARLIER APPLICATION NUMBER: 60/056,880	
31	EARLIER FILING DATE: 1997-08-22	
32	EARLIER APPLICATION NUMBER: 60/056,894	
33	EARLIER FILING DATE: 1997-08-22	
34	EARLIER APPLICATION NUMBER: 60/056,911	
35	EARLIER FILING DATE: 1997-08-22	
36	EARLIER APPLICATION NUMBER: 60/056,636	
37	EARLIER FILING DATE: 1997-08-22	
38	EARLIER APPLICATION NUMBER: 60/056,874	
39	EARLIER FILING DATE: 1997-08-22	
40	EARLIER APPLICATION NUMBER: 60/056,910	
41	EARLIER FILING DATE: 1997-08-22	
42	EARLIER APPLICATION NUMBER: 60/056,864	
43	EARLIER FILING DATE: 1997-08-22	
44	EARLIER APPLICATION NUMBER: 60/056,631	
45	EARLIER FILING DATE: 1997-08-22	
46	EARLIER APPLICATION NUMBER: 60/056,845	
47	EARLIER FILING DATE: 1997-08-22	
48	EARLIER APPLICATION NUMBER: 60/056,892	
49	EARLIER FILING DATE: 1997-08-22	
50	EARLIER APPLICATION NUMBER: 60/057,761	
51	EARLIER FILING DATE: 1997-08-22	
52	EARLIER APPLICATION NUMBER: 60/047,595	
53	EARLIER FILING DATE: 1997-05-23	
54	EARLIER APPLICATION NUMBER: 60/047,599	
55	EARLIER FILING DATE: 1997-05-23	
56	EARLIER APPLICATION NUMBER: 60/047,588	
57	EARLIER FILING DATE: 1997-05-23	
58	EARLIER APPLICATION NUMBER: 60/047,585	
59	EARLIER FILING DATE: 1997-05-23	
60	EARLIER APPLICATION NUMBER: 60/047,586	
61	EARLIER FILING DATE: 1997-05-23	
62	EARLIER APPLICATION NUMBER: 60/047,590	
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66	EARLIER APPLICATION NUMBER: 60/047,589	
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68	EARLIER APPLICATION NUMBER: 60/047,593	
69	EARLIER FILING DATE: 1997-05-23	
70	EARLIER APPLICATION NUMBER: 60/047,614	
71	EARLIER FILING DATE: 1997-05-23	
72	EARLIER APPLICATION NUMBER: 60/043,578	
73	EARLIER FILING DATE: 1997-04-11	

EARLIER APPLICATION NUMBER: 60/043,576  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/047,501  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,670  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/056,632  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,664  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,876  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,881  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,909  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,875  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,862  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 9.2%; Score 539.5; DB 4; Length 168;  
Best Local Similarity 59.3%; Pred. No. 4.3e-27;  
Matches 99; Conservative 36; Mismatches 31; Indels 1; Gaps 1;  
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Db 1 MLLSLAAPSIVSVSYLLALLSVTSPIRYKVIQAIQKSDGHPFRAYLESEVISEE 60  
Qy 1058 LVQKYSNSALGVNSTIKELRFLVDLSLKFVLMVFTYVVGALFNGLTLLIALI 1117  
Db 61 AFHYMNAAMVHINRAKLIIRLFLVDLSLKFVLMVFTYVVGALFNGLTLLIALI 120  
Qy 1118 SLFSPVYERHQQIDHYLGANKSVKDMAKIQAKIPGL-KRKAD 1163  
Db 121 LIFSVPVYKQIDHYGVGIARDQTSIVEKIQAKIPGLGIAXKAE 167

RESULT 11  
US-09-270-767-45132  
Sequence 45132, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: Patent in Ver. 2.0  
SEQ ID NO 45132  
LENGTH: 219  
TYPE: PPT  
ORGANISM: Drosophila melanogaster  
US-09-270-767-45132

Query Match 8.9%; Score 522.5; DB 4; Length 219;

Best Local Similarity 47.8%; Pred. No. 7.8e-26;  
Matches 97; Conservative 48; Mismatches 55; Indels 3; Gaps 1;  
Qy 957 EKEDRSLSA---VLSAELSKTSVVDLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAY 1013  
Db 1 EHRERSVGKPNLNRKXSNRLLESLLYWRDVKSGIVFGAGLITLAAISFSVISVPAY 60  
Qy 1014 IALALLSVTSIFRIYKVIQAIQKSDGHPFRAYLESEVISELQKYSNSALGVNST 1073  
Db 61 LSLTLFTGTVAFRIYKSVTQAVKTNEGHPKDYLEDLTLSEKVNQIAGVAHNGF 120  
Qy 1074 IKELRRLFLVDLSLKFVLMVFTYVVGALFNGLTLLIALISLSPVYERHQQV 1133  
Db 121 ISELRLFLVEDIIDSIKFGVILMVFTYVVGAFNGMTLVILAFVSLFTLPKVYNNKQSI 180  
Qy 1134 DHYLGANKSVKDMAKIQAKIP 1156  
Db 181 DTHLDLVRSLKLTETDKIRVAIP 203

RESULT 12  
US-08-700-607-3  
Sequence 3, Application US/08700607  
Patent No. 5858708  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Au-Young, Janice  
APPLICANT: Goli, Surya K.  
APPLICANT: Hillman, Jennifer L.  
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/700,607  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0114 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: THPINOB01  
CLONE: 31870  
US-08-700-607-3

Query Match 8.9%; Score 519; DB 2; Length 241;  
Best Local Similarity 59.4%; Pred. No. 1.5e-25;  
Matches 95; Conservative 33; Mismatches 32; Indels 0; Gaps 0;  
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Db 44 SSCAVHDLIXWRDVKKTGFVFGTLLMLSLAAPSIVSVSYLLALLSVTSPIRYKSV 103





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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:29:05 ; Search time 150.865 Seconds  
(without alignments)  
2960.058 Million cell updates/sec

Title: US-09-830-972-2  
Perfect score: 5848  
Sequence: 1 MEDIDQSLNVSSTDSPPR.....VKDAMAKIQAKIPGLKPKAD 1163

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1714042

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
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21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	5848	100.0	1163	9	US-09-893-348-18
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3	5312.5	90.8	1162	16	US-10-633-423-10
4	5312.5	90.8	1162	16	US-10-427-741-10
5	5307	90.7	1163	15	US-10-267-502-431
6	4403.5	75.3	1192	9	US-09-758-140-6
7	4403.5	75.3	1192	9	US-09-972-599A-6
8	4403.5	75.3	1192	14	US-10-060-036-71
9	4398.5	75.2	1192	9	US-09-789-386-2
10	4398.5	75.2	1192	9	US-09-893-348-23
11	4398.5	75.2	1192	15	US-10-267-502-429
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Sequence 18, Appl					
Sequence 10, Appl					
Sequence 431, App					
Sequence 6, Appli					
Sequence 71, Appl					
Sequence 2, Appli					
Sequence 23, Appl					

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15	4398.5	75.1	1192	15	US-10-408-967-7
16	1513	25.9	379	14	US-10-205-194-164
17	1411.5	24.1	360	9	US-09-893-348-20
18	1411.5	24.1	360	16	US-10-810-653-20
19	1191	20.4	373	9	US-09-789-386-6
20	1191	20.4	373	9	US-09-765-205-6
21	1191	20.4	373	9	US-09-893-348-24
22	1191	20.4	373	14	US-10-060-036-72
23	1191	20.4	373	15	US-10-408-967-8
24	1191	20.4	373	16	US-10-810-653-24
25	1183	20.2	373	17	US-10-347-669-6
26	1183	20.2	373	16	US-10-466-258-4
27	925	15.8	199	9	US-09-893-348-21
28	925	15.8	199	16	US-10-810-653-21
29	908	15.5	199	9	US-09-893-348-25
30	908	15.5	199	15	US-10-660-946-1
31	908	15.5	199	16	US-10-810-653-25
32	901	15.4	199	15	US-10-408-967-9
33	899	15.4	199	11	US-09-378-360A-467
34	888	15.2	289	9	US-09-789-386-4
35	868	14.8	199	16	US-10-466-258-11
36	801	13.7	777	14	US-10-205-219-93
37	792	13.5	780	15	US-10-267-502-432
38	789.5	13.5	776	15	US-10-660-946-5
39	789.5	13.5	776	15	US-10-267-502-430
40	789.5	13.5	776	16	US-10-723-860-1481
41	716.5	12.3	356	15	US-10-660-946-6
42	706.5	12.1	593	15	US-10-108-260A-2892
43	685	11.7	208	15	US-10-660-946-7
44	671	11.5	267	14	US-10-205-194-127
45	671	11.5	267	15	US-10-660-946-8
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Sequence 467, App					
Sequence 4, Appli					
Sequence 11, Appl					
Sequence 93, Appl					
Sequence 432, App					
Sequence 5, Appli					
Sequence 430, App					
Sequence 1481, Ap					
Sequence 6, Appli					
Sequence 2892, Ap					
Sequence 7, Appli					
Sequence 127, App					
Sequence 8, Appli					

ALIGNMENTS

RESULT 1  
US-09-893-348-18  
; Sequence 18, Application US/098933348  
; Patent No. US20020072493A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN, Irun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SCHWARTZ=2A  
; CURRENT APPLICATION NUMBER: US/09/893,348  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 1163  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-09-893-348-18

Query Match 100.0%; Score 5848; DB 9; Length 1163;  
Best Local Similarity 100.0%; Pred. No. 1.9e-256;  
Matches 1163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;







Qy 61 PAAGLSAAVPPAAAAAPLLDFSSDSVPPAPRGPLPAAAPPAEROPSWERSPAAPSLP 120  
Db 60 PAAGLSAAVPP- AAAPLLDFSSDSVPPAPRGPLPAAAPTAPEROPSWERSPAAPSLP 118  
Qy 121 PAAAVLPKLPEDDDPPPPPPPPAGASPLAEPAPSTPAAPKRRGSGVDLTFALP 180  
Db 119 PAAAVLPKLPEDDDPPAR- PPAPAGASPLAEPAPSTPAAPKRRGSGVDLTFALP 176  
Qy 181 AASEPVPSSAEKINDLMEQPCNTVSSGOEPFSSVLLLETAASLSPLSTVSKHGYL 240  
Db 177 AASEPVPSSAEKINDLMEQPCNTVSSGOEPFSSVLLLETAASLSPLSTVSKHGYL 236  
Qy 241 GNLASVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELYSENGSFFKSPKGES 300  
Db 237 GNLASVASTEGTIEETLNEASRELPERATNPFVNRDESAEFVLESENGSFFNGSPKGES 296  
Qy 301 AILVENTKEEVIVRSKOKEDLVCSAALHSPESP-----VKEDRVVSPKMTDIFNMQ 355  
Db 297 AMLVENTKEEVIVRSKOKEDLVCSAALHSPQESPATLTKVVKEDGVMSPEKMTDIFNBMK 356  
Qy 356 MSVAVPREEYADPKPFEQAEVKDITYEGSRDVLAAARANVESKYDRKCLEDSLQKSLGK 415  
Db 357 MSVAVPREEYADPKPFEQAEVKDITYEGSRDVLAAARANMESKYDKCFEDSLQKSHGK 416  
Qy 416 DSEGRNEDASPPSTPEPVKDSRAYITCASPTSATSTANTFPLLEDHTSENKTDKKI 475  
Db 417 DSESENENASPPSTPELVKDSRAYITCDSFTSATESAANI FVLEDTHTSENKTDKKI 476  
Qy 476 BERKAAIITEKTSPTKSNPFLVAVODSEADYVTTDTLSKVTEAAVSNMPEGLTDPDLVQEA 535  
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Qy 536 CESELINEATGKIAYETKVDLVQTSSEATQESLYPTAQICPSFEAEATPSPVLVDI VMEA 595  
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Qy 656 EPESFNAAVQTEAPYISIACDLIKETKLSSTEPSPDFSNYSIAIAKFKSVPEHAELVEDS 715  
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Qy 716 SPSEPVDLFDDSDIPEVPTQEEAVMLMKESLTVSETVTAQHK- EERLSASPOELCKPY 774  
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Qy 835 DSSPIEIIIDPFTFVSAKDDSPKLAKEYTDLVEDSKSEIANIQSGADSLPCLLEPCDLSF 894  
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Db 894 KNTYPKDEAHVSDREFSKRSVSKVPDLLPNVSALESQIEGNTGVKPVLTKEAEKLPS 953  
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Db 954 DTEKEDRLTAVLSAELNKTSDVLLIYWRDIKKTGVYFGASLFLILLSLTVFSTVSTAY 1013  
Qy 1014 IALALLSVTISFRIYKGVIAIQKSDSEGHPPFRAYLESEVAISEELVQKYSNLSALGHVNST 1073  
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Qy 1134 DHYGLANKSVKIDAMAKIQAKIPGLKERKAD 1163  
Db 1134 DHYGLANKSVKIDAMAKIQAKIPGLKERKAE 1163  
RESULT 6  
US-09-758-140-6  
; Sequence 6, Application US/09758140  
; Patent No. US20020012965A1  
; GENERAL INFORMATION:  
; APPLICANT: Strittmatter, Stephen M.  
; TITLE OF INVENTION: No. US20020012965A10 Receptor-Mediated Blockade of Axonal Growth  
; FILE REFERENCE: 44574-5073-US  
; CURRENT APPLICATION NUMBER: US/09/758,140  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/175,707  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: US 60/207,366  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/236,378  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-758-140-6  
Query Match 75.3%; Score 4403.5; DB 9; Length 1192;  
Best Local Similarity 75.9%; Pred. No. 4.8e-191;  
Matches 909; Conservative 104; Mismatches 145; Indels 39; Gaps 20;  
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Db 1 MEDLDQSPVLSVSS--DSPPRPQAPKYOFTVREPEDEE-EEEEEEDEDEDEDELEVLERK 58  
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Db 59 PAAGLSAAVPTAPAAAGAPLMDFGNDVFPAPRGPLPAAAPVAPERQSPWDPSPVSTVTP 118  
Qy 116 APSLPPAAAVLPKLPEDDDPPPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166  
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Qy 167 RG-SGSDVDELTPALPAASEBVIPISSAEKINDLMEQPCNTVSSGOEDPFSVLLETAASLPS 225  
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Qy 286 SEMGSSFKGSPKGESAILVENTKEEVIVRSKOKED-LVCSAALHSPQESVPG-----KED 339  
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Qy 340 RVVSPKMTDIFNEMQMSVAVPREEYADPKPFEQAEVKDITYEGSRDVLAA-----RANV 395  
Db 358 EYVSSSEKAKDSFNEKRVAVAPMREEYADPKPFEVWVEVKDSKEDS-DMLAAGKIKESNL 416  
Qy 396 ESKVDRLKCLSDLSLEOKSLGKDSGRNEDASFPSTPEPVKDSRAYITCASFT-SATESSTT 454  
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Qy 455 ANTFFPLEDHTSENKTDKKIEERKAAQIITEK-TSPKTSNPFVAVODSEADYVTTDTLS 513  
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Qy 514 KVTEAAVSNMPEGLTDPDLVQEAACESELNEATGKIAYETKVDLVQTSSEATQESLYPTAQOL 573  
Db 537 KVTEEVVANMPEGLTDPDLVQEAACESELNEVTGKIAYETKMDLVQTSSEVWQESLYPAAQL 596

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 DB 656 PPHYEAMSVLKVGSGIKKEIKEPENINAAQVETAPYISACDLIKETKLSAPAPDF 715  
 QY 693 SNYSEIAKFEKSVPEHAELVEDSSPESPVDFSDDSIPEVPQTOEEAVMLKESLITEVS 752  
 DB 716 SDYSEMAKVEQVPDHSSELVEDSSPESPVDFSDDSIPDVQKQDETVMVKESLTETS 775  
 QY 753 -ETVAQHK-EERLSASPOELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISIQMBEF 809  
 DB 776 FESMIEYENKEKLSALPPEGKPYLESFKLSLNTKDTLLPDEVSTLSKKEKIPLOMBEL 835  
 QY 810 NTAIYNSNDLLSKEDKIKESSTFSDSPIEIIDFPPTFVSAKDD-PSKLAKETDLEVS 868  
 DB 836 STAVYNSNDLFTSKAQIRETETTFSDSPIEIIDFPPTLISKTDSFKLAREYTDLEVS 895  
 QY 869 DKSEIANIQSGADSLPCLPELPCDLGPKNTYPK--DEVHVSDFSENRSVSKASISPSNV 926  
 DB 896 HKSEIANAPDGAGSLPCTELPHDLNLKNTQPKVEEKISFSDDFSKNGSATS KVL LPPDV 955  
 QY 927 SALEPQTEMGSIKSVKSLTKAEKKLPSTTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK 986  
 DB 956 SALATAQAEIESIVKPKVLKAEKKLPSTTEKEDRSPSAIFSAELSKTSVVDLLYWRDIK 1015  
 QY 987 KTVGVFGASLFLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIOAQKSDGHPFRA 1046  
 DB 1016 KTVGVFGASLFLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIOAQKSDGHPFRA 1075  
 QY 1047 YLESEVAISEELVQKYSNALSALGHVNSTIKELRRLFLVDDLVDLSLKFVAVLMMVFTYVGALF 1106  
 DB 1076 YLESEVAISEELVQKYSNALSALGHVNSTIKELRRLFLVDDLVDLSLKFVAVLMMVFTYVGALF 1135  
 QY 1107 NGTLTLLIALISLFSIPVIYERHQQIDHYLGANKSVKDAKIOAKIPGLKRAK 1163  
 DB 1136 NGTLTLLIALISLFSIPVIYERHQQIDHYLGANKSVKDAKIOAKIPGLKRAE 1192  
 RESULT 7  
 US-09-972-599A-6  
 ; Sequence 6, Application US/09972599A  
 ; Patent No. US20020077295A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: STRITTMATTER, STEPHEN M.  
 ; TITLE OF INVENTION: NOCO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH  
 ; FILE REFERENCE: C077 CJP US  
 ; CURRENT APPLICATION NUMBER: US/09/972,599A  
 ; CURRENT FILING DATE: 2001-10-06  
 ; PRIOR APPLICATION NUMBER: PCT/US01/01041  
 ; PRIOR FILING DATE: 2001-01-12  
 ; PRIOR APPLICATION NUMBER: 09/758,140  
 ; PRIOR FILING DATE: 2001-01-12  
 ; PRIOR APPLICATION NUMBER: 60/236,378  
 ; PRIOR FILING DATE: 2000-09-29  
 ; PRIOR APPLICATION NUMBER: 60/207,366  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: 60/175,707  
 ; PRIOR FILING DATE: 2000-01-12  
 ; NUMBER OF SEQ ID NOS: 57  
 ; SOFTWARE: Patent in Ver. 2.1  
 ; SEQ ID NO 6  
 ; LENGTH: 1192  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-972-599A-6

Query Match 75.3%; Score 4403.5; DB 9; Length 1192;  
 Best Local Similarity 75.9%; Pred. No. 4.8e-191;  
 Matches 909; Conservative 104; Mismatches 145; Indels 39; Gaps 20;

QY 1 MEDIDQSLVSSSTDSPPRPPAPFKYQVTTPEDEDEDEDEDEDEDEDEDEDEDELEVLERK 60  
 DB 1 MEDLDQSLVSS--DSPRPQPAFKYQVREPEDEE-EEEEEEDEDEDEDELEVLERK 58  
 QY 61 PAAAGLSAAVPP--PAAAAPLIDFSDSVPPAPRGRPLPAAPPAAPRQSWERSPAA---P 115  
 DB 59 PAAAGLSAAVPTAPPAAGAPLMDFGNDFVPPAPRGRPLPAAPPVAPRQSWDSFVSSVTP 118  
 QY 116 APSLPPAAVLPKLPDEDEPPARPPPPAGASPLAE-----PAAPESTPAAPKR 166  
 DB 119 APSLPLAAVSPKLPDEDEPPARPPPPASVSPAEPVMTTPPAPAPAAPSTPAAPKR 178  
 QY 167 RG-SSVDETLFPALPAASEPVISSAEKIMOLMEOPGNTVSSGQDDFPVSLLETAASLPS 225  
 DB 179 RGSQSGVDETLFPALPAASEPVISSAEKIMOLMEOPGNTI SAGQDDFPVSLLETAASLPS 237  
 QY 236 LSPILSTVFKHGYLGNLSAVSSSEGTTEETLNEASKELPERATNPPVNRDLAEFSELEY 285  
 DB 238 LSPLSAASFKEHYLGNLSTVLPTEGTLOENVSEASKSEKAKTLLIDRLDTEFSELEY 297  
 QY 286 SEMGSPFKGSPKGESAILVENTKEEVIYRSKDKED-LVCSAALHSPQSPVPG-----KED 339  
 DB 298 SEMGSPSVSPKAEASAVIANPREBII VKNKDEEKLVSNNILHNQOBLPTALTALTKLVKED 357  
 QY 340 RVVSPKTMDFENOMQSVVAPVREYADFKPFQEAWEVKOTYEGSRDLAA---RANV 395  
 DB 358 EYVSEKAKDFNEKRVAPVAPVREYADFKPFERVWEVKOSKEDS-DMLAAGGKIESNL 416  
 QY 396 ESKVDRKCLEDSLEQSLGKDSSEGNEDASPPSTPEPVKDSRAYITCASFT-SATESPT 454  
 DB 417 ESKVKKCFADSLQNTHEKSESNDSTSPSTPEGIDKDRSGAVITCAPFNPAATESA 476  
 QY 455 ANTPFLLEDHTSENKTDKKEERKAAQIITEK-TSPKTSNPFVAVQSEADYVTTDTLS 513  
 DB 477 TNIPFLGDPSTSENKTDKKEEKAQIVTEKNTSTKTSNPFVAAQDSEYDVTYVTTDNL 536  
 QY 514 KVTAAVSNMPEGLTPDLVQEAQSEFNEACTKIAYETKVDTLQVTSIAOESLPTAQL 573  
 DB 537 KVTAEVAMNPEGLTPDLVQEAQSEFNEACTKIAYETKMDLVQTSSEVQESLPPAAQL 596  
 QY 574 CPSFEAEATPSVLPDIWMEAPLNSLLPSAGASVVPQSVSPLEAPPVSVYSIKLEPEN 633  
 DB 597 CPSFESEATPSVLPDIWMEAPLNSAVPSAGASVIQSPSSPLEA-SSVNYESI KHEPEN 655  
 QY 634 PPHYEAMNVALKAL-GTKEGIKEPESFNAAQVETAPYISACDLIKETKLSSTPSPDF 692  
 DB 656 PPHYEAMSVLKVGSGIKKEIKEPENINAAQVETAPYISACDLIKETKLSAPAPDF 715  
 QY 693 SNYSEIAKFEKSVPEHAELVEDSSPESPVDFSDDSIPEVPQTOEEAVMLKESLITEVS 752  
 DB 716 SDYSEMAKVEQVPDHSSELVEDSSPESPVDFSDDSIPDVQKQDETVMVKESLTETS 775  
 QY 753 -ETVAQHK-EERLSASPOELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISIQMBEF 809  
 DB 776 FESMIEYENKEKLSALPPEGKPYLESFKLSLNTKDTLLPDEVSTLSKKEKIPLOMBEL 835  
 QY 810 NTAIYNSNDLLSKEDKIKESSTFSDSPIEIIDFPPTFVSAKDD-PSKLAKETDLEVS 868  
 DB 836 STAVYNSNDLFTSKAQIRETETTFSDSPIEIIDFPPTLISKTDSFKLAREYTDLEVS 895  
 QY 869 DKSEIANIQSGADSLPCLPELPCDLGPKNTYPK--DEVHVSDFSENRSVSKASISPSNV 926  
 DB 896 HKSEIANAPDGAGSLPCTELPHDLNLKNTQPKVEEKISFSDDFSKNGSATS KVL LPPDV 955  
 QY 927 SALEPQTEMGSIKSVKSLTKAEKKLPSTTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK 986  
 DB 956 SALATAQAEIESIVKPKVLKAEKKLPSTTEKEDRSPSAIFSAELSKTSVVDLLYWRDIK 1015  
 QY 987 KTVGVFGASLFLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIOAQKSDGHPFRA 1046  
 DB 1016 KTVGVFGASLFLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIOAQKSDGHPFRA 1075  
 QY 1047 YLESEVAISEELVQKYSNALSALGHVNSTIKELRRLFLVDDLVDLSLKFVAVLMMVFTYVGALF 1106

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Db 1076 YLESEVAISELVQKYSNLSALGHVNTCTIKELRRLFLVDDLVLKFAVLMVFTVVGALF 1135
Qy 1107 NGLTLLILALISLSPVPIYERHQQVQIDHYLGLANKSVKDMAKIOAKIPGLKRAKAD 1163
Db 1136 NGLTLLILALISLSPVPIYERHQQVQIDHYLGLANKSVKDMAKIOAKIPGLKRAE 1192

RESULT 8
US-10-060-036-71
; Sequence 71, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Daxin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060.036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-036-71

Query Match 75.3%; Score 4403.5; DB 14; Length 1192;
Best Local Similarity 75.9%; Pred. No. 4.8e-191;
Matches 909; Conservative 104; Mismatches 145; Indels 39; Gaps 20;

Qy 1 MEDIDQSLVSSSTDSPRRPPAFKQYQVTPEDDEDEDEDEDEDEDEDEDEDEDELEEVLERK 60
Db 1 MEDIDQSLVSS--DSPPRPQAFKQYQVREPDEE--EEEEEEDEDEDEDELEEVLERK 58

Qy 61 PAAGLSAAVPP--PAAAPLIDFSDSVPPAPRGLPAAAPPAAPRQSWERSPAA---P 115
Db 59 PAAGLSAAVPTAAGALMDFGNDFVPPAPRGLPAAAPVAPRQSPMDPSVSTVP 118

Qy 116 APSLPPAAVLPSKLPEDDEPPARPPPPAGASPLAE-----PAAPESTPAAPKR 166
Db 119 APSLPSAAVSPSKLPEDDEPPARPPPPASVSPQAEPPVTPPAPAPAAPSTPAAPKR 178

Qy 167 RG-SGSDVDTLFAALPAASEPIVPSAEKIMDLMEQPGNTVSSGOEDFPFVILLETAAALPS 225
Db 179 RGSAGSDVDTLFAALPAASEPIVIRSSAEN-MDLKEQPGNTISAGQEDFPFVILLETAAALPS 237

Qy 226 LSPILSTVFKKHGYLGNLSAVSSSEGTTEETINASKELPRANVFNVRDLAEFSELEY 285
Db 238 LSPLSAASFKEHYLGNLSTVLTPTGTLQENVSEASKEVSEKAKTLAIDRLDTFSELEY 297

Qy 286 SEMSSFKGSPKGSAILVENTKEVIVRSKDED-LVCSAALHSPQESPVG-----KED 339
Db 298 SEMSSFSVSPKASAVIANPREIIVKNDEBEKLVNNILNHQBELFTALTKLVKED 357

Qy 340 RVWPEKTMDFNEMQMSVAVPVEEYADFPFQAEVMDKTYEGSRDLVLA-----RANV 395
Db 358 EVVSEKAKDSFNEKRVAVEAPMEEYADFPFVVEVMDKSKEDS-DMLAAGKIESNL 416

Qy 396 ESKVDRKCLSDLEQKSLGKDSSEGNEDASFPSTPEPVKDSRAYITCASFT-SATESTT 454
Db 417 ESKVDKCFADSLQETHKDSSESNDDTSFPSTPEGIKDRSGAYITCAPNPAATESIA 476

Qy 455 ANTPELLDHTSENKTKDEKKLEERKAOIITEK-TSPKTSNPLFVAVDSEADYVTTTSL 513
Db 477 TNIFLLGDPSTSENKTKDEKKLEERKAOIVTEKNTSTKTSNPLFVAAQDSEYDVTNLT 536

Qy 514 KVTEAAVSNMPEGLTPDLVQACESELNEATGTIAVETKVDLVQTSIAIQESLYPTAQL 573
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Db 537 KYTEEVANMEGLTPDLVQACESELNEVTGTIAVETKVDLVQTSSEVMQESLYPAAQL 596
Qy 574 CPSPFEAEATSPVLPDI VMEAPLNSLLPSAGASVQSPSPLEAPPVSVDSIKLEPEN 633
Db 597 CPSPFESEATSPVLPDI VMEAPLNSAVPSAGASVIOFSSSPLEA-SSVNTYESIKHEPEN 655
Qy 634 PPYEEMANVAKAL-GTKEGKEPESFNAAVQTEAPYISIAICDLIKETKLSLSTEPSPDF 692
Db 656 PPYEEMAMSVLSKKVSGIKKEIPENINAAQTEAPYISIAICDLIKETKLSABPAPDF 715
Qy 693 SNYSEIAKFEKSPVEHAELVEDSSPEPVDLFDSDSIPEVPTQEEAVMLMKESLSTVS 752
Db 716 SDYSEMAKVEQVPDHSSELVEDSSPDSEPDVLDSDSIQVQKQDETVMVLKESLSTVS 775
Qy 753 -ETVAQHK-BERLSASQBELGKPYLESFQPNLHSTKOA-ASNDIPTLTKKKISLQMBEF 809
Db 776 FESMIEYENKELKALPPEGKPYLESFKLSLNDTKDTLLPDEVSTLSKKEKIPLOMBEL 835
Qy 810 NTALYSNDDLLSSKEDKIKESFESDSSPTEIIDFFTFVSXKDDSPKLAKEYTDLREVS 868
Db 836 STAVYSNDDLLFISKEAQIRFETEFSDSPTEIIDFFTLISSKTSFKLARETTDLREVS 895
Qy 869 DKSEIANIQSGADSLPCLDELPCDLSPKNIYPK--DEVHVSDEFSENSSSVKASISPSNV 926
Db 896 HKSEIANAPDAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDV 955
Qy 927 SALEPQTEMGSIKVSLSLTKEAEKKLPDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK 986
Db 956 SALATQAEIESIVKPKVLVKEAEKKLPDTEKEDRSLSAELSKTSVVDLLYWRDIK 1015
Qy 987 KTGWFVCGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDSGHPRA 1046
Db 1016 KTGWFVCGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDSGHPRA 1075
Qy 1047 YLESEVAISELVQKYSNLSALGHVNTCTIKELRRLFLVDDLVLKFAVLMVFTVVGALF 1106
Db 1076 YLESEVAISELVQKYSNLSALGHVNTCTIKELRRLFLVDDLVLKFAVLMVFTVVGALF 1135
Qy 1107 NGLTLLILALISLSPVPIYERHQQVQIDHYLGLANKSVKDMAKIOAKIPGLKRAKAD 1163
Db 1136 NGLTLLILALISLSPVPIYERHQQVQIDHYLGLANKSVKDMAKIOAKIPGLKRAE 1192

RESULT 9
US-09-789-386-2
; Sequence 2, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: MICHALOVICH, DAVID
; APPLICANT: PRINJHA, RABINDER KUMAR
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-789-386-2

Query Match 75.2%; Score 4398.5; DB 9; Length 1192;
Best Local Similarity 75.9%; Pred. No. 8.1e-191;
Matches 908; Conservative 104; Mismatches 146; Indels 39; Gaps 20;
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Db 1076 YLESEVAISELVQKYSNAGLHVNCITIKELRRFLVDDLSLKPFAVLMMVTVYVGLF 1135
QY 1107 NGTLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAWAKIOAKIPGLKRKAD 1163
Db 1136 NGTLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAWAKIOAKIPGLKRKAE 1192

RESULT 12
US-10-327-213-9
; Sequence 9, Application US/10327213
; Publication No. US20040121341A1
; GENERAL INFORMATION:
; APPLICANT: FILBIN, MARIE T.
; APPLICANT: DOMENICONI, MARCO
; APPLICANT: CAO, ZIXUAN
; TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)
; TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION
; FILE REFERENCE: CUNY/003
; CURRENT APPLICATION NUMBER: US/10/327,213
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-327-213-9

Query Match 75.2%; Score 4398.5; DB 16; Length 1192;
Best Local Similarity 75.9%; Pred. No. 8.1e-191;
Matches 908; Conservative 104; Mismatches 146; Indels 39; Gaps 20;

QY 1 MEDIDQSSLVSSSTGPPPPPAFKYQFVTEPEDEDEDEDEDEDEDEDEDEDEDELEVELEK 60
Db 1 MEDLDQSLVSSS-DSPRPQPAFKYQFVREPEDEE-EEEEEEDEDEDEDELEVELEK 58
QY 61 PAAGLSAAVPP--PAAALPLDFSSDVPAPRGPLPAAPPAAPAPQPSWERSPAA---P 115
Db 59 PAAGLSAAVPTAPAGAPLMDGNDVFPAPRGPLPAAPPAAPQPSWDFSPVSTVP 118
QY 116 APSLPPAAAVLPSKLPEDDEPPAPPPPPAGASPLAE-----PAAPSTPAAPKR 166
Db 119 APSPLSAAVSPSKLPEDDEPPAPPPPPPPASVPOAEVPTPAPPAAPSTPAAPKR 178
QY 167 RG-SGSVDETLPAALPAASEPVIPISSAEKIMDLMEQPGNTVSSQGEDFPVSLLETAASLPS 225
Db 179 RGSQSGVDETLPAALPAASEPVIPISSAEN-MDLKEQPGNTISAGQEDFPVSLLETAASLPS 237
QY 226 LSPSLTVSKHGYLGNLSAVSSSEGTIBETLNEASKELPERATNPFVNRDLAFSELEY 285
Db 238 LSPLSAASFKEHYLGNLSTVLTEGLQENVSEASKEYSEKAKTLLIDRLDTEFSELEY 297
QY 286 SEMGSSFKGSPKGESAILVENTKEEVIIVRSKDED-LVCSAALHSPOESVPG-----KED 339
Db 298 SEMGSSFSVSPKAEAVIVANPREELIVKNKDEEKLVSNNILHNOQELPTALTUKVKED 357
QY 340 RVVSPKTDIFNEMQMSVVAVPREEYADFKPFEQAWVEVKDITYEGSRDVLAA-----RANV 395
Db 358 EVVSESEKAKDSFNEKRVAVEAPREYADFKPFEVWEVKDSKEDS-DMLAAGGKTESNL 416
QY 396 ESKVDKRLCDSLEQSLKQSDGRNEDASFPSTPEPVKDSRPAYITCASFT-SATESST 454
Db 417 ESKVDKRCFADSLQNTNHEKSSSNDTTFSPSTPEGIDKDPGAYITCAPFNPAAATESIA 476
QY 455 ANTFPLEDHTSNKTKDEKKIEBKQAITEK-TSPKTSNPFVLVAVQDSEADVVTVDTL 513
Db 477 TNIFPLLGDTSNKTKDEKKIEBKQAIVTEKNTSTKTSNPFVLAQDSEDTVITDNL 536
QY 514 KVTEAAVSNMPEGLTDPDLVQAECESELNEATGKIAYETKVDLVQVSEAIQESLYTAQL 573
Db 537 KVTEEVVANNPEGLTDPDLVQAECESELNEVTGKIAYETKMDLVQVSEVQESLYPAAQL 596
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QY 574 CPSFEAEATSPVLPDVIWMEAPLNSLLPSAGASVQPSVSPLEAPPVPPVSDYSIKLEPN 633
Db 597 CPSFESEATSPVLPDVIWMEAPLNSAVPSAGASVQPSSSPLEA-SSVNYESIKEHPN 655
QY 634 PPPEEAMNVALKAL-GTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSSTPSPDF 692
Db 656 PPPEEAMSVSLKKVSGIKKEIKEPENINAAALQETEAPYISIACDLIKETKLSASPADF 715
QY 693 SNYSIAKPEKSVPEHAELVEDSSPESPVDLFSDDSIPDVQTOEEAVMLKESLITEVS 752
Db 716 SDYSEMAKVEQVPDHSSELVSSPDSPVDLFSDDSIIPDVQKQDETVMVKESLITETS 775
QY 753 -ETVAQHK-EERLSASPOELGKPYLESFQPNLHSTKDA-ASNDITLTKKEKISLQMBEF 809
Db 776 FESMIEYENKEKLSALPPEGGKPYLESFKLSLNDTKOTLLPDEVSTLKSKEKIPLOMEEL 835
QY 810 NTAYISNDDLLSSKEDKIKESFTFSDSPIELIIDEFTFVSAKODS-PKLAKEYTDLVS 868
Db 836 STAVYSNDDLFISKQAQIRETETFSDDSPIELIIDEFTLISSTKDSFKLAKEYTDLVS 895
QY 869 DKSEIANIQTSGADSLPCLELPCDLSFKNIYPK--DEVHVSDBFSENRSVSKASISPSNV 926
Db 896 HKSEIANAPDAGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDV 955
QY 927 SALEPQTEMGSIKVSLSLTKEAEKLPSTDEKEDSLSAVLSAELSKTSVVDLLYWRDIK 986
Db 956 SALATQAEIESIVKPKVLKAEKLPSTDEKEDSPSAIFSAELSKTSVVDLLYWRDIK 1015
QY 987 KTGVSFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRA 1046
Db 1016 KTGVSFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRA 1075
QY 1047 YLESEVAISEELVQKYSNAGLHVNCITIKELRRFLVDDLSLKPFAVLMMVTVYVGLF 1106
Db 1076 YLESEVAISEELVQKYSNAGLHVNCITIKELRRFLVDDLSLKPFAVLMMVTVYVGLF 1135
QY 1107 NGTLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAWAKIOAKIPGLKRKAD 1163
Db 1136 NGTLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAWAKIOAKIPGLKRKAE 1192

RESULT 13
US-10-466-258-9
; Sequence 9, Application US/10466258
; Publication No. US20040132096A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: ASSAY
; FILE REFERENCE: P80966 GCW
; CURRENT APPLICATION NUMBER: US/10/466,258
; CURRENT FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-466-258-9

Query Match 75.2%; Score 4398.5; DB 16; Length 1192;
Best Local Similarity 75.9%; Pred. No. 8.1e-191;
Matches 908; Conservative 104; Mismatches 146; Indels 39; Gaps 20;

QY 1 MEDIDQSSLVSSSTGPPPPPAFKYQFVTEPEDEDEDEDEDEDEDEDEDEDEDELEVELEK 60
Db 1 MEDLDQSLVSSS-DSPRPQPAFKYQFVREPEDEE-EEEEEEDEDEDEDELEVELEK 58
QY 61 PAAGLSAAVPP--PAAALPLDFSSDVPAPRGPLPAAPPAAPAPQPSWERSPAA---P 115
Db 59 PAAGLSAAVPTAPAGAPLMDGNDVFPAPRGPLPAAPPAAPQPSWDFSPVSTVP 118
QY 116 APSLPPAAAVLPSKLPEDDEPPAPPPPPAGASPLAE-----PAAPSTPAAPKR 166
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QY 574 CPSFEAEATPSPVLPDIYMEAPLNSLLPSAGASVQPSVPLEAPPVVSYSIKLEPEN 633
DB 597 CPSFEAEATPSPVLPDIYMEAPLNSVQPSVPLEAPPVVSYSIKLEPEN 655
QY 634 PPPEEAMNVALKAL-GTKEGKEPESFNAVQETAPYISACOLIKETKLTSPSPDF 692
DB 656 PPPEEAMNVALKAL-GTKEGKEPESFNAVQETAPYISACOLIKETKLTSPSPDF 715
QY 693 SNYSIAKFEKSPVPEHAEVLVEDSSPESBVDLFSDDSIPEVQTOBEAAMKESLTVS 752
DB 716 SDYSEMAKVEQVPDHSSELVEDSSPESBVDLFSDDSIPEVQTOBEAAMKESLTVS 775
QY 753 -ETVAQHK- EERLSASPOELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISIQMEEF 809
DB 776 FESMIEYENKEKLSALPPEGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISIQMEEF 835
QY 810 NTAIYNSNDLLSSKEDKIKESLTVSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSGDEHPRA 868
DB 836 STAVYNSNDLLFISKEAQIRETETFSDDSPIEIDFPTLISKTSFSLAREYTDLEVS 895
QY 869 DKSEIANIOSGADSLPCLPELPCDLSFKNIYPK-DEVHVSDFSENRSVSKASISPSNV 926
DB 896 HKSEIANAPDAGSLPCTELPHDLNLSKNIPQVKEKISFSDDFSKNGSATSKVLLLPDV 955
QY 927 SALEPOTENGSIYKSKLSLKEAEKLPSTDEKDRSLSAVLSAELSKTSVVDLLYWRDIK 986
DB 956 SALATQAEIESIVKPKVLVKEAEKLPSTDEKDRSPSAIFSAELSKTSVVDLLYWRDIK 1015
QY 987 KTVGVFASLFLLSLTVSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSGDEHPRA 1046
DB 1016 KTVGVFASLFLLSLTVSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSGDEHPRA 1075
QY 1047 YLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGALF 1106
DB 1076 YLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGALF 1135
QY 1107 NGLTLLILALISLFSIPVIYERHQVQIDHYGLANKSVKDMAKIQAOKIPGLKRKAD 1163
DB 1136 NGLTLLILALISLFSIPVIYERHQVQIDHYGLANKSVKDMAKIQAOKIPGLKRKAE 1192

RESULT 15
US-10-408-967-7
; Sequence 7, Application US/10408967
; Publication No. US20040063161A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn Company
; APPLICANT: Yan, Riqiang
; APPLICANT: Lu, Yifeng
; TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease
; FILE REFERENCE: 00925
; CURRENT APPLICATION NUMBER: US/10/408,967
; CURRENT FILING DATE: 2003-04-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-967-7

Query Match 75.1%; Score 4389.5; DB 15; Length 1192;
Best Local Similarity 75.8%; Pred. No. 2.1e-190;
Matches 907; Conservative 104; Mismatches 147; Indels 39; Gaps 20;

QY 1 MEDIDOSLVSTSDSPSPAPAFKYQVTEDEDEDEDEDEDEDEDEDEDEDEDELEVLERK 60
DB 1 MEDIDOSLVSTSDSPSPAPAFKYQVTEDEDEDEDEDEDEDEDEDEDEDEDELEVLERK 58
QY 61 PAAGLSAAAVP--PAAAAALLDSSDVPVPPAPRGPLPAAPPAAPRQPSWERSPAA--P 115
DB 59 PAAGLSAAAVP--PAAAAALLDSSDVPVPPAPRGPLPAAPPAAPRQPSWERSPAA--P 115
```

```
QY 116 APSLPAAAVLPSKLPEDDEPPAPPPPPPPAGASPLAE-----PAAPSTPAAPKR 166
DB 119 APSLPAAAVLPSKLPEDDEPPAPPPPPPPPPAGASPLAE-----PAAPSTPAAPKR 178
QY 167 RG-SSVDETLFPALPAASEPVPSSAEKIMDLMEOPGNTVSSGOEDFSSVLLETASLPS 225
DB 179 RGSSGVSDETLFPALPAASEPVPSSAEKIMDLMEOPGNTVSSGOEDFSSVLLETASLPS 237
QY 236 LSPLSTVTFKHYGLNLSAVSSSGCTTTEETLINEASKELPERATNPFVNRDILAESELEY 285
DB 238 LSPLSAAAFKHEYLGNLSVLPTEGTLQENVSEAKSEKAKTLLIDRLDTESELEY 297
QY 286 SEMGSSFKGSPKGESAILVENTKEBIVRSKDKED-LVCSAALHSPQSPVPG-----KED 339
DB 298 SEMGSSFKGSPKGESAILVENTKEBIVRSKDKED-LVCSAALHSPQSPVPG-----KED 357
QY 340 RVVSPKTMDFINEMQMSVAVPVEEYADFKPPEQAEWKDTYEGSRDVLAA----RANV 395
DB 358 EYVSEKAKDSFKNEKRVAVEAPMREYADFKPPEQAEWKDTYEGSRDVLAA----RANV 416
QY 396 ESKVDRKCLDESLEQSLGKDSSEGRNEDASPPSTPEPVKDSRAYITCASFT-SATESST 454
DB 417 ESKVDRKCLDESLEQSLGKDSSEGRNEDASPPSTPEPVKDSRAYITCASFT-SATESST 476
QY 455 ANTPPLLEDHTSENKTDKKEIKERKAAQIITEK-TSPKTSNPFPLVAVQSEADYVTTDLIS 513
DB 477 TNIPFLGDPSTSENKTDKKEIKERKAAQIITEK-TSPKTSNPFPLVAVQSEADYVTTDLIS 536
QY 514 KVTAAVSNMPEGLTPDLVQACESELNEATGTIAYETKVDLVOTSAIQSLPPTAQL 573
DB 537 KVTAAVSNMPEGLTPDLVQACESELNEATGTIAYETKVDLVOTSAIQSLPPTAQL 596
QY 574 CPSFEAEATPSPVLPDIYMEAPLNSLLPSAGASVQPSVPLEAPPVVSYSIKLEPEN 633
DB 597 CPSFEAEATPSPVLPDIYMEAPLNSVQPSVPLEAPPVVSYSIKLEPEN 655
QY 634 PPPEEAMNVALKAL-GTKEGKEPESFNAVQETAPYISACOLIKETKLTSPSPDF 692
DB 656 PPPEEAMNVALKAL-GTKEGKEPESFNAVQETAPYISACOLIKETKLTSPSPDF 715
QY 693 SNYSIAKFEKSPVPEHAEVLVEDSSPESBVDLFSDDSIPEVQTOBEAAMKESLTVS 752
DB 716 SDYSEMAKVEQVPDHSSELVEDSSPESBVDLFSDDSIPEVQTOBEAAMKESLTVS 775
QY 753 -ETVAQHK- EERLSASPOELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISIQMEEF 809
DB 776 FESMIEYENKEKLSALPPEGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISIQMEEF 835
QY 810 NTAIYNSNDLLSSKEDKIKESLTVSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSGDEHPRA 868
DB 836 STAVYNSNDLLFISKEAQIRETETFSDDSPIEIDFPTLISKTSFSLAREYTDLEVS 895
QY 869 DKSEIANIOSGADSLPCLPELPCDLSFKNIYPK-DEVHVSDFSENRSVSKASISPSNV 926
DB 896 HKSEIANAPDAGSLPCTELPHDLNLSKNIPQVKEKISFSDDFSKNGSATSKVLLLPDV 955
QY 927 SALEPOTENGSIYKSKLSLKEAEKLPSTDEKDRSLSAVLSAELSKTSVVDLLYWRDIK 986
DB 956 SALATQAEIESIVKPKVLVKEAEKLPSTDEKDRSPSAIFSAELSKTSVVDLLYWRDIK 1015
QY 987 KTVGVFASLFLLSLTVSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSGDEHPRA 1046
DB 1016 KTVGVFASLFLLSLTVSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSGDEHPRA 1075
QY 1047 YLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGALF 1106
DB 1076 YLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMMVFTYVGALF 1135
QY 1107 NGLTLLILALISLFSIPVIYERHQVQIDHYGLANKSVKDMAKIQAOKIPGLKRKAD 1163
DB 1136 NGLTLLILALISLFSIPVIYERHQVQIDHYGLANKSVKDMAKIQAOKIPGLKRKAE 1192
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Search completed: June 16, 2005, 13:03:58  
Job time : 156.865 secs

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**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 12:55:32 ; Search time 34.9713 seconds  
(without alignments)  
3199.767 Million cell updates/sec

Title: US-09-830-972-2

Perfect score: 5848

Sequence: 1 MEDIDQSLVSSSTDSPPR.....VKDAMAKIQAKIPGLKERAD 1163

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	789.5	13.5	776	2 A46583	neuroendocrine-spe
2	685	11.7	208	2 I60904	neuroendocrine-spe
3	671	11.5	267	2 A60021	tropomyosin-relate
4	517	8.8	2484	2 T26216	hypothetical prote
5	503.5	8.6	2607	2 T26215	hypothetical prote
6	328.5	5.6	5327	2 T13564	microtubule-associ
7	322	5.5	7962	2 I38346	elastic titin - hu
8	320	5.5	222	2 T26213	hypothetical prote
9	304.5	5.2	873	2 A47283	calphotin - fruit
10	302.5	5.2	1829	2 T24583	hypothetical prote
11	295.5	5.1	865	2 A47282	calcium-binding pr
12	292	5.0	3507	2 T34513	hypothetical prote
13	291.5	5.0	2364	2 A56577	microtubule-associ
14	288.5	4.9	971	2 T19431	hypothetical prote
15	284	4.9	2464	1 QRMSP1	microtubule-associ
16	281	4.8	3488	2 T34418	hypothetical prote
17	279.5	4.8	1262	2 T22523	hypothetical prote
18	277	4.7	1621	2 A92255	hypothetical prote
19	275.5	4.7	3924	2 S37431	ankyrin 2, neurona
20	275	4.7	1299	2 T47182	hypothetical prote
21	273.5	4.7	1029	2 T30351	mucin-like protein
22	273.5	4.7	1274	2 T16251	hypothetical prote
23	273	4.7	1558	2 B71603	RESA-H3 antigen pF
24	272.5	4.7	3534	2 T42567	tegument protein 2
25	270	4.6	1230	2 T22458	hypothetical prote
26	269.5	4.6	2187	2 T30826	nascent polypeptid
27	267	4.6	1684	2 JWO057	gravin - human
28	265.5	4.5	1828	2 A40115	microtubule-associ
29	263	4.5	1825	2 S13507	microtubule-associ

ALIGNMENTS

RESULT 1

A46583

neuroendocrine-specific protein, splice form A - human

N:Contains: neuroendocrine-specific protein, splice form B

C:Species: Homo sapiens (man)

C:Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 09-Jul-2004

C:Accession: A46583; I60903

R:Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; J.

J. Biol. Chem. 269, 13439-13447, 1993

A:Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spe

A:Reference number: A46583; MUID:93293865; PMID:7685762

A:Accession: A46583

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-776 <ROE1>

A:Cross-references: UNIPROT:Q16799; GB:L10333; NID:G307306; PIDN:AAA59950.1; PID:G307307

A:Accession: I60903

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 421-776 <ROE2>

A:Cross-references: GB:L10334; NID:G307308; PIDN:AAA59951.1; PID:G307309

C:Genetics:

A:Gene: GDB:RTN1; NSP

A:Cross-references: GDB:203968; OMIM:600865

A:Map position: 14q21-14q22

Query Match 13.5%; Score 789.5; DB 2; Length 776;

Best Local Similarity 31.2%; Pred. No. 8.5e-25;

Matches 243; Conservative 115; Mismatches 252; Indels 169; Gaps 28;

Qy	487	TSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVNNMPEGLTPDLVQACSELSNEATGT	546
Db	65	SGPARQSP--VAMETASTAGVSSAMDHFTSTTKDGE-----SCYSLI-----S	110
Qy	547	KIAYETKVDLVQVSEAIQ-ESLYPTAQLCPSEFAEATPSPVLPI--VMEAPLNS----	599
Db	111	DICYPPOEDSTYFGILQKENGHVITISEP---RELGTGPGSLPDVPGIESRGLFSSDSG	167
Qy	600	--LLPSAGASVQVQSPVSFLEAPPVSY-----DSIKLEPNPPPYEEA-----M	641
Db	168	IEMTPAESSTEVNKILADPLDQMAEAYKYIDITRPEEVKHOEQHHPELEDKDLDFKNKDT	227
Qy	642	NVALKALGTGEGKEPE-----SFNAAVQETAPYISACDLIKETKLSTE--PSP	690
Db	228	DISIK-----PEGVREPKPAPVEGKIIXHLLSESTFAPYID---DLSEORRAPQITTP	280
Qy	691	DFSNYSYIAKFEKSVPSGHAELVEDSSPESPVDLIF-SDDDSIPEV----PQOEBAVLMK	745
Db	281	VKITLTIE-----PSVETTTQETPEKQDICLKPSPDIVPTVTVSEPEDDSFGSITPP	334
Qy	746	ESLTEVSETVAQHK-----EERLSASPOELGKPYLESFQP-----NLHSTKDAAND	792





[illegible]

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Db 2032 SASSEYKQAVDSGEIGRELLDNVEQIRQVKEPIVDSLHKAAYDGVGDVHV-ETVNAV- 2089
QY 589 PDVMEAPLNSLLPSAGASVQPSVSPLEAPPVSDYSIKLEPENPPPYEEAMNVALKAL 648
Db 2090 DDVFREAE-----KOLPESVVP-----2106
QY 649 GKKEGKBPESFNAAVQETAEPIVISTACDLIK-----ETKLETPSPDFSNYSIAKPEK 703
Db 2107 -----EKIETPE-----PLVDLHDTVDKVDHEDVNFLETRPTTPE-----2142
QY 704 SVPEHAELVEDSPSEPEVDLSDSDSIPVQTOQBEAVMLKESLT-----EVSETVAQHK 760
Db 2143 -----TDDVAPLSDDKPQGNQT-PE-----EDETTFDRKGLPTIPEVEKAAAQNN 2189
QY 761 ERLSASQBLGPKYLESFOPNLHSTKDA-----ASNDIPTLTKKKIKSLQMEFNTAI 813
Db 2190 D-----LDDFPLVTSNTGAAGAAVGAAGAAAVESLITEEMFGHQ--KFETVP 2234
QY 814 YSNDLLSSKEDKIKESETFSSPIEIIDETPTFVSADDDSP--KLAKEYTDLEVSOKS 871
Db 2235 RPTTPPKOISDEDVKS-----TVNLGFSHHHPSPHHSILKHGDWIDFKT 2284
QY 872 EIANIQSG-----ADSLPCLE-----LPCDLSFKNIYKPKDEHV 904
Db 2285 VPPCAQNAFSGEIMFLLAFFVYLSCFASFPSKSLPLLDNLLSLVYLISLI-----IH 2339
QY 905 VSDE-----FSENRSVSKASISPSNVSA-----LEPOTMGSIYKSKSLTKAEAK 950
Db 2340 VKHRRKFRWNEBQATMSKLGAVGRGLYALIAFIVNIVLRGLNVALVGVAVSAHEAYK 2399
QY 951 KLPSDTEKEDRSLSAVLSAELSKTSVDLLYWRDICKTGWFGASIFLLLSITVFSIVS 1010
Db 2400 LTKS-----SGVLRKKEVLDVYWRDACKSAIVLSLALVLLVFLAKYPLLTIV 2446
QY 1011 TAYIALALSVTISPRIYKGVTOAQKSGDEGHPFRAYLSEVAISEELYQKYSNLSALGHV 1070
Db 2447 VTYSLLLALGAAGFRVFKKVEAQIKKTSEHPFSEILLAQDLTLQEKVHAQADVFEHA 2506
QY 1071 NTKIELRLFLVDDLSKFAVLWVTVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYV 1130
Db 2507 TCIANKKLKLVPESPLESIKGLVMSLTYIASWFSGFTLAILGLLVFSVPKVVESNQ 2566
QY 1131 VOIDHYGLGLANKSVKDMAKIQAKIPGLK 1159
Db 2567 EAIIDPHLATISHLKKNVQNIIDEKUPFLR 2595

RESULT 6
T13564
Microtubule-associated protein homolog - fruit fly (Drosophila melanogaster)
N:Alternate names: hypothetical protein EG:4984.1
C:Species: Drosophila melanogaster
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T13564
R:Spanos, L.; Papagiannakis, G.; Siden-Kiamos, I.; Louis, C.
submitted to the EMBL Data Library, April 1999
A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A:Reference number: Z17689
A:Accession: T13564
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5327 <SPA>
A:Cross-references: UNIPROT:O76891; EMBL:AL031128; PIDN:CAA20006.1
C:Genetics:
A:Cross-references: FlyBase:FBgn0025392
A:Introns: 24/2; 52/3; 104/3; 179/1; 232/1; 1669/3; 2566/1; 4798/3; 5272/1
A>Note: EG:4984.1
C:Superfamily: Drosophila 576K microtubule-associated protein homolog

Query Match 5.6%; Score 328.5; DB 2; Length 5327;
Best Local Similarity 22.7%; Pred. No. 5.5e-05;
Matches 255; Conservative 176; Mismatches 453; Indels 236; Gaps 54;

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Db      7179  PAKKPEAPPKVPPEAP-KEVVPPEKKVPVPPPKKPEVPPPTKVPEVPKAAVPEKKVPEAIPP 7237
QY      570  TAOLCFS--PEEAETPS-----PV-LPDIVMEAPLNSLLPGAGASVWOPSPLE 617
Db      7238  KPSPPPPEVEPEESESAPPKKPEVPPVTVPEVPEKVVPEKKVPAAPPK--KPEVTIVK 7295
QY      618  AP-----PPVS-----DSIKLEPENPPP--YEE 639
Db      7296  VPEAPKEVVPEKKVPVPPPKKPEVPPTKVPEVPKVA/PEKKVPEAIPPKPESPPEVPEE 7355
QY      640  AMNVALKALGTKEGIEKPEPSFNA-----VQETEARPISTACDLIKETKLSTEP 688
Db      7356  PEEVALEE-PPAEVVEPEP--AAPQVTVPPKPNVPEKKAPAV-----VAKPELPPVK 7407
QY      689  SPDFSNSYETAKPEKVPSEHAELVEDSSPESEBPVDFSDSIPEVPQTOEAVMLMKESL 748
Db      7408  VPVP--KEVVP-EKKVP-----LVVPKPEAPA-----KVPEVP-----KEVV 7444
QY      749  TEVSETVAQHEERLSASQSELGPKPYLESQPNLHSTKDAASNDIPTLTKEKISLQME 808
Db      7445  PEKKVAVPKKPEVPVPAKVPPEVKKVLEE-KPAVPVPRAESPPPEVVEPEEPIAPEE- 7502
QY      809  FNTAIYSNDDLLSSKEDK--IKES-----TFSSSPIEIIDEPPTFFSAKODSPKLA 859
Db      7503  -----IAPSEKVPVVAESEEPEVPPPAVPEEPKKIIPKPKVPVIKPEAPP-P 7550
QY      860  KEYTDLEVDKSRIANIQSGADSLPCLELPCDLSFK-NIYPKDVHVSDFSFENRSSVSK 918
Db      7551  KPPEPKVIEKPKLKKRPPPPPPPPPPPKPKEDVKEKIFQLKAIPKKCV-----PENPVPEK 7604
QY      919  ASISPSNVSALEPQTEMGSIVKSKSTKEAEKKLP--SDTEKEDRSLSAVL 967
Db      7605  VELTPLKVPGE-----KKVKLLPERKPEPEVVLKSVL 7640

RESULT 8
T26213
hypothetical protein W06A7.3b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26213
R;Ainscough, R.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z20173
A;Accession: T26213
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-222 <W1>
A;Cross-references: UNIPROT:Q23188; EMBL:Z78066; PIDN:CAB01523.1; GSPDB:GN000023
A;Experimental source: clone W06A7
C;Genetics:
A;Gene: CESP.W06A7.3b
A;Map position: 5
A;Introns: 27/1; 77/2; 201/2

Query Match 5.5%; Score 320; DB 2; Length 222;
Best Local Similarity 32.1%; Pred.No.1.5e-06;
Matches 59; Conservative 47; Mismatches 78; Indels 0; Gaps 0;

QY      976  VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIAI 1035
Db      27  ILDVIYWRDAKSAIVLSLALLVLFVLAKYPLLTIVTVYSLLLALGAAGAFVFKKVEAQI 86
QY      1036  QKSDGEHPRAYLESEVAISEELVQKYSALGNHVNSTIKELRRLFLVDDVLSLKEAVL 1095
Db      87  KKTDSHPFSEILAQDLTLTPOEKVHAQADVFEHATCIANKLKGJFVFSPLSESIKFGVL 146
QY      1096  MWVFTVVGALENGLTLLILALISLFSIPVYERHQVIDHYLGLANKSVKDAMAKIOAKI 1155
Db      147  LMSLTIVASWFSFTLAILLGLGVSPVKYNSQEAIDPHLATISLGHUKNVQNIIDEKL 206
QY      1156  PGLK 1159

```

505	Db	PIDNVLGEAAITVPAPPVEVTTEVAVADVAPEEAEDLIIIEPVEPPAPIPDLLQQTTS	564
730	QY	IPEVPTQEEAAVMLMKESLTVSETVAQHKERLSASPOBELGKPYLESFQPNLHSTKDA	789
565	Db	VPAVEAAESTGSPITSLPPPNEAVA--SPEVAVAPITAPRPIPEP-EPSLATETPEI	620
790	QY	SNDIPTLTKEKISLQMEEFNTALYSNDLLSSKEOKIKESSEFSSPIELIIDEPPTV	849
621	Db	VPEAPV-----VQEAVDAVEVPVTETSTSPETTVEPEAV	657
850	QY	SAKDPSPLKAKEYTDLEV-SDKSFIANIQSGAD----SLPCLPECDLSFKNIYPKDEVH	904
658	Db	AEKVLDPDAI-----TEAPVTTQEPDVAINDGAPATEITTPAVEI-----VT	699
905	QY	VSDSEFSENRSVSKASISPSNVSALE-PTQEM--GSIVKSLSLTTKEAKKLPSDTEKDR	961
700	Db	AAAEVSDTAIPLIDPPV-PQEIAVAIEPIETETPAEVIVEQS-TTIEAPVPEVSVKAP	757
962	QY	SLSAVLISAELSKTS	975
758	Db	VISEAPAAAEVPIA	771

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RESULT 10
T24583
hypothetical protein T06D8.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T24583
R/Falmer, S.
submitted to the EMBL Data Library, April 1995
A/Reference number: Z19909
A/Accession: T24583
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1829 <WIL>
A/Cross-references: UNIPROT.Q22248; EMBL.Z49130; PIDN.CAA88964.1; GSPDB:GN00022
A/Experimental source: clone T06D8
C/Genetics:
A/Gene: CESP:T06D8.1
A/Map position: 2
A/Introns: 1391/3; 1432/3; 1470/3; 1505/1; 1520/1; 1616/1; 1644/1; 1687/3; 1747/3
Query Match 5.2%; Score 302.5; DB 2; Length 1829;
Best Local Similarity 21.1%; Pred. No. 0.00014;
Matches 233; Conservative 157; Mismatches 469; Indels 245; Gaps 38
QY 2 EIDQSSIVSSSTDSPPR-----PPAPKQFVTEPEDEE-----DDEEE-----E 42
Db 212 EETTVAVVGSGEGEPASSSTSIPTELSKDQVTEASGEETITAAATEASEETTISAVTE 271
QY 43 DDEEDDELEELEVLKPKAAGLSAAAVPPAAAAPLLDFSSDVPPAPRG---PLPAAP 99
Db 272 GSGEDTTVAVVELSGEPAS--SSTSIP-----TELSKDQVTEASGEETTTAAATE 322
QY 100 AAPERQPS-----WERPAPAPSLPAAAVLSKLPEDDE--PPARPPP 143
Db 323 ASEETTTSVATGSGEETTVAVVGSGEGEPASS-----STSIPTELSKDQVTEASGEET 378
QY 144 PPAGASPLAEAPAAPSTPAAPKRRGSGVDETLFAL-----PAASEPVIIPSSAEKIND 196
Db 379 TTAATEASE-----EITTSVATGSGE-DTTVAVVGSGEGEPASSSTSIPTELSKDQ 432
QY 197 LMEQPGN-----TVSGQEDFPVSLLETAAASLPISLPLSTVTSFKH 432
Db 433 VTEASGEETTAAATEASEETTTSAVTEGSGEDTTVAVVGSGEGEPASSSTSIPT----- 488
QY 238 GYLGNLSAVSSSGEITIEITLINEASKEPLERATNPFFVNRDLAEFTSELEYSEMGSFKGSPK 297
Db 489 -ELSKDQVTEASG--EETTTAAATEASEETTTSAVTEGSGEETTVAVVGSGEGEPAS 544
QY 298 GESAILVENTKEEIVRSKOKEDIVCSAALHSPQESPV-----GKEDRVVSPKTMID 350

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Db 545 SSTSIPTLSKDDKVKTEASGETTTAAATDASSEETTTTSAVTEGSGEETTVAVVVSSD- 603  
Qy 351 FNMQMSVVPVREYADFKFEQAEWKDTEGSRDVLAAARANVESKVDRKCLDSLEQ 410  
Db 604 -EPPASSSTSIPTLSKDDQVTEASGETTT-----AAATEASEETTTSAVTEGSGEE 655  
Qy 411 KSLGKDSGRNEDASFPTSPFVKDSSRAYITCASFTSATESTTANTPLLEDHTSENKT 470  
Db 656 TTVAVAVSSGEEPPASSSTSIPTLSKDDKVKTEA---SGEETTTAAATDASSEETTTSAV 712  
Qy 471 DEKLEERKQIILTEKSPK-TSNPFLVAVODSEADYVTTTLKSVTEAAVSNMPEGLTP 529  
Db 713 TEGSGEETTVAVAVSSGEEPPASSSTSIPTLSKDDQVTEASGETTTTAAATEASEETTT 772  
Qy 530 DLVEACESELN-----EATG-----TKLAYETKVDLVOTSEAIQESLYPTAQLCPSF 577  
Db 773 SAVTEGSGEETTVAVAVSSGEEPPASSSTSIPTLSKDDQVTEASGEE-----TTAAATE 828  
Qy 578 EEABATSPVLVDIWEAPLNSLLPSAGASVQVSPLEAPPVPPVSDIKLEPENPPPY 637  
Db 829 ASEETTTSAVTEGSGEDTTVAVAVSSGEE---QPASSSTSIPTLS----- 871  
Qy 638 EEMNVALKATGTEKIGEKPEPSFNAVOETAPYISACDLIKETKLTSTEPSDFSNYSE 697  
Db 872 -----KDDQVTEASGETTT---AAATEASEETTTSAVTEGSGEETT 911  
Qy 698 IAKFEKSVPEHAELVEDSSPESEPVDFSDDSIPEV---POTQEEAVMLKESLVEYSET 754  
Db 912 VAVVSSGEEPA-----SSSTSIPTLSKDDQVTEASGEEETTAAATEASEETTTSAVT 966  
Qy 755 VAQHEERLSAQBELGPKYLESPQ-----NLHSTKDAASN----- 791  
Db 967 EGSGETTTSAVTEGSGEETTTSAPVEGENSTTEAPAVTGSIEIIPSSRESSTTTTHDP 1026  
Qy 792 DIPLTKKEKLSQMEENTAIYNDLLSKEDKIKESET-FSDSSPIEIIDEPFVVS 850  
Db 1027 SIPVITPKPSVSTIENVMKSTSE---AAEKKIIGEHOTGKDDAGKEDENMPAFVT 1083  
Qy 851 A-----KDDSPKLAKETVDLEVDSDKSIANIQSGADSLPCLLEPCD 891  
Db 1084 ANPAGTSTTESAENVSTGEDENIKMKELGKQFAADLAKLA----- 1126  
Qy 892 LSFKNIPKORVHVSDFFSNRVSASISPSNVSALEPQTEMGSIYKSKSLTKEAEKK 951  
Db 1127 -----AKQGVNLT-ETADAKDGETAHVEDEQVSSTE--SSIGSBETTTVNKETTEE 1176  
Qy 952 LPSDTEKEDRSLSAVLAEKLSKTS 975  
Db 1177 HHEASGEEDDAPAFVVTGAPTDSTT 1200

RESULT 11  
A47282  
calcium-binding protein calphotin - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C:Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: A47282  
R:Martin, J.H.; Benzer, S.; Rudnicka, M.; Miller, C.A.  
Proc. Natl. Acad. Sci. U.S.A. 90, 1531-1535, 1993  
A:Title: Calphotin: a Drosophila photoreceptor cell calcium-binding protein.  
A:Reference number: A47282; MUID:93165729; PMID:8094559  
A:Accession: A47282  
A:Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-865 <MAR>  
A:Cross-references: UNIPROT:Q02910; GB:L02111; NID:g157031; PIDN:AAA28405.1; PID:g157031  
A:Experimental source: photoreceptor cells  
A:Note: sequence extracted from NCBI backbone (NCBIN:124955, NCBI:P:124956)  
C:Genetics:  
A:Gene: FlyBase:Cpn  
A:Cross-references: FlyBase:FBgn0010218  
C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;  
C:Keywords: calcium binding

Query Match 5.1%; Score 295.5; DB 2; Length 865;  
Best Local Similarity 21.3%; Pred. No. 9.5e-05;  
Matches 217; Conservative 127; Mismatches 379; Indels 295; Gaps 41;  
Qy 62 AAGLSAAAVPAAAPLDFSSDVPAPGRLPAAPAAAPER-----QPSWERSPAAPAP 117  
Db 11 SAPVAAPVTPSGAAPVQVVSAAVAPAPAPIAVTPVAPPPTLASVQPATVTIP-ADAP 69  
Qy 118 ----SLPAAAVLPSKLPDEDDPPARPPPPPPAGA-----SPLAEAPAPSTP- 161  
Db 70 IAAASVTPFVASVAPVVAAPTPPAASPVSTPVAAQIPVAVSAPVAPVAAATPTPVQIP 129  
Qy 162 -AAPKRRGSGVDTELFALP--AASEP-----VIPSSAEKIMDLMEQPGNT---VSSGQED 211  
Db 130 VAAP-----VIATPVAASAPTPAAVTPVISPVIASPPVVPVANTTVPVAAVAA 178  
Qy 212 PPSVLLTAAASL-PSLSPLSTVSPKEHYGLNLSAVSSSECTIETETLNEAKHEPERATN 270  
Db 179 VPAAVPPVAPVLADAPAVAPVAVVVAETPAPPVVAEIPVA--TIPECVAPLIPVSVWATK 236  
Qy 271 PFVNRDLAEFSELEYSEMGSSFKGSPKESAILVENTKEEVIYRSKOKEDLVCSAALHSP 330  
Db 237 PLA-----AAEPVVVAPPATETPVVAPAAASP 263  
Qy 331 QESPVGKEDRVVSPEKTMDFNEMQMSVAVPVREYADFKFEQAEWKDTEGSRDVL 390  
Db 264 HVS-----VAP-----AVETAVAPV- 279  
Qy 391 ARANVESKVRKCLDSLEQKSL-----GKQSEGRNEDASFPSTPEPVKDSRAYITCASF 446  
Db 280 -SASTEPVAAAATLTAPETPALAPVVAESQVAANTVVATPTTAPETIAPVVAETP 338  
Qy 447 TSATESITANTFPLLEDHTSENKTDEKKIEERKQIITEKTSPTKTSRPLVAVODSEADY 506  
Db 339 EVASVAVAEVTPPVVPPVAAES-----IPAPVAVTTPVATLAVTDPD--- 381  
Qy 507 VTDTLSKTEAAVSNMPEGLTDLVQESSELNEATGKIAVETKVDLVOTSEAIQES 566  
Db 382 -----VTASAVPELPVVIAPSPVPSA-----VAETPVDLA-----PPV 414  
Qy 567 LYP-TAQLCPSF--EEABATSPVLVDIWEAPLNSLLPSAGASVQVSPVSLRAP----- 619  
Db 415 LPPVAAEPVPAVVAEETPTPAPASAPVTI-AALD--IPEVAPVIAAPSDAPAEAPASAA 471  
Qy 620 PPUSYDSIKLEPENPPPYEEMNVALKATGTEKIGEPESFNAVQIETAPYISACD- 677  
Db 472 PIVS-----TPPT-----TASVPETTPAAPAVPTPEPI 498  
Qy 678 ---LIKETKLTSTEPSDFSNVSEIAKPEKSVPEHAE--LVEDSSPESGEPVDFLSD-DSIP 731  
Db 499 DVSVLSEAAIETPVAPPEVTEVAVADVAPPEAAADLIIEPVPEPAPIPLLQTTTSPV 558  
Qy 732 EVPTQTEAAVLMKESLTVSETVQAHKEERLSASPOELGPKYLESPQNLHSTKDAASN 791  
Db 559 AVEAAESTSSPIPETSLPPNEAVA--SPEVAVAPITAPEPIPEP-EPSLATPTETPIPV 614  
Qy 792 DIPLTKKEKLSQMEENTAIYNDLLSKEDKIKESETFSDSSPIEIIDEPPTFVSA 851  
Db 615 EAPV-----VIOEAVDAVEVPVVTETSTSTPETTVEPPEAVAE 651  
Qy 852 KDDSPKLAKETVDLEV-SDKSEIANIQSGAD-----SLPCLLE-----PCDLSFKNIYP- 899  
Db 652 KYLDPAI-----TEAPVTTQEPDVANINDGAPATEITTPAVEIVTAAAEVSDIALPIDPDP 707  
Qy 900 -KDEHVHSDFFSNRVSASISPSNVSALEPQTEMG----- 936  
Db 708 VPQEIAVA-EIPETDTKPAEIVVEQSTIPIEAPVPEVSKVAEPVISEAPAAEVPITAGDN 766  
Qy 937 ----SIVKSKSLTKEAEKKLPDTEKEDRSLSAVLAEKLSKTSVVDLILYRDIKKTGV 990  
Db 767 PDNTSVGISVWPTIAEKVEEVPETSIPEQSSSPSDSPVPAKITPLL--RDLQTTDV 822

RESULT 12  
T34513  
hypothetical protein ZK783.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T34513  
R:Ravello, A.; Vaudin, M.  
submitted to the EMBL Data Library, August 1994  
A:Description: The sequence of C. elegans cosmid ZK783.  
A:Reference number: Z21536  
A:Accession: T34513  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-3507 <FAV>  
A:CROSS-references: UNIPROT:Q23587; EMBL:U13646; PIDN:AAC24418.1; GSPDB:GN00021; CESP:ZK783  
A:Experimental source: strain Bristol N2; clone ZK783  
C:Genetics:  
A:Gene: CESP:ZK783.1  
A:Map position: 3  
A:Introns: 14/1; 48/2; 84/1; 196/3; 303/1; 381/1; 586/1; 605/1; 1175/3; 1207/1; 1409/2; 3504/1  
Query Match 5.0%; Score 292; DB 2; Length 3507;  
Best Local Similarity 20.6%; Pred. No. 0.00092;  
Matches 226; Conservative 146; Mismatches 491; Indels 236; Gaps 37;  
QY 11 SSSDTPPPPPAFKYQFVTEPEDEDEDEDEDEDEDL--EELEVLERKPAAGLSAA 68  
DB 2043 SSSSEAPLTSPTATTEVITESVSKTTPKESSEITVKLSKSPETVSSVKSSTP 2102  
QY 69 AVPPAAAPLLDFSDSVPPAPRGLPAAAPP-----AAPERQSWERSPA-----APAPSL 119  
DB 2103 STTSQSVTSTVTPETSKSTVLSSEAPVTSTPTSEVTSTSTKPSGASSTTGTNTSTPST 2162  
QY 120 PPAAVLPKLPDEDEPPAPPPPPAGASP--LAEP-----AAPSTPAAPKRGGSV 172  
DB 2163 SSLASVKSTSAPEGTS--ASVAPVKLSLSPVQSPSTKTFPATSESTVQASSETSGTSV 2220  
QY 173 DET-----LFALPAASEPI--PSSAEKIMDLMEQPGNTVSSQEDFP-----SV 215  
DB 2221 KSTSPESHVTKLSTSSNPSSVPVTPSKPTVPPESTEQTSTTPSGQSLTPWNSSE 2280  
QY 216 LLETA---ASLPSLPLSTVSKHEGYLGNLSAVSSSEGTIEETNEASKELPERAT--N 270  
DB 2281 VLTTEPHVLSLSPDVQSSQSTTPNNLSESTVETPKTSSSEVLSNSEEPSTTEAPTILS 2340  
QY 271 PV-----NRDLAEFSEL---EYSEMGSSPKGSPKG-----BSAILVENTKEEIVRSKD 317  
DB 2341 PDLSTTTNNLQSSSTVSTEDRSEISSENSEKPTSAPELVTSVTHVASSSDPDVPTESSE 2400  
QY 318 KEDLVCSAALHSPQ-----ESPVGKEDRVVSPKTMDFNEMQMSVVAVPREYADPK 370  
DB 2401 PDLATGSSSTENIPEASSKQTISSITPTPTTASEEPTKSTMSPDLSSTNSVLSSTTP 2460  
QY 371 PFEQAWEVKDTVEGRDVLAAANVESKVDKCLDSLEKQSLGKDSOGRNEDASFPSTP 430  
DB 2461 ESSSKSPVSSSTEG---ISVVTSTFKVPSTISSVLE-----EDLT--KTP 2504  
QY 431 EPVKDSSRAYITCASFTSAT-----ESTANTPFLLEDHTSENKTDSEKIEE 477  
DB 2505 SPILSEI-----TTASETSPLTEDSLTVSVRHELTTSSENVKSESESTTSSESKEPQ 2560  
QY 478 RKAQIITEKSTKTNPFVAVQDSEADYVTTDLTKSVTEAAVSNMPEGL-----TPDLV 532  
DB 2561 EPAGILTSVVVPTSSVSLITASEIEA--ITSNTPFKQGRTPITTSKSLVKSTTSPSTV 2618  
QY 533 --QACESLNEATGKIAYETKVDLVQTSIAQESLYPTAQLCPSEFEAEATPSPVLDP 590  
DB 2619 TSSEPSSESTKRTVSTVSTTPTTETTTTSSLIILTAAPSK---PTESTESSEAPTTP- 2674  
QY 591 IVMAPLNSLLPSAGASVVPQSVSPLEAPPVSYDSIKLEPENPPPYEAMVVALKLT 650

DB 2675 -----AKTSETKPS-----NVSSTSRKS 2692  
QY 651 KEGIKEPESFNAAVQETAPYISIACDLIKETKLTSTEPSDPFSNYSEIAKFKSKVPEHAE 710  
DB 2693 TENVETSTSQSGLESS-----TMSSTSEPETNAPAVTVSSSEASTLSE 2738  
QY 711 LVEDSSPESEPVDLFSDDSIPEVPQTOBEAVNLMKESLTVSETVAQHKELRLSASPOE 769  
DB 2739 NSSTSPSTSSSEASVKLSLFPF--SITSEAVTVSSRAPAEITMSSSHREITVSSSEPSE 2796  
QY 770 LCKPYLESFQPNLHSTKDAASNDITLTKKEKISIQMEEFNTAIYSNDDLLSS----- 822  
DB 2797 PEIPLSTTVSPNVVTASSIPSEE--PILSSVSSSTPRVRLITG--TPDDLIVSVTVPSHG 2853  
QY 823 -KEDKIKSETFSDS--SPIEIDEPTTVSAKDDSKPLAKETDLEVDKSIANIQSGA 880  
DB 2854 NRRQNTITASSVPFSNSTSPILPSESLTTPQPPPTTTTAKPAT-----TSCK 2900  
QY 881 DSLPCLLELPCLDSFKNIYPKDEHVHVSDEFSENRSVSKASISPSNVSALEPOTEMGSIYK 940  
DB 2901 RGPFSIQPPAEM-----FTTAPPPPPSGGYGEE----- 2929  
QY 941 SKSLTKEAEKKLPSTDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVWFGASLFLLL 1000  
DB 2930 -----TNQEEQVTSITTTTAPSLCSTVCHSLATCE-----QSTGVCLCRDGFCD 2976  
QY 1001 SLTVFSIVSVTAYIALALL 1019  
DB 2977 GTTACKSKSTADCSLPSL 2995  
RESULT 13  
A56577  
microtubule-associated protein MAP 1B - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
R:Zauner, W.; Kratz, J.; Staunton, J.; Feick, P.; Wiche, G.  
Eur. J. Cell Biol. 57, 66-74, 1992  
A:Title: Identification of two distinct microtubule binding domains on recombinant rat  
A:Reference number: A56577; MUID:92347374; PMID:1639092  
A:Accession: A56577  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-2364 <ZAU>  
A:CROSS-references: UNIPROT:P15205; GB:X60550  
A:Experimental source: brain  
A:Note: nucleotide sequence not given; conceptual translation not complete  
C:Superfamily: microtubule-associated protein MAP1B  
Query Match 5.0%; Score 291.5; DB 2; Length 2364;  
Best Local Similarity 20.0%; Pred. No. 0.00056;  
Matches 220; Conservative 167; Mismatches 456; Indels 255; Gaps 44;  
QY 30 TEPEDEDEDEDEDEDEDEDEDEDEDELEVLERKPAAGLSAAVPPAAAPLLDFSSDSVPPA 89  
DB 913 SEEGEEDEKAEADAREDEHDPDKTE-----AEDYVNAVVDKAAEAGVTEDQYDFL---- 963  
QY 90 PRGPLPAAAPAPRQPSWERSPAAAPSLPAAAVLPKLPDEDEPPARPPPPPPAGAS 149  
DB 964 -----GTPAKQ-----PGVQSPSPREPASSIHDETLPGGSEAT-----AS 999  
QY 150 PLAEPAAPSTPAAPKRGGSGVDETLFPALPAASEPVPSSAEKIMDLMEQGN---TVS 206  
DB 1000 DEENREDQPEEPTAT---SGYTQST---IEISSEPTMDENSTPRDVTMDTNNBETS 1052  
QY 207 SQGE-----DPESVLLETAASLP---SLSPLS---TVSFKEHGYLGNLSAVSSSEGTE 254  
DB 1053 PSQEFVNTKYESSLYSQEYKPVVASFNGUSDGSKTDATDGRDNTASASTISPPSSMEE 1112  
QY 255 ETLNEAS-----KELPERATNPFVNRDLAEF--SELEYSEMG--- 289  
DB 1113 DKFSKSLRADYRPRETDVKTGAELDIKDVSDERLSPAKSPSLSPSPPIEKTPLGERS 1172



QY 920 SIS 922  
Db 907 SVS 909

RESULT 15  
QMSPI

microtubule-associated protein MAP1B - mouse  
N:Alternate names: microtubule-associated protein MAP1(X); microtubule-associated protein  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text\_change 09-Jul-2004  
C:Accession: S07549; S44387; A33645  
R:Noble, M.; Lewis, S.A.; Cowan, N.J.  
J. Cell Biol. 109, 3367-3376, 1989  
A:Title: The microtubule binding domain of microtubule-associated protein MAP1B contains  
A:Reference number: A33645; MUID:90094539; PMID:2480963  
A:Accession: S07549  
A:Molecule type: mRNA  
A:Residues: 1-2464 <NO>  
A:Cross-references: UNIPROT:P14873; EMBL:X51396; NID:g52999; PIDN:CAA35761.1; PID:g53000  
R:Sanchez, C.; Padilla, R.; Paciucci, R.; Zabala, J.C.; Avila, J.  
Arch. Biochem. Biophys. 310, 428-432, 1994  
A:Title: Binding of heat-shock protein 70 (hsp70) to tubulin.  
A:Reference number: S44387; MUID:94234720; PMID:8179328  
A:Accession: S44387  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 653-663, 'IC' <SAN>  
C:Superfamily: microtubule-associated protein MAP1B  
C:Keywords: microtubule binding; phosphoprotein; tandem repeat  
F:589-786/Domain: microtubule binding #status experimental <MTB>  
F:589-592,639-642,649-652,655-658,660-663,668-671,674-677,679-682,683-686,687-690,691-694  
R:X-E/D-X)

F:1861-2064/Region: 17-residue repeats  
F:91,116,351,888,1124,1153,1168,1208,1662,1877,1918,2003,2030,2054,2083/Binding site: ph  
F:147,969,1336,1562,1563,1702,1708,1990,2057,2063,2419/Binding site: phosphate (Thr) (Co  
F:1953/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 4.9%; Score 284; DB 1; Length 2464;  
Best Local Similarity 20.7%; Pred. No. 0.0012;  
Matches 233; Conservative 159; Mismatches 424; Indels 312; Gaps 51;

QY 31 EPEDEDEDEDEED-----DELELE-----VLERKPAAG-----LSAAAVP 71  
Db 1009 EAEQSEEGEEDKAEAREEGVEPDKTEADYVMAVADKAAEAGVTEQYGLGTSKQ 1068

QY 72 PAAAPLPLDFSS-----DSVPPAPRGLPAPAPAPAPRQP-----SWERSPAAPA 116  
Db 1069 PGIQSPSRFPASSIHDETLPGGSESEATASDENREDQEEFTATSGYTQSTIEISSEPT 1128

QY 117 P---SLPPAAAVLPKLPEDDEPPARP-----PPPPAGASPLAEP-- 155  
Db 1129 PMDENSTPRDVMSTENNEETESPSQEFVNITKYESSLYSQEYKPAVASFNGLSEGSKT 1188

QY 156 -----APSTPAAPKRGSGVDLTFALPA-----ASEVIPSSAEKIMDLMEQ 200  
Db 1189 DATDGKDYNNASASTISPP-----SNNEEDKFSKALRDAYCSEKELKASAE--LDIKDV 1241

QY 201 PGNTVSSGQEDFPFVLELTAASLPSPSLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEA 260  
Db 1242 SDERLS-----PAKSPSLP-----SPSPSIEKT----- 1265

QY 261 SKELPERATNPFVNRDLAFS-----ELEYSEMGSSPKGPKGSAAILVEN--TKGEVIVR 314  
Db 1266 --PLGERSVN-----FSLTPNEIKVSAEGEARSVPGVTOAVVEHCHASPEKITLE 1314

QY 315 SKDKEDLVCSAALHSP-QESPVGKEDRVVSPKTMWDFNEMQMSVVA-PVREYADF-- 370  
Db 1315 VVSPQSVGTGSAHTPIYQSP-----TDEKSSHLPTVESENQAQVPSFESEAKDE 1366

QY 371 -----PFEQAWEVKDTYEGSRDVLAAAPANVESKVDKCLD--SLEQSLGKDS---- 417

Search completed: June 16, 2005, 13:31:49  
Job time : 42.9713 secs

Db 1367 NERASLPMDE--PVPDSSEPVKEVLSPLRSPPLLGSESPYEDFLSADSKVLGRSESPF 1424  
QY 418 EGRNEDASFPSTPEPVKDSRAYITCASFTSATSTTANTPTPLLEDHTSENKT----- 470  
Db 1425 EGKNGKQGFDPRESFVSLT---STGLYQDKQBEKSTGFIPKEDFGPEKKTSDVETMS 1480  
QY 471 -----DEKKI-----EERKAQIITEKTSPKTSNPFLVAVQDSEAD 505  
Db 1481 SOSALALDERKILGGVSVPTQIDVSGFKEDTKMSISEGTVSDKSATPVDSEGV--AET 1538  
QY 506 YTTTDTLTKVTEAAV--SNMPEGLTPDLVQACASELNEATGKIAYETKVLVOTSEAI 563  
Db 1539 YSHMEGVA SVSTASVATSFPEPTDD-VSPSLHAEVGSPHSTVEDDLSLSVSVVPTTF 1597  
QY 564 QES-LYPTAQICP--SPEEAEATP-----SPVLPDIMEAPLMSLL-- 601  
Db 1598 QETEMSPSKEECPRMSISPPDFSPKTAKSRTVPQDHRSEQSSMSIEFQESPEHSFAMD 1657  
QY 602 -----PSAGASVVQPSVPLEAPPVSYD-----SIKLEPENPPPEEAMNVA 644  
Db 1658 FSRQPDHPTLGLASVLIHITEN--GPTVDVSPCDIQSSLSHKIPPTPEEPSTQONDLS 1714  
QY 645 LKALGTKEGKEIPESFNAAVOETEAPYISACDLIKETKLTSTEPSPDFSNYSEIAKFEKS 704  
Db 1715 -ELISVSQVEASPTSSAHTPS-----QIASPLQEDTLSDVVPPREMSLYASLA---- 1762  
QY 705 VPEHAELVEDSPSEPVDLFSDDSIPEVPOTQEEAVML-----MKESLTVSETVAQHK 760  
Db 1763 ----SEKVV--SLEGEKLSPKSDIS---PLTPRESSPLYSFGFSDSTSAAKETAAAH-- 1810  
QY 761 ERLSASP--QELGKPY-----LESFQPNLHSTKDAASNDIPTLTKEKISLQWERN 810  
Db 1811 -QASSPPIIDAATAEPYGFRRSMLPDTQHHALNARDLTTSSV-----EKDSGKTPGDPN 1865  
QY 811 TAIYVNDLLSKEDKIKESETFSDSPSIEIIDEFTFVSANKDDSPK-----LAKSYTDLE 866  
Db 1866 YAYQKPENAAGSPDEEDVYB--SQEKTIRTHDVVRYVYKERTIKSPCDSGSYVETIE 1923  
QY 867 VSDKSEIANIOSGADSLPCLELPCLSPKNYIPKDEHVHVSDEFSENRSVSKAS----- 920  
Db 1924 KTKTTP-----EDGG-----YTCEITKTRTPEEGYSYSEIKTTRTPEVSGYTV 1972  
QY 921 -----ISPSNVSALEPQTEMGSI VKSKSLTKEAKKLPSDTEKEDRS 962  
Db 1973 TERSRLDDISNGYDDTDGCHTLGDCSYVETTEKITSPESESYS 2020



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:33:51 ; Search time 157.778 Seconds  
(without alignments)  
3774.604 Million cell updates/sec

Title: US-09-830-972-2

Perfect score: 5848

Sequence: 1 MEDIDQSLVSSSTDSPPRP.....VKDAMAKIQAKIPGLKRRAD 1163

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5848	100.0	1163	1 RTN4 RAT	Q9Jk11 rattus norv
2	5312.5	90.8	1162	2 Q8BGM9	Q8Bgm9 mus musculu
3	5307	90.7	1163	2 Q8K3G8	Q8K3g8 mus musculu
4	4501.5	77.0	1046	2 Q8BGK7	Q8Bgk7 mus musculu
5	4403.5	75.3	1192	1 RTN4 HUMAN	Q9ncq3 homo sapien
6	3627.5	62.0	986	2 Q7Tnb7	Q7Tnb7 mus musculu
7	3299.5	56.4	720	2 Q7Tnb7	Q8Iua4 homo sapien
8	2926	50.0	639	2 Q8K290	Q8K290 mus musculu
9	2610	44.6	578	2 Q8QW95	Q8Qw95 mus musculu
10	1664	28.5	658	2 Q8RS88	Q6rs88 gallus gall
11	1620	27.7	1043	2 Q6JRV0	Q6Jrv0 xenopus lae
12	1616	27.6	1055	2 Q6JRV1	Q6Jrv1 xenopus lae
13	1596.5	27.3	1032	2 Q6JRV7	Q6Jrv7 xenopus lae
14	1586.5	27.1	1044	2 Q6JRV8	Q6Jrv8 xenopus lae
15	1554.5	26.6	1024	2 Q6JRV2	Q6Jrv2 xenopus lae
16	1539	26.3	1013	2 Q6JRV9	Q6Jrv9 xenopus lae
17	1416	24.2	375	2 Q8BHf5	Q8Bhf5 mus musculu
18	1314.5	22.5	356	2 Q8BHf8	Q8Bhf8 mus musculu
19	1304	22.3	357	2 Q8K3G7	Q8K3g7 mus musculu
20	1283.5	21.9	392	2 Q96B16	Q96b16 homo sapien
21	1060	18.1	343	2 Q6IPN0	Q6ipn0 homo sapien
22	917	15.7	199	1 RTN4 MOUSE	Q9p972 mus musculu
23	908	15.5	199	2 Q7YRW9	Q7Yrw9 bos taurus
24	904	15.5	199	2 Q6IM70	Q6im70 sus scrofa
25	899	15.4	199	2 Q7PCJ7	Q7pcj7 macaca fasc
26	896	15.3	187	2 Q6IG15	Q6ig15 sus scrofa
27	876	15.0	199	2 Q7T224	Q7t224 gallus gall
28	850	14.5	250	2 Q6IG16	Q6ig16 sus scrofa
29	844	14.4	179	2 Q9GM33	Q9gm33 macaca fasc
30	807.5	13.8	315	2 Q6IFY4	Q6ify4 xenopus tro
31	806	13.8	1013	2 Q6T930	Q6t930 homo sapien

32	803	13.7	945	2 Q6T929	Q6t929 mus musculu
33	801	13.7	777	1 RTN1 RAT	Q64548 rattus norv
34	797.5	13.6	311	2 Q6JRV3	Q6jrv3 xenopus lae
35	797	13.6	330	2 Q6JRV4	Q6jrv4 xenopus lae
36	796.5	13.6	964	2 Q8RFB4	Q8rfe4 mus musculu
37	792.5	13.6	940	2 Q6RJR6	Q6rjr6 rattus norv
38	792	13.5	780	2 Q8K4S4	Q8k4s4 mus musculu
39	789.5	13.5	776	1 RTN1 HUMAN	Q16799 homo sapien
40	788	13.5	780	2 Q8K0T0	Q8k0t0 mus musculu
41	777	13.3	316	2 Q6JRW2	Q6jrw2 xenopus lae
42	774	13.2	193	2 Q6IFX5	Q6ify5 xenopus tro
43	770.5	13.2	323	2 Q6JRW1	Q6jrw1 xenopus lae
44	767.5	13.1	882	2 Q6R8K6	Q6r8k6 mus musculu
45	767	13.1	304	2 Q6JRW0	Q6jrw0 xenopus lae

ALIGNMENTS

RESULT 1  
ID RTN4 RAT STANDARD; PRT: 1163 AA.  
AC Q9Jk11; Q9Jk10; Q9ROD9; Q9WUE9; Q9WUF0;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DE 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Poccen)  
DE (Glut4 vesicle 20 kDa protein).  
GN Name=RTn4; Synonyms=Nogo;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.  
RC STRAIN=Sprague-Dawley; TISSUE=Adipocyte;  
RX MEDLINE=99249816; PubMed=10231557; DOI=10.1016/S0167-4899(99)00033-6;  
RA Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lienhard G.E.;  
RT "Cloning and characterization of a 22 kDa protein from rat adipocytes:  
a new member of the reticulon family";  
RL Biochim. Biophys. Acta 1450:68-76(1999).  
RN [2]  
SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RX MEDLINE=20129258; PubMed=10667796; DOI=10.1038/35000219;  
RA Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,  
RA Spillmann A.A., Christ F., Schwab M.E.;  
RT "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an  
antigen for monoclonal antibody IN-1";  
RL Nature 403:434-439(2000).  
RN [3]  
SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).  
RC STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;  
RA Ito T., Schwartz S.M.;  
RT "Cloning of a member of the reticulon gene family in rat: one of two  
minor splice variants";  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
RN [4]  
FUNCTION.  
RX MEDLINE=22033691; PubMed=12037567; DOI=10.1038/417547a;  
RA GrandPre T., Li S., Strittmatter S.M.;  
RT "Nogo-66 receptor antagonist peptide promotes axonal regeneration";  
RL Nature 417:547-551(2002).  
CC -1- FUNCTION: Potent neurite outgrowth inhibitor which may also help  
block the regeneration of the nervous central system in adults (By  
similarity).  
CC -1- SUBUNIT: Binds to RTN4R. Interacts with Bcl-x1 and Bcl-2 (By  
similarity).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the  
membrane of the endoplasmic reticulum through 2 putative  
transmembrane domains (By similarity).  
CC -1- ALTERNATIVE PRODUCTS:  
Event=Alternative splicing; Named isoforms=4;  
Name=1; Synonyms=Nogo-A, NI-220-250;







Db 63 SEPVPSSAEKIMDLKEQNGNTVSSQEQEDFPSPVLFTAAASPLSLSTVSPFKHGYLEGN 122  
Qy 243 LSAVSSSECTIETLINEASKELPERATNPPFVNDRDLAEFSELYSEWSSGSKGSPKGEAI 302  
Db 123 LSAVASTECTIETLINEASRELPERATNPPFVNRESAEFSLVLEYSEWSSGSKGSPKGEAI 182  
Qy 303 LVENTKEEVVRSKDKEDLVCSAALHSPQESP-----VGKEDRVVSPSEKTMDFINEMQMS 357  
Db 183 LVENTKEEVVRSKDKEDLVCSAALHNPQESPATLTKVVKEDGVMSPEKTMDFINEMQMS 242  
Qy 358 WVPVREYADPKPEQAEVWEDTTEGSRDVLAAANVESKVDKCLDESLSEKSLGKDS 417  
Db 243 WVPVREYADPKPEQAEVWEDTTEGSRDVLAAANVESKVDKCLDESLSEKSLGKDS 302  
Qy 418 EGRNEDASFPSPPEPVKDDSSRAYITCASFTSATESTTANTPELLSDHTSENKTDSEKLEE 477  
Db 303 ESRNENASFPPTPELVKDGSRAYITCDSFSSATESTTANIPVLEDHTSENKTDSEKLEE 362  
Qy 478 RKAQIITEKTSPTKSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEA 537  
Db 363 RKAQIITEKTSPTKSNPFLVAIHDSADYVTTDNLSKVTEAVVATMPEGLTPDLVQEA 422  
Qy 538 SELNEATGKTAYETKVDLVOTSEAIQESLPTAQLCSPFEAEATPSPVLPIVMEAPL 597  
Db 423 SELNEATGKTAYETKVDLVOTSEAIQESLPTAQLCSPFEAEATPSPVLPIVMEAPL 482  
Qy 598 NSLLPSAGASVVPQSPVPLEAPPVSYDSIKLEPNPPPYEAMNVALKGTKEGKEP 657  
Db 483 NSLLPSTGASVAQPSASPLEVSPVSYDGIKLEPNPPPYEAMNVALKGTKEGKEP 542  
Qy 658 ESFNAVAQETAPYISACDLIKETKLTSTEPSDFSNYSSEIAKFSKVPSEAEALVEDSSP 717  
Db 543 ESFNAVAQEAAPYISACDLIKETKLTSTEPSDFSNYSSEIAKFSKVPSEAEALVEDSSP 602  
Qy 718 ESEPVDLFSDSDSIPVPQTEBAVMKESLTVSETVQAUK-BERLSASPOELGKPYLE 776  
Db 603 ESEPVDLFSDSDSIPVPQTEBAVMKESLTVSETVQAUK-BERLSASPOELGKPYLE 662  
Qy 777 SFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDLLSSKEDKIKESFTFSDS 836  
Db 663 SFQPNLHSTKDAASNEIPTLTKEKISLQMEEFNTAIYSNDLLSSKEDKIKESFTFSDS 722  
Qy 837 SPIEIIDFPPTFVSAKDSPLAKETDLEVSDEKSEIANIQSGADSLPCLPLCDLSPKN 896  
Db 723 SPIEIIDFPPTFVSAKDDSP---KEYTDLEVSNNKSEIANVQSGANSLPCLSPDLSPKN 779  
Qy 897 IYPKDEIVHVSDEFSENRSVSKASISPSNVSALEPQTEMGSIKSLTKAEKPLPSDT 956  
Db 780 TYPKDEAHVSDSEFSKRSVSKVPILLPNVSALESQIEMGNIVKPKVLTKAEAEKPLPSDT 839  
Qy 957 EKEDRSLSAVLSAELSKTSVVDLLVWRDIKKTGVVFGASLFLLLSLTVFSTVSTAYTAL 1016  
Db 840 EKEDRSLSAVLSAELSKTSVVDLLVWRDIKKTGVVFGASLFLLLSLTVFSTVSTAYTAL 899  
Qy 1017 ALLSVTISFRIYKGVIOAKSDSEGHPPFRAYLESEVAISEBLVQKYSNSALGHVNSTIKE 1076  
Db 900 ALLSVTISFRIYKGVIOAKSDSEGHPPFRAYLESEVAISEBLVQKYSNSALGHVNSTIKE 959  
Qy 1077 LRRFLVDDLVDSLKFAVLMVFTVVGALFNGLTLLILALISLSPVPIYERHQVQIDHY 1136  
Db 960 LRRFLVDDLVDSLKFAVLMVFTVVGALFNGLTLLILALISLSPVPIYERHQVQIDHY 1019  
Qy 1137 LGLANKSVKDAWAKIQAKIPGLKRAK 1163  
Db 1020 LGLANKSVKDAWAKIQAKIPGLKRAE 1046

## RESULT 5

RTN4\_HUMAN

ID RTN4\_HUMAN STANDARD; PRT; 1192 AA.

AC Q9NQC3; Q94962; Q9BG5; Q9H212; Q9H313; Q9Q42; Q9Y293; Q9Y2Y7;

AC Q9Y5U6;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Reiculon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Pocent)  
DE (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific  
protein C homolog) (RTN-x) (Reiculon 5) (My043 protein).  
GN Name=RTN4; Synonyms=ASY, KIAA0886, NOGO;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RP MEDLINE=20129242; PubMed=10667780; DOI=10.1038/35000287;  
RA Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G.,  
Michalovich D., Simmons D.L., Walsh F.S.;  
RT "Inhibitor of neurite outgrowth in humans.";  
RL Nature 403:383-384(2000).  
RN [2]  
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RP TISSUE=Brain;  
EX MEDLINE=21010696; PubMed=11126360; DOI=10.1038/sj.onc.1203948;  
RA Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;  
RT "A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on  
endoplasmic reticulum and reduces their anti-apoptotic activity.";  
RL Oncogene 19:5736-5746(2000).  
RN [3]  
SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RP MEDLINE=20237542; PubMed=10773680;  
RA Yang J., Yu L., Bi A.D., Zhao S.-Y.;  
RT "Assignment of the human reticulon 4 gene (RTN4) to chromosome  
2p14--2p13 by radiation hybrid mapping.";  
RL Cytogenet. Cell Genet. 88:101-102(2000).  
RN [4]  
SEQUENCE FROM N.A. (ISOFORM 4).  
RA Jin W.-L., Ju G.;  
RT "Developmentally-regulated alternative splicing in a novel Nogo-A";  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).  
RC TISSUE=Placenta, and Skeletal muscle;  
RA Ito T., Schwartz S.M.;  
RT "Cloning of a member of the reticulon gene family in human.";  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
RN [6]  
SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE=Fibroblast;  
RA Yutsudo M.;  
RT "Isolation of a cell death-inducing gene.";  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
RN [7]  
SEQUENCE FROM N.A. (ISOFORM 3).  
RC TISSUE=Pituitary;  
RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,  
Luo B., Hu R., Chen J.;  
RT "Human neuroendocrine-specific protein C (NSP) homolog gene.";  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
RN [8]  
SEQUENCE FROM N.A. (ISOFORM 3).  
RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,  
Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,  
Yu J., Han L.H.;  
RT "Novel human cDNA clones with function of inhibiting cancer cell  
growth.";  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
RN [9]  
SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Brain;  
EX MEDLINE=99156230; PubMed=10048485;  
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosewa M.,  
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
RT "Prediction of the coding regions of unidentified human genes. XII.  
The complete sequences of 100 new cDNA clones from brain which code  
for large proteins in vitro.";

RL DNA Res. 5:355-364(1998).

RN [10]

RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).

RC TISSUE=Brain, Ovary, Pancreas, and Skeletal muscle;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,

RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [11]

RP SEQUENCE FROM N.A. (ISOFORM 3).

RC TISSUE=Umbilical cord blood;

RX MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200;

RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,

RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,

RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.,

RT "Cloning and functional analysis of cDNAs with open reading frames for

RT 300 previously undefined genes expressed in CD34+ hematopoietic

RT stem/progenitor cells."

RL Genome Res. 10:1546-1560(2000).

RN [12]

RP SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).

RC TISSUE=Brain;

RA Mao Y.M., Xie Y., Zheng Z.H.;

RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.

RN [13]

RP SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1).

RC TISSUE=Testis;

RA Sha J.H., Zhou Z.M., Li J.M.;

RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

RN [14]

RP TOPOLOGY.

RC TISSUE=Brain;

RX MEDLINE=20129259; PubMed=10667797; DOI=10.1038/35000226;

RA GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.;

RT "Identification of the Nogo inhibitor of axon regeneration as a

RT Reticulon protein."

RL Nature 403:439-444(2000).

RN [15]

RP FUNCTION.

RC TISSUE=Brain;

RX MEDLINE=21069055; PubMed=11201742; DOI=10.1038/35053072;

RA Fournier A.E., GrandPre T., Strittmatter S.M.;

RT "Identification of a receptor mediating Nogo-66 inhibition of axonal

RT regeneration."

RL Nature 409:341-346(2001).

RN [16]

RP REVIEW.

RC MEDLINE=2188956; PubMed=11891768; DOI=10.1002/jnr.10134;

RA Ng C.E.L., Tang B.L.;

RT "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron

RT regeneration."

RL J. Neurosci. Res. 67:559-565(2002).

CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help

CC block the regeneration of the nervous central system in adults.

CC Isoform 2 reduces the anti-apoptotic activity of Bcl-xl and Bcl-2.

CC This is likely consecutive to their change in subcellular

location, from the mitochondria to the endoplasmic reticulum,

after binding and sequestration.

-!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2.

-!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic

reticulum. Anchored to the membrane of the endoplasmic reticulum

through 2 putative transmembrane domains.

-!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=4;

CC Name=1; Synonyms=RTN 4A, Nogo-A, RTN-xL;

CC IsoId=09NQC3-1; Sequence=Displayed;

CC Name=2; Synonyms=RTN 4B, Nogo-B, RTN-xS, Foccen-M;

CC IsoId=09NQC3-2; Sequence=VSP\_005655;

CC Name=3; Synonyms=RTN 4C, Nogo-C, Foccen-S;

CC IsoId=09NQC3-3; Sequence=VSP\_005652, VSP\_005653;

CC Name=4;

CC IsoId=09NQC3-4; Sequence=VSP\_005654;

CC TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain

and testis and weakly in heart and skeletal muscle. Isoform 2 is

widely expressed excepted for the liver. Isoform 3 is expressed in

brain, skeletal muscle and adipocytes. Isoform 4 is testis-

specific.

-!- SIMILARITY: Contains 1 reticulon domain.

CC -!- CAUTION: Ref.11 sequence differs from that shown due to

frameshifts in positions 1149 and 1156.

CC -----

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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).

CC -----

DR EMBL; AJ251383; CAB99248.1; -

DR EMBL; AJ251384; CAB99249.1; -

DR EMBL; AJ251385; CAB99250.1; -

DR EMBL; AB040462; BAB18927.1; -

DR EMBL; AB040463; BAB18928.1; -

DR EMBL; AF148537; AAG12176.1; -

DR EMBL; AF148538; AAG12177.1; -

DR EMBL; AF087901; AAG12205.1; -

DR EMBL; AF320999; AAG40878.1; -

DR EMBL; AF132047; AAD31021.1; -

DR EMBL; AF132048; AAD31022.1; -

DR EMBL; AB015639; BAA83712.1; -

DR EMBL; AF077050; AAD27783.1; -

DR EMBL; AF177332; AAG17976.1; -

DR EMBL; AB020693; BAA74909.2; ALT\_INIT.

DR EMBL; BC001035; AAH01035.1; -

DR EMBL; BC007109; AAH07109.1; -

Query Match 75.3%; Score 4403.5; DB 1; Length 1192;

Best Local Similarity 75.9%; Pred. NO. 2.4e-152;

Matches 909; Conservative 104; Mismatches 145; Indels 39; Gaps 20;

QY 1 MEDIDSSIVSSSTDSPPRPAPFKYQVTRPEDEDEDEDEDEDEDEDEDEDEDELEVLK 60

DB 1 MEDLDQSLVSSS-DSPPRPAPFKYQVTRPEDEE-EEEEEEDEDEDELEVLK 58

QY 61 PAAGLSAAAVP--PAAAAPLDFFSDSVPPAPRGLPAPAPAPAPRQPSWERSPAA--P 115

DB 59 PAAGLSAAVPTAPAPAGAPLMDFGNDFFVPAPRGLPAPAPVAPRQPSWDSVSTVP 118

QY 116 APSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPSTPAAPKR 166

DB 119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVQAPVMTTPAPAPAPSTPAAPKR 178

QY 167 RG-SCSVDETFLAPAASEPVTIPSAEKIMDLMEQNTVSSGQDFPSVLETAASLPS 225

DB 179 RGSSGVDETFLAPAASEPVTIRSAEN-MDLKEQFGNTISAGQDFPSVLETAASLPS 237

QY 226 LSPSTVTFKGHGYLGNLSAVSSSGTTEETINEASKELPERATNPFVNRDLAEPSELEY 285

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Db 238 LSPLSAAFKEHEYLGNLSTVLTGTLQENVSSEASKEVSEKAKTLLIDRLDTFSELEY 297
Qy SEMGSSFKGSPKESAIIVENTKERVIVRSXDKED-LVCSAALHSPQSPVPG-----KED 339
Db 286 SEMGSSFKGSPKESAIIVENTKERVIVRSXDKED-LVCSAALHSPQSPVPG-----KED 339
Db 298 SEMGSSFKGSPKESAIIVENTKERVIVRSXDKED-LVCSAALHSPQSPVPG-----KED 339
Qy 340 RVSPSEKTMIDIFNEMQSVAVPVRREYADFKPFQAEWVVDKTYEGSRDVLAA-----RANV 395
Db 358 EVVSEKAKDSFNEKRVAVPVRREYADFKPFQAEWVVDKTYEGSRDVLAA-----RANV 395
Qy 396 ESKVDKCLDSLEQSLGKSGSEGNEDASPPSPPEPVKDSRAYITCASFT-SATESTT 454
Db 417 ESKVDKCLDSLEQSLGKSGSEGNEDASPPSPPEPVKDSRAYITCASFT-SATESTT 454
Qy 455 ANTPFLLEDHTSENKTKTEERKAQIITK-TSPKTSNPFVAVQSEADYVTTDTLS 513
Db 477 TNIPFLGDPITSENKTKTEERKAQIITK-TSPKTSNPFVAVQSEADYVTTDTLS 513
Qy 514 KVTEAAVSNMPEGLTPDLVQACESELNEATGTKIAYETKVDLVQTSBAIQESLYPTAQL 573
Db 537 KVTEAAVSNMPEGLTPDLVQACESELNEATGTKIAYETKVDLVQTSBAIQESLYPTAQL 573
Qy 574 CPSFEABATSPVLPDITWMEAPLNSLLPSAGASVQVQSPVPLERAPPVVSVDISKLPEN 633
Db 597 CPSFEABATSPVLPDITWMEAPLNSLLPSAGASVQVQSPVPLERAPPVVSVDISKLPEN 633
Qy 634 PPPVEEAMNVALKAL-GTKEGIKEPESNAVAQTEAPYISIACDLIKETKLSSTEPDPDF 692
Db 656 PPPVEEAMNVALKAL-GTKEGIKEPESNAVAQTEAPYISIACDLIKETKLSSTEPDPDF 692
Qy 693 SNYSIEIAKFEKSVPEHAELVEDSPSPFVDFSDSIPPEVQPTQEEAVMLKESLSEVS 752
Db 716 SDYSEMAKVEOPVPHSELVEDSPSPFVDFSDSIPPEVQPTQEEAVMLKESLSEVS 752
Qy 753 -ETVAQHK-ERLGSAPQELKPYLESQPNLHSTKDA-ASNDIPTLKKEKISLQMBEF 809
Db 776 FESMIEYENKEKLSALPPEGGKPYLESQPNLHSTKDA-ASNDIPTLKKEKISLQMBEF 809
Qy 810 NTALYSNDLLSKEDKIKESSETSDSPIIIDEFFTFVSAKDDSPKLAKEYTDLEVS 868
Db 836 STAVYSNDLLSKEDKIKESSETSDSPIIIDEFFTFVSAKDDSPKLAKEYTDLEVS 868
Qy 869 DKSBIANTQSGADSLPCLPCLDSFKNIPK--DEVHVSDEFSENRSSVSKASISPSNV 926
Db 896 HKSIANAPDAGSLPCTELPHDLKNIQPKVEKISFSDFSKNGSATSKVLLLPDV 955
Qy 927 SALEPQTMGSIKSLTKBAEKKLPSTDEKEDRSJSAVLABELSKTSVVVDLLYWRDIK 986
Db 956 SALATQABIESIVKPKVLVKEAEKKLPSTDEKEDRSJSAVLABELSKTSVVVDLLYWRDIK 1015
Qy 987 KGVVFGASLLSLVTSFVSIVTAYIALALLSVTISFRIYKGVIOAIQKSDSGHPRA 1046
Db 1016 KGVVFGASLLSLVTSFVSIVTAYIALALLSVTISFRIYKGVIOAIQKSDSGHPRA 1075
Qy 1047 YLESEVAISELVQKYSNLSALGHVNSTIKELRRLFLVDDLVSLKFAVLMVVFYVVGALF 1106
Db 1076 YLESEVAISELVQKYSNLSALGHVNSTIKELRRLFLVDDLVSLKFAVLMVVFYVVGALF 1135
Qy 1107 NGLTLLIALISLSPVIVYERHQVQIDHYIHLANKSVKDMAMAKIQAIPGLKRAKAD 1163
Db 1136 NGLTLLIALISLSPVIVYERHQVQIDHYIHLANKSVKDMAMAKIQAIPGLKRAKAE 1192
RESULT 6
Q81UA4 ID Q81UA4 PRELIMINARY; PRT; 986 AA.
AC Q81UA4;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DE 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE RNT4 (RTN4 isoform Ab) (RTN4 isoform D) (RTN4 isoform E) (RTN4 isoform
DE F) (RTN4 isoform G) (RTN4 isoform Aa).
GN Name=RTN4;
```

```
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT "Genomic structure and functional characterisation of the promoters of
RL human and mouse nogo/rtn4.";
RL J. Mol. Biol. 325:299-323(2003).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN (3)
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX Oertle T., Schwab M.E.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102285; AAM64244.1; -
DR EMBL; AY123246; AAM64250.1; -
DR EMBL; AY123247; AAM64251.1; -
DR EMBL; AY123248; AAM64252.1; -
DR EMBL; AY123249; AAM64253.1; -
DR EMBL; AY123250; AAM64254.1; -
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon.
DR PROSITE; PS0845; RETICULON.
SQ SEQUENCE 986 AA; 108449 MW; 0CDE8F647036415A CRC64;

Query Match 62.0%; Score 3627.5; DB 2; Length 986;
Best Local Similarity 75.4%; Pred. No. 3.3e-124;
Matches 745; Conservative 96; Mismatches 126; Indels 21; Gaps 13;

Qy 195 MDLMEQPGNTVSSQEDFPFVLLTAASLPSLSTVSPKHEGYLGNLSAVSSEGTIE 254
Db 1 MDLKEQPGNTISAGQEDFPFVLLTAASLPSLSTVSPKHEGYLGNLSAVLPTGTLQ 60
Qy 255 ETLNEASKELPERATNPFVNRDLAEFSELEYSESGSFKGSPKESAILVNTKBEIVR 314
Db 61 ENTSEASKVESEKAKTLLIDRLDTFSELEYSESGSFKGSPKESAVIVANPREIIVK 120
Qy 315 SKOKED-LVCSAALHSPQSPVPG-----KEDRVVSPSEKTMIDIFNEMQSVAVPVRREYAD 368
Db 121 NKDEEEKLVSNLILHNOQLPTALTCLKVEDEVVSVSEKAKDSFNEKRVAVPVRREYAD 180
Qy 369 FKPEQAEWVVDKTYEGSRDVLAA-----RANVESKVDKCLDSLEQSLGKSGSEGNED 424
Db 181 FKPFERYVWEKDSKEDS-DMLAAGKIESNLESKVKKCFADSLSEQTNHSEKSSNDT 239
Qy 425 SFPSTPSPVKDSSRAYITCASFT-SATESTTANTFPLEDHTSENKTKTEERKAQI 483
Db 240 SFPSTPSPVKDSSRAYITCASFT-SATESTTANTFPLEDHTSENKTKTEERKAQI 483
Qy 484 TEK-TSPKTSNPFVAVQSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQACESELNE 542
Db 300 TEKNTSTKTSNPFVAVQSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQACESELNE 359
Qy 543 ATGTKIAYETKVDLVQTSBAIQESLYPTAQLCPSFEABATSPVLPDITWMEAPLNSLLP 602
Db 360 VTGTKIAYETKMDLVQTSBAIQESLYPTAQLCPSFEABATSPVLPDITWMEAPLNSLLP 419
Qy 603 SAGASVQVQSPVPLERAPPVVSVDISKLEPENPPPYEAMNVALKAL-GTKEGIKEPESFN 661
Db 420 SAGASVQVQSPVPLERAPPVVSVDISKLEPENPPPYEAMNVALKAL-GTKEGIKEPESFN 478
Qy 662 AAVQETEPAYISIACDLIKETKLSSTEPSPDFSNYSIEIAKFEKSVPEHAELVEDSPSEB 721
Db 662 AAVQETEPAYISIACDLIKETKLSSTEPSPDFSNYSIEIAKFEKSVPEHAELVEDSPSEB 721
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479 AALQETAPYISIAADLIKETKLSAPADPDSYSEMAKVQVPDHSSELVSDSSDPSEP 538

722 VDLFSDSDSIPVPTQEEAVMLMKESLITEVS-ETVAQHK-EERLSASPQBLKPYLESFQ 779

539 VDLFSDSDSIPDVQPQKQDETVMVKESLITETSPFSEMIETENKELSLAPPGGKPYLESFK 598

780 PNLHSTKDA-ASNDIPTLTKKEKISLOMBEFTNTAIYSNDDLLSSKEDKIKESFTTFSDSSP 838

599 LSLDNTKDTLLPDEVSTLSKKEKIPLOMBELSTAVYSNDDLFITSKEAQIRETETTFSDSSP 658

839 IETIDEPPTFVSAKDS-PKLAKEYTDLEVDSKSETANTIOSGADSLPCLPELPCDLSPKNI 897

659 IETIDFPPTLSKTSFSLKLAKEYTDLEVSHKSEIANADPGAGSUPCTELPHDLSLUNI 718

898 YPK--DEVHVSDFSENRSSVSASISPSNVSALEPQTEMGSIYKGSKSLTKEAEKKLPSP 955

719 QPKVEKISPSDFSEKNGSATSKVLLPPDVSAALATQAEIESIVKPKVLKAEKKLPSP 778

956 TEKEDRSLSAVLSAEISKTSVVDLLKYWRDIKKTGVVFGASLFLLLLSLTVFSIVSVTAYIA 1015

779 TEKEDRSPSAIFSASLKSIVVDLLKYWRDIKKTGVVFGASLFLLLLSLTVFSIVSVTAYIA 838

1016 LALLSVTISPRIYKGVIOAQKSDGEPFPAYLSEVAISEVSEIYKGSVNSALGHVNSTIK 1075

839 LALLSVTISPRIYKGVIOAQKSDGEPFPAYLSEVAISEVSEIYKGSVNSALGHVNSTIK 898

1076 ELRRLFLVDDLVSLLKFAVLMMVFTYVGVLFNGLTLLILALISLFSIPVIYERHQVQIDH 1135

899 ELRRLFLVDDLVSLLKFAVLMMVFTYVGVLFNGLTLLILALISLFSVPVIYERHQVQIDH 958

1136 YLGLANKSVKDAWMAKIQAKIPLKRXAD 1163

959 YLGLANKVNVKDAWMAKIQAKIPLKRXAE 986

RESULT 7

Q7TNB7 PRELIMINARY; PRT; 720 AA.

AC Q7TNB7

CD Q7TNB7

AD Q7TNB7

DT 01-OCT-2003 (T-EMBLrel. 25, Created)

DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE Hypothetical protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RP [1]

RN SEQUENCE FROM N.A.

RP STRAIN=C57BL/6; TISSUE=Brain;

RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Srausberg R.L., Feingold E.A., Grouse L.H., Deige J.G.

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalek U., Smallus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences".

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RP [2]

RN SEQUENCE FROM N.A.

RP



OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Straube R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Klausner R.D., Zeeberg B., Bueow K.H., Schaefer C.F., Bhat N.K.,  
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Hopkins R.F., Maruina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Diatchenko L., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Brownstein M.J., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Raha S.S., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
RA Straube R.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC022192; AAH22192.1; -;  
DR MGD; MGI:1918635; Rcn4.  
DR GO; GO:0005783; C:cytoplasmic reticulum; IEA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
SQ SEQUENCE 639 AA; 70312 MW; 309A19DA37603F11 CRC64;  
  
Query Match 50.0%; Score 2926; DB 2; Length 639;  
Best Local Similarity 91.6%; Pred. No. 6.5e-99;  
Matches 588; Conservative 20; Mismatches 30; Indels 4; Gaps 2;  
  
Qy 523 MPEGLTPDLVQACESENEATGKIAYETKVDLVQTEAIOESLYPTAQICPSFEAE 582  
Db 1 MPEGLTPDLVQACESENEATGKIAYETKVDLVQTEAIOESLYPTAQICPSFEAE 60  
  
Qy 583 TPSPVLPDIVMEAPLNSLLPSGASVQPSVPLEAPPVSDSIKLEPENPPPYEAMN 642  
Db 61 TPSPVLPDIVMEAPLNSLLPSGASVQPSVPLEAPPVSDSIKLEPENPPPYEAMN 120  
  
Qy 643 VALKALGTKEGKEPESFNAVAQTEAPYISACDLIKETKLTSTPSPDFSNYSEIAKFE 702  
Db 121 VALKTSDAKEELKEPESFNAVAQTEAPYISACDLIKETKLTSTPSPDFSNYSEIAKFE 180  
  
Qy 703 KSVPEHAELVEDSPSEPPVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHK-EE 761  
Db 181 KSPVDPCHLVDSDSPSEPPVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHK-EE 240  
  
Qy 762 RLSASQBLGKPYLESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTAISNDLLS 821  
Db 241 RLSASQBLGKPYLESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTAISNDLLS 300  
  
Qy 822 SKEDKIKESFTSDSSPIEIIIDEPPTFVSAKDDSPKLAKEYTDLEVSKSEIANIQSGAD 881  
Db 301 SKEDKIKESFTSDSSPIEIIIDEPPTFVSAKDDSPKLAKEYTDLEVSKSEIANIQSGAN 357  
  
Qy 882 SLPCLEPCDLISFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALPQTEMGSIVKS 941  
Db 358 SLPCLEPCDLISFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALPQTEMGSIVK 417

Qy 942 KSLTKEAEKLPSPDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLS 1001  
Db 418 KSLTKEAEKLPSPDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLS 477  
  
Qy 1002 LTVFSIVSVTAYIALALLSVTISPRIYKGVTOAQKSDGHPFRAYLSEVAISELVOK 1061  
Db 478 LTVFSIVSVTAYIALALLSVTISPRIYKGVTOAQKSDGHPFRAYLSEVAISELVOK 537  
  
Qy 1062 YSNSALGHVNSTIKELRRLFLVDDDLVDSLKFAVLMWVFTYVYVGFALPGLTLLILALISLFS 1121  
Db 538 YSNSALGHVNSTIKELRRLFLVDDDLVDSLKFAVLMWVFTYVYVGFALPGLTLLILALISLFS 597  
  
Qy 1122 IPVTYERHQVIDHYLGLANKSVKDAKIAKIPGLKRAKAD 1163  
Db 598 IPVTYERHQVIDHYLGLANKSVKDAKIAKIPGLKRAKAE 639  
  
RESULT 9  
Q80W95  
ID Q80W95 PRELIMINARY; PRT; 578 AA.  
AC Q80W95;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Nogo-A (Fragment)  
GN Name=Nogo-A;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tozaki H., Hirata T.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB073672; BAC75974.1; -;  
DR GO; GO:0005783; C:cytoplasmic reticulum; IEA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
FT NON\_TER 1  
SQ SEQUENCE 578 AA; 63696 MW; 832670C171E4AC61 CRC64;  
  
Query Match 44.6%; Score 2610; DB 2; Length 578;  
Best Local Similarity 90.7%; Pred. No. 1.8e-87;  
Matches 527; Conservative 18; Mismatches 32; Indels 4; Gaps 2;  
  
Qy 584 PSPVLPDIVMEAPLNSLLPSGASVQPSVPLEAPPVSDSIKLEPENPPPYEAMN 643  
Db 1 PSPVLPDIVMEAPLNSLLPSGASVQPSVPLEAPPVSDSIKLEPENPPPYEAMN 60  
  
Qy 644 ALKALGTKEGKEPESFNAVAQTEAPYISACDLIKETKLTSTPSPDFSNYSEIAKFE 703  
Db 61 ALKTSDAKEELKEPESFNAVAQTEAPYISACDLIKETKLTSTPSPDFSNYSEIAKFE 120  
  
Qy 704 SVPEHAELVEDSPSEPPVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHK-BER 762  
Db 121 SVPDCHLVDSDSPSEPPVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHK-BER 180  
  
Qy 763 LSASQBLGKPYLESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTAISNDLLS 822  
Db 181 LSASQBLGKPYLESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTAISNDLLS 240  
  
Qy 823 KEDKIKESFTSDSSPIEIIIDEPPTFVSAKDDSPKLAKEYTDLEVSKSEIANIQSGADS 882  
Db 241 KEDKIKESFTSDSSPIEIIIDEPPTFVSAKDDSPKLAKEYTDLEVSKSEIANIQSGANS 297  
  
Qy 883 LPLCLEPCDLISFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALPQTEMGSIVKS 942  
Db 298 LPLCLEPCDLISFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALPQTEMGSIVK 357  
  
Qy 943 SLTKEAEKLPSPDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLS 1002  
Db 358 SLTKEAEKLPSPDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLS 417

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QY 1003 TVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDSGHPFRAYLSEVAISEELVQRY 1062
Db 418 TVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDSGHPFRAYLSEVAISEELVQRY 477
QY 1063 SNSALGHVNSTIKELRRFLVDDVSLKFAVLMVFTYVGGALFNGLTLLIILALISLFSI 1122
Db 478 SNSALGHVNSTIKELRRFLVDDVSLKFAVLMVFTYVGGALFNGLTLLIILALISLFSI 537
QY 1123 PVIYERHOVIDHYLGLANKSVKDMAKIOAKIPGLKRAKAD 1163
Db 538 PVIYERHOVIDHYLGLANKSVKDMAKIOAKIPGLKRAKAD 578

RESULT 10
Q6RSS8
ID Q6RSS8 PRELIMINARY; PRT; 658 AA.
AC Q6RSS8;
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Neurite outgrowth inhibitor NOGO-A (Fragment).
GN Name:NOGO;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP SEQUENCE FROM N.A.
RA Calharp S.A., Pira C.U., McNeill D.S., Liwnicz B.H., Oberg K.C.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY494005; AAS18427.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
FT NON_TER
SQ SEQUENCE 658 AA; 72075 MW; 14B7A000C5E8CDA5 CRC64;

Query Match 28.5%; Score 1664; DB 2; Length 658;
Best Local Similarity 56.7%; Pred. No. 66-53;
Matches 379; Conservative 82; Mismatches 168; Indels 40; Gaps 17;

QY 524 PGLTPDLVQEAACESEINATGCTKIAYETKVLDTVOTSEAIQBSLYPTAQLCPSEFAEAT 583
Db 1 PGLTPDLVQEAACESEINATGCTKIAYETKVLDTVOTSEAIQBSLYPTAQLCPSEFAEAT 60
QY 584 PGPVLPDIWNEAPLNSLLPSAGASVQPSVPLEA-PPPVSVSDSIKLEPNPPPYEEAMN 642
Db 61 PGPVLPDIWNEAPLNSLLPSAGASVQPSVPLEA-PPPVSVSDSIKLEPNPPPYEEAMN 120
QY 643 VAL-KALGKKEGI--KEPESFNAQVQETAPYISIACTLIKETKISTE-PPDPFSNYSE 697
Db 121 MFLTQAEAKBELTLKADRESSTSPEDLETPTIYISIACTLIKETKIVSGESASPLTDYST 180
QY 698 IAKFE---KSVPEHAELVSDSPESPEVDLFDSDSIPEVP--QTQEEAVMLKESLTVS 752
Db 181 TPTTEHLSQDVSEHKEAELKSPQFGKDLFRQVMPDFGKESEDQTLILNGKSVENIE 240
QY 753 ETVAQKKEERLASPOELKPKVLESFQPNLHSTKDAASN-DIPT---LTKKEKISLOWEE 808
Db 241 ---TDEEQRRLVDSLAATGPKVLESFQDELSDSKIVTTPQSEFTPAKIAKAKIPLQWEE 297
QY 809 FNTAIVNDLLSSKEDKIKESSTFSDSPIETIDFTFVSAKDSPKLAKETDLEVS 868
Db 298 LNALAYST-DVSVAMEPKGDSKGLSPSPVSVEDDFVMLVPKCTEFVA-EVTDRETV 355
QY 869 DKSE---IAN-IQSGADSLPCLELPCDLSFKNIYPK--DEVH-----VSDSEFSENK 914
Db 356 HKNESKDISNEIRDEKRQAPLTCLPCDLSVRNVKVTEDDAHALKKSLQAIQREVPE--- 412
QY 915 SVSKASISFNSVALEPQPTMGISIVKSKSLTKAEAKLPDTEKEDRSLSAVLSAELSKT 974

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Db 413 -VSMVSLPATGTSPSTKEIVSVGKPEAFKEAERGAASAKEKE--KPTAVFSAKLNV 469
QY 975 SVVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIA 1034
Db 470 SVVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIA 529
QY 1035 IQKSDGHPFRAYLSEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDVSLKFAV 1094
Db 530 IQKSDGHPFRAYLSEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDVSLKFAV 589
QY 1095 LMWFTYVGGALFNGLTLLIILALISLFSIPVIYERHOVIDHYLGLANKSVKDMAKIOAK 1154
Db 590 LMWFTYVGGALFNGLTLLIILALISLFSIPVIYERHOVIDHYLGLANKSVKDMAKIOAK 649
QY 1155 IPGLKRAKAD 1163
Db 650 IPGLKRAKTE 658

RESULT 11
Q6JRV0
ID Q6JRV0 PRELIMINARY; PRT; 1043 AA.
AC Q6JRV0;
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE RTN4.1-A1.
GN Name:RTN4;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]_TaxID=8355;
RP SEQUENCE FROM N.A.
RA Klinger M., Diekmann H., Heinz D., Hirsch C., Hannbeck von Hanwehr S.,
RA Petrusch B., Oertle T., Schwab M.E., Stuermer C.A.;
RT "Identification of two NOGO/RTN4 genes and analysis of Nogo-A
expression in Xenopus laevis";
RL Mol. Cell. Neurosci. 25:205-216(2004).
DR EMBL; AY316197; AAQ82646.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 1043 AA; 113994 MW; 6AF170C14DD2CB1A CRC64;

Query Match 27.7%; Score 1620; DB 2; Length 1043;
Best Local Similarity 37.2%; Pred. No. 4.4e-51;
Matches 464; Conservative 153; Mismatches 337; Indels 292; Gaps 45;

QY 5 DOSSIVSSSTDSPPPPPA-----FKQFVTEPEDEDEEE 41
Db 3 EQSPDISSSHSGDERREPAQGERKPDLDLDTLGAGQFQSPFGSGHPARDIEEE 62
QY 42 EDEEEDDELELEVLERKPAAGLSAAVPPAAAAFLDFSDSDSVPPAP----RGPLPAA 97
Db 63 EDEEERGANW-----DSLESPVPEEPGSDSI 91
QY 98 PPAAPERQPSWERSPAAPAPSLPPAAVLPKLPEDDEPPAPPPPPPPAGASPLAEPAP 157
Db 92 SPVSP-----HSPAVP-----SAPMEEPER 112
QY 158 PSTPAAPKRGSGVDETLFPALPAASEPVPSSAEKIMDLMEQNGTVSSGGEDRPPSVLL 217
Db 113 PAPCTAP----SGVDENLFTLPAASAHLMHASAKIM----EPYSTVSTGQEEFASVLL 164
QY 218 ETAASLPISLSTVTSFKHEGYLGNLSAVSSSEGTIEETLNFEASKELPERATNPFVNRDL 277
Db 165 QSTASLSSLPISLSTDSSEK-----AETVAFTGLAATEALQEPDNDM----- 208

```





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      :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
872 SVFISVSLAYIALALLSVTISFRIYKGLVLAQKSEEGHPRFSLNLAALPEDVQKH 931
      :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
1063 SNSALGHVNSTIKELRRLFLVDLVDLSKFAVLMVFTVVGALFNGLTLLIILALISLPSI 1122
      :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
932 CTVALNQVNRVTAELRRLFLVDLVDLSKFAVLMVFTVVGALFNGLTLLIILALISLPSI 991
      :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
1123 PVIYERHQVQIDHYLGLANKSVKDMAMAKIQAIPGLKRXAD 1163
      :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
992 PVIYERHQVQVHDYLLALINKNLKNTSDLLAKVPLGKRKSE 1032

RESULT 14
Q6JRV8
ID Q6JRV8 PRELIMINARY; PRT; 1044 AA.
AC Q6JRV8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE RTN4.2-A2.
GN Name=RTN4;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Wholemount embryos;
RX PubMed15019938; DOI=10.1016/j.j.mcn.2003.09.021;
RA Klinger M., Diekmann H., Heinz D., Hirsch C., Hannbeck von Hanwehr S.,
RA Petrusch B., Oertle T., Schwab M.E., Stuermer C.A.;
RT "Identification of two NOGO/RTN4 genes and analysis of Nogo-A
RT expression in Xenopus laevis";
RL Mol. Cell. Neurosci. 25:205-216 (2004).
DR EMBL; AY316189; AAQ82638.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon.1.
DR PROSITE; PS0845; RETICULON.1.
SQ SEQUENCE 1044 AA; 115088 MW; 34FB48351A6C9888 CRC64;

Query Match 27.1%; Score 1586.5; DB 2; Length 1044;
Best Local Similarity 37.4%; Pred. No. 7,3e-50;
Matches 465; Conservative 171; Mismatches 320; Indels 287; Gaps 54;

QY 6 QSSLVSTSDSPRRP-----PAFYQFVT-----EPEDDEDEEERDE 44
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
4 QSSDISSHEPGDTKPWEDDDVLDLTGGAGQFSPTFPVSPARHMEKEEENEDEE 63
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
45 EDDDELELEVLERKPAAGLSAAVPPAAAPLLDFSSDVPAPRGPLPAAPPAER 104
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
64 KSKESLASPVLE-----DQGST-----GSSPTPHSP--PEFSAPTEEP 104
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
105 QPSWERSPAAPAPSLPPAAAVLPSKLPDEBPAPPPPPAGASPLAEPAPSTPAAP 164
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
105 PPA-----TCAPSSSLAYTVLAQLRKE----- 128
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
165 KRGSGSVDETLFALPAASEVPVPSAEXKINDLMQPNQNTVSSQEDPSPVLLTAASLP 224
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
129 -----DENLFLPAAASAHMLHLSADKIM-----EPSSTVSTGQEDPASVLLQSTASLS 176
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
225 SLSPLSVTSFKHGHYGLNLSAVSSSEGTIEETLNKASKELPERATNPF--VNRDLAEFSEL 283
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
177 SLPSLSS---KEH-----VQVAFSTGL-----AANEALQPTNTYTSRSLDTLET 222
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
284 EYSEMGSSFGKSPKGESAILVETKERVIVRSKOKEDLVCSAALHSP--QESPVGKEDRV 341
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
223 K-----ALDQFKKEVIFSDK-----GVVHEHPTSQETISEEHAK 257
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
342 VSPKTMDFINEMQMSVAVPRE-----EYADFPP-----EQAEVVKDTYEGSR 386
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
258 LYSQSAKEMFGMLQSVAPPHEEFTDIKEVDYQYVDFKPFIFSSNSRSDIGYEVKDAE--- 314

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QY 387 DVLAAANVESKVRKCKLEDLSLEQSLGKDSGRNEDASFSTPBPVXDSSRAYITCASPF 446
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
315 KLHVRMLNESTAKHE--EKSEEEKEM-----DISDIS--PLTPEVLSDSSTYENP----- 362
QY 447 TSATESITTANTPP--LLEDHTSENKTDKKEIKERKAAQIITEKTS-----PKTSPPL-V 497
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
363 :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
498 AVQDSEADYVTTDTLSKVTAAVSNMPEGLTPDLVQBAECESBELNATGKIAYETKVDLV 557
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
414 SAQESE--YVTTG---ATRVQVSTKAEQPTDVIQEAYESAYDTGISKLYEPNIDLV 467
QY 558 QT-SEAIQESLVPQAOLCPSFEERBATPSVLPDITVMEAPLNSLPSAGASVQVQSVSPL 616
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
468 QTAATSMQEKVSPTAQV--PALLE--DSVSSVLPDITVMEAPLASTL--CLETMALKEPDISPV 524
QY 617 EAPPVVSYSIKLEPPNPYPPEEAMNVALKALG-----TKEGIKEPESFNAVQBT 667
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
525 RIEPPARDEKTKARPEKPPSYEAEVTEVLQDQGPAAADLGDQKQ-----AVVKEA 576
QY 668 EA-----PVIACDLIKETKLTSTPSPDFSNYSYSEIAKFSV--PEHAELVEDSSPEBP 721
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
577 EAPYISPYIACDLIKGTQSA-----SDTFEFSKEQHEFDSQFMEPSDESSPDS- 629
QY 722 VDLFSDDSIPVPOQBEAVMLKESLTVSET-----VAQHKERLSASP 767
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
630 :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
768 QELGKPYLESQPNLHSTK--DAASNDIPT--LTKKEKISLOWEEFNATYISNDLLSSKE 824
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
679 --SKPYLASQPEIYVSKATDLPAKGLDTEISIPQERHLHMERFDEGLYSS--KLPGSKY 734
QY 825 DKIKESETFSSSPEIET---DEPFTFVSAKODSPKLAKEYTDLDEVSKSEIANIQSGAD 881
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
735 SPVSESPFPR--LSPEELTSKHEEIQTHI--AKHPEDKLQKN-----KDKLDF----- 778
QY 882 SLPCLELPCLDLSFKNIYPKDVEHVHVSDEFSNRSVSKASISPSNVSALEPOTEMSSIVKS 941
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
779 :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
942 KSLTKAEAF--KKLPSTDEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLL 1000
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
825 EPPSKDDEVSKLP--KKESKAPSTVPSSDFRNSVDLIYWRDIKRGVGVFGASLFLLL 881
QY 1001 SLTVFSIVSVTAYIALALLSVTISFRIYKGLVLAQKSEEGHPRFSLNLAALPEDVQ 1060
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
882 SLTVFSIVSVLAYIALALLSVTISFRIYKGLVLAQKSEEGHPRFSLNLAALPEDVQ 941
QY 1061 KYSNSALGHVNSTIKELRRLFLVDLVDLSKFAVLMVFTVVGALFNGLTLLIILALISL 1120
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
942 KCTVALNQVNRVTAELRRLFLVDLVDLSKFAVLMVFTVVGALFNGLTLLIILALISL 1120
QY 1121 SIPVYERHQVQIDHYLGLANKSVKDMAMAKIQAIPGLKRXAD 1163
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
1002 SIPVYERHQVQVHDYLLALINKNLKNTSDLLAKVPLGKRKSE 1044

RESULT 15
Q6JRV2
ID Q6JRV2 PRELIMINARY; PRT; 1024 AA.
AC Q6JRV2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE RTN4.1-A3.
GN Name=RTN4;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]

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RP SEQUENCE FROM N.A.
RC TISSUE=Wholemount embryos;
RX PubMed=15019938; DOI=10.1016/j.j.mcn.2003.09.021;
RA Klinger M., Diekmann H., Heinz D., Hirsch C., Hambeck von Hanwehr S.,
RA Petrausch B., Oertle T., Schwab M.E., Stuermer C.A.;
RT "Identification of two NOGO/RTN4 genes and analysis of Nogo-A
RT expression in Xenopus laevis.";
RL Mol. Cell. Neurosci. 25:205-216(2004).
DR EMBL; AY316195; AAQ82644.1; -
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS00845; RETICULON; 1.
SQ SEQUENCE 1024 AA; 112016 MW; 79197ACA7D29C5C CRC64;

Query Match 26.6%; Score 1554.5; DB 2; Length 1024;
Best Local Similarity 36.4%; Pred. No. 1e-48;
Matches 454; Conservative 149; Mismatches 332; Indels 311; Gaps 46;

QY 5 DQSSLVSSSTDSPPRPPA-----FKYQVTEPEDEDEEE 41
DB :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
DB 3 EQSPDISSSHGSDERREPAQPGERKPWDDLVDLDTGGAGQFSQPFSGSHPARDIEEE 62
QY 42 EDEEEDDELELEVLERPAAGLSAAVPPAAAPLLDFSSDVPPAP-----RGPLPAA 97
DB :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
DB 63 EDEEERGAWK-----DSLEPSPVEEPGSDISI 91
QY 98 PPAAPERQPSWERSPAAPAPSLPPAAAVLPKLPEDEPPARPPPPPPAGASPLAEPAP 157
DB :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
DB 92 SPVSP-----HSPAVP-----SAPMEEPERP 112
QY 158 PSTPAAPKRRGSGVDETILFALPAASEVPIPSAEKIMDLMEQPGNTVSSGGEDPSPVLL 217
DB :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
DB 113 PAPCTAP-----SGSVD-----KIM-----EPYSTVSTGQEEFASVLL 145
QY 218 ETAASLPSLSPSTVSFKHGYLGNLSAVSSSEGTIEETLNASKELPERATNPFVNRDL 277
DB :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
DB 146 QSTASLSLSPSLSTDSKSH-----AETVAPPTGLAATEALQEPDNNY----- 189
QY 278 AEFSELEYSEMSSFKGSPKGSAILVENTKEEVIVRSKDEDLVCSAALHSP--QESPV 335
DB :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
DB 190 -----SVSRITSHLPLSDNLESKAL-DQVKEVIFSEK-----GYVVDHPTSQOETI 235
QY 336 GKEDRVVSPKEMDIFNEMQMSVAP-----VREYADFKEP-----EQAEVKD 380
DB :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
DB 236 SEEHAKLYSQSAKEMFSGMLQSVAPPHEEFTDIEKYDYPYDFKPTMSSKSGDVGVEVD 295
QY 381 TYEGSRDLAARAVESKYDRKCLEDSLQKSLGKDSGRNEDASPPSTPEPVKDSRAY 440
DB :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
DB 296 VAE-KFQVDVGRNLNLESAVKHE-----EKSSEMEIDSISDDIS-PLTPELLPD----- 342
QY 441 ITCASFTSATESTANTFFLLED-----HTSENKTDEKKIERKQIITEKTS--- 488
DB :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
DB 343 -----STDYDMFATVEQNIIPFSFGGHVAGNKTDEKKIEDIEAQ-----KTSVGF 387
QY 489 ----PKTSNPLF-VAVQDSADYVTTDLTKSVTEAAVSNMPEGLTPDLVQEAACESELNEAT 544
DB :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
DB 388 GLKVATVNPFFYBESAQES--YVTHVATH-----VSTKPEGTPDIVEAESEAYDTG 440
QY 545 GTKIAYETKVDLVOT--SEALQESLYPTAQICPSFEAEATPSPVLPIVMEAPLNSLLPS 603
DB :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
DB 441 IPKQKYESNIDLVTQTAANSVQEKVPTAQAPARLEETDSVSSPVLPIVMEAPLASALET 500
QY 604 AGASVVQPSVSPLEAPPPVSDSIKLEPENPPPYEEAMNVALK-----AL-GTKEGIKE 656
DB :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
DB 501 V----ALKPDISPVGIKPPARVEKTKAEPEKPPSYEEAVTEVLQNQDLAAALGSGKQ--- 554
QY 657 PESFNAVQETEAPYISACDLIKETKLTSTEPSPPDFSNTYSEIAKFEKSPVEHAELVEDSS 716
DB :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
DB 555 -----AVVEETETPYISACDLIKGTESVASGTFEPSKLQ-NEFESQFMPS---DESS 605
QY 717 PESEPVDLFSDDSIPEVPQ-----TQBEAVMLMKESILTEVSETVAQHK-----EERLSASP 767
DB :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||

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Search completed: June 16, 2005, 13:17:33

Job time : 164.778 secs

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Db 606 PDSE-----CSEPSYKQWDEVVQKEAFSIKTSEVNAQSIIPQKQVFPQKSEESP 658
QY 768 QELGKPYLESFQPNL---HSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKE 824
Db 659 ---SKSYLDSQPEICVSKATSDLFPAKGLTTLQEK--PLQWEELDEGI-SLEKIPCTKY 712
QY 825 DKIKSETFSOSSPIEIIDEPPTFVSADKDPKLAKETVDTLSEVSKSEIANIOSGADSLP 884
Db 713 SPVSES---PEPRSPVPEDLSLKGDIQKEVLIQAKPEDKVKQKNSNLDVPENIEFTF 769
QY 885 CLELPCDLKFKNIIYPKDEVHVSDSENRSSVSKASISPSNVSALEPQTEMGSIV---- 939
Db 770 AVQKPD-----SGKAVSDTF-----GGLDTTKGSAVHEVKV 803
QY 940 -KSKSLTKEAE-KKLPSTDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVFGASLF 997
Db 804 DKPKPPSKEDDGGSKLP---KKESKASTVSSSDF-MNSVVDLIYWRDIKRSVGFASLF 858
QY 998 LLLSLTVFSIVSVTAIYALALLSVTISFRIYKGVIOAKSDEGHPPFRAYLESEVAISEE 1057
Db 859 LLLSLSVFSIVSVLAYIALALLSVTISLRIYKGIILQAIKSEEGHPPFRSILESNLAVPD 918
QY 1058 LVQKYSNLSALGHVNSTFIKELRELFLVDDLDVSLKEAVLMMVFTYVYVYVYVYVYVYV 1117
Db 919 LVQKTCNVALNHNCTVKELRHLFLVEDLVSLKFAVLMVFTYVYVYVYVYVYVYVYV 978
QY 1118 SLFSPVIVYERHQVIDHYLGLANKSVKDAMAKIOAKIPGLKRRKAD 1163
Db 979 SLFSPVIVYERHQVDHYLALVNKNLKSSTDLILSKVPGLKRAE 1024

```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:55:32 ; Search time 5.68322 Seconds  
(without alignments)  
3199.767 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163

Perfect score: 925

Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRAKAD 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_79.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	679	73.4	208	2 I60904	neuroendocrine-spe
2	679	73.4	776	2 A46583	neuroendocrine-spe
3	665	71.9	267	2 A60021	tropomyosin-relate
4	321	34.7	2484	2 T26216	hypothetical prote
5	321	34.7	2607	2 T26215	hypothetical prote
6	320	34.6	222	2 T26213	hypothetical prote
7	194	21.0	255	2 B84899	hypothetical prote
8	182	19.7	271	2 T13013	hypothetical prote
9	163	17.6	275	2 T05595	hypothetical prote
10	142	15.4	393	2 S67763	probable membrane
11	135.5	14.6	242	2 B85016	hypothetical prote
12	134	14.5	183	2 A84527	hypothetical prote
13	131.5	14.2	295	2 S59439	probable membrane
14	123	13.3	206	2 T01153	probable seed matu
15	109.5	11.8	264	2 T47948	hypothetical prote
16	107.5	11.6	203	2 T47571	hypothetical prote
17	94	10.2	288	2 B90043	conserved hypothet
18	93.5	10.1	457	2 H85095	hypothetical prote
19	92.5	10.0	458	2 A72258	hypothetical prote
20	92.5	10.0	677	2 F95232	immunity protein,
21	92.5	10.0	680	2 H98096	conserved hypothet
22	91	9.8	160	2 C84422	hypothetical prote
23	90.5	9.8	442	2 C75057	hypothetical prote
24	89	9.6	224	2 D71915	hydrogenase, cytoc
25	89	9.6	468	2 A38223	nicotinic acetylch
26	87	9.4	1065	2 E69795	acridin flavin resista
27	86	9.3	589	2 F84201	transport ATP-bind
28	86	9.3	1055	2 H90023	hypothetical prote
29	85.5	9.2	296	2 S46018	probable membrane

30	85.5	9.2	299	2 B69155	hypothetical prote
31	85	9.2	299	2 C64397	hypothetical prote
32	85	9.2	459	2 G86264	F3F19 hypothetical
33	85	9.2	689	2 T09007	ABC-transporter ho
34	84.5	9.1	151	2 G96705	unknown protein, 7
35	83.5	9.0	445	2 A02358	glucosyltransferas
36	83.5	9.0	570	2 S52765	secB protein - Str
37	83.5	9.0	823	2 H83724	hypothetical prote
38	83	9.0	180	2 E97200	probable phosphata
39	83	9.0	252	2 G97886	hypothetical prote
40	83	9.0	388	1 D70006	conserved hypothet
41	82.5	8.9	410	2 A95044	conserved hypothet
42	82.5	8.9	502	2 F70316	conserved hypothet
43	82.5	8.9	675	2 T50332	STC1 homolog SPB1
44	82.5	8.9	937	2 T41400	probable peroxisom
45	82	8.9	224	1 A64599	hydrogenase (EC 1.

ALIGNMENTS

RESULT 1

I60904

neuroendocrine-specific protein C - human

C:Species: Homo sapiens (man)

C>Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 09-Jul-2004

C:Accession: I60904

R:Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; V

J. Biol. Chem. 268, 13439-13447, 1993

A:Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spe

A:Reference number: A46583; MUID:93293865; PMID:7685762

A:Accession: I60904

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-208 <RES>

A:Cross-references: UNIPROT:Q16799; GB:L10335; NID:g307310; PIDN:AAA59952.1; PID:g307311

C:Genetics:

A:Gene: GDB:RTN1; NSP

A:Cross-references: GDB:203968; OMIM:600865

A:Map position: 14q21-14q22

Query Match 73.4%, Score 679; DB 2; Length 208;

Best Local Similarity 67.9%; Pred. No. 3.6e-52;

Matches 127; Conservative 31; Mismatches 29; Indels 0; Gaps 0;

Qy	3	VDLLYWRDIKKTGVVFGASLFLLLSLTVFSTVSVTAVIALALLSVTISFRYKGVQIAIQ	62
Db	22	IDLLYWRDIKQTGIVFGSFLLLSFLSTQFSVSVVAYLALAAALSATISFRYKSVLQAVQ	81
Qy	63	KSDEGHPFRAYLSEVAISELVEQYKQYDCLQFYVNSTLKELRRLFLVDLVDLSLKFAVLM	122
Db	82	KTDEGHPFKAYLEILITLSQEQIKYDCLQFYVNSTLKELRRLFLVDLVDLSLKFAVLM	141
Qy	123	WVFTYVGALENGLLTLLALISLPSIPVYERHQVQIDHYGLANKSVKDMAKIQAKIP	182
Db	142	WLLTYVGALENGLLTLLMAVSMETLPAVYVHQVQIDQYGLVTRTHNAVVAQIKQAKIP	201
Qy	183	GLKREKAD 189	
Db	202	GAKRHAE 208	

RESULT 2

A46583

neuroendocrine-specific protein, splice form A - human

N:Contains: neuroendocrine-specific protein, splice form B

C:Species: Homo sapiens (man)

C>Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 09-Jul-2004

C:Accession: A46583; I60903

R:Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; V

J. Biol. Chem. 268, 13439-13447, 1993

A:Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spe

A:Reference number: A46583; MUID:93293865; PMID:7685762





RESULT 7  
E84899  
hypothetical protein At2g46170 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: E84899  
R.;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: E84899  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-255 <STO>  
A:Cross-references: UNIPROT:O82352; GB:A5002093; NID:g3702332; PIDN:AAC62889.1; GSPDB:GN  
C:Genetics:  
A:Gene: At2g46170  
A:Map position: 2

Query Match 21.0%; Score 194; DB 2; Length 255;  
Best Local Similarity 27.6%; Pred. No. 1.2e-09;





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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 12:31:51 ; Search time 27.2927 Seconds  
(without alignments)  
2678.292 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163

Perfect score: 925

Sequence: 1 SVVDLLYWRDIKTKGVVFGA.....VKDAMAKIQAKIPGLKRRAD 189.

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	925	100.0	361	3 AAY71385	Aay71385 Alternati
2	925	100.0	1163	3 AAY71310	Aay71310 Rat neuro
3	925	100.0	1163	3 AAY71384	Aay71384 Alternati
4	925	100.0	1163	5 ABB81074	Abb81074 Rat neuro
5	925	100.0	1163	8 ADO26399	Ado26399 Rat trunc
6	925	100.0	1163	8 ADP45572	Adp45572 Rat NogoA
7	922	99.7	379	7 ADB85283	Adb85283 Rat foocoe
8	921	99.6	199	5 ABB81077	Abb81077 Rat neuro
9	921	99.6	360	3 AAY71383	Aay71383 Rat neuro
10	921	99.6	360	5 ABB81076	Abb81076 Rat neuro
11	921	99.6	522	3 AAY71312	Aay71312 Rat neuro
12	919	99.4	199	3 AAY71559	Aay71559 Rat Nogo
13	919	99.4	359	3 AAY71558	Aay71558 Rat Nogo
14	919	99.4	403	3 AAY71563	Aay71563 Rat Nogo
15	919	99.4	1162	3 AAY71557	Aay71557 Rat Nogo
16	917	99.1	1162	8 ADT89537	Adt89537 Mus muscu
17	908	98.2	893	3 AAY95012	Aay95012 Human sec
18	908	98.2	983	6 ABU11573	Abu11573 Human MDD
19	908	98.2	1178	3 AAY71311	Aay71311 Human neu-
20	908	98.2	1192	3 AAY56967	Aay56967 Human MAG
21	908	98.2	1192	4 AAB82349	Aab82349 Human NOG
22	908	98.2	1192	4 AAU04591	Aau04591 Human NOG
23	908	98.2	1192	5 ABG30938	Abg30938 Human NOG
24	908	98.2	1192	5 ABP68600	Abp68600 Human pan
25	908	98.2	1192	5 ABB81078	Abb81078 Human neu

## ALIGNMENTS

## RESULT 1

AAY71385  
ID AAY71385 standard; protein; 361 AA.

XX AC AAY71385;

DT XX  
DT 02-NOV-2000 (first entry)

DE AAY71385  
DE Alternative version of rat neurite growth inhibitor Nogo B.

XX Rat; neurite growth inhibitor; Nogo B; neural cell; myelin; CNS;  
KW central nervous system; neoplastic disease; antiproliferative; glioma;  
KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
KW structural plasticity; screening.

XX Rattus sp.

Key	Location/Qualifiers
PH Region	1. .172
FT Region	/note= "Corresponds to amino acids 1-172 of Nogo A protein shown in AAY71310"
FT Inhibitory-site	1. .171
FT Inhibitory-site	/note= "Inhibits NIH 3T3 fibroblast spreading"
FT Modified-site	30
FT Modified-site	/note= "Casein kinase II site"
FT Region	31. .58
FT Region	/note= "Acidic region"
FT Region	173. .361
FT Region	/note= "Corresponds to amino acids 975-1163 of Nogo A protein (AAY71310)"
FT Region	174. .361
FT Region	/note= "This region is common to Nogo A, B and C isoforms"
FT Domain	186. .221
FT Domain	/label= Transmembrane domain
FT Domain	/note= "C-terminal hydrophobic region"
FT Modified-site	222
FT Modified-site	/note= "Protein kinase C (PKC) site"
FT Modified-site	269. .271
FT Modified-site	/note= "Asn is N-glycosylated"
FT Modified-site	271
FT Modified-site	/note= "Protein kinase C (PKC) site"
FT Modified-site	287
FT Modified-site	/note= "Protein kinase C (PKC) site"
FT Domain	288. .323

26	908	98.2	1192	6 ABR59667	AbR59667 Human NOG
27	908	98.2	1192	8 ADO08103	Ado08103 Human pol
28	908	98.2	1192	8 ADO26400	Ado26400 Human tru
29	908	98.2	1192	8 ADP45551	Adp45551 Human NOG
30	908	98.2	1192	8 ADP67234	Adp67234 Human NOG
31	908	98.2	1192	8 ADRI3966	Adri3966 Human NOG
32	906.5	98.0	1163	8 ADO08105	Ado08105 Mouse pol
33	905	97.8	200	4 AAB64514	Aab64514 Human sec
34	904	97.7	199	2 AAW53947	Aaw53947 Human NSP
35	904	97.7	199	2 AAW78313	Aaw78313 Fragment
36	904	97.7	199	3 AAB12805	Aab12805 Human NSP
37	904	97.7	199	4 AAB82348	Aab82348 Human NOG
38	904	97.7	199	5 ABB81080	Abb81080 Human neu
39	904	97.7	199	8 ADP67236	Adp67236 Human NOG
40	904	97.7	373	3 AAY53624	Aay53624 A bone ma
41	904	97.7	373	3 AAY56969	Aay56969 Human MAG
42	904	97.7	373	3 AAB24242	Aab24242 Human NOG
43	904	97.7	373	4 AAB82350	Aab82350 Human NOG
44	904	97.7	373	5 AAM47954	Aam47954 Human RTN
45	904	97.7	373	5 ABG30937	Abg30937 Human NOG





FT	/note= "This region is not essential for inhibitory activity"	FT	/note= "This region is not essential for inhibitory activity"
FT	Misc-difference	FT	Region
FT	223	FT	976. .1163
FT	/label= Unknown	FT	/note= "C-terminal common region found in Nogo A, B and C isoforms"
FT	/note= "There is Leu at this position in the sequence shown in AA71310"	FT	988. .1023
FT	233	FT	/label= Transmembrane domain
FT	/note= "Protein kinase C (PKC) site"	FT	/note= "C-terminal hydrophobic region"
FT	242. .244	FT	1024
FT	/note= "Asn is N-glycosylated"	FT	/note= "Protein kinase C (PKC) site"
FT	291	FT	1071. .1073
FT	/note= "Protein kinase C (PKC) site"	FT	/note= "Asn is N-glycosylated"
FT	235	FT	1073
FT	/note= "Protein kinase C (PKC) site"	FT	/note= "Protein kinase C (PKC) site"
FT	404	FT	1089
FT	/note= "There is Ile at this position in the sequence shown in AA71310"	FT	/note= "Protein kinase C (PKC) site"
FT	436	FT	1090. .1125
FT	/note= "Protein kinase C (PKC) site"	FT	/label= Transmembrane domain
FT	468. .470	FT	/note= "C-terminal hydrophobic region"
FT	/note= "Asn is N-glycosylated"	FT	1141. .1143
FT	469	FT	/note= "Asn is N-glycosylated"
FT	/label= Unknown	FT	1143
FT	/note= "There is Lys at this position in the sequence shown in AA71310"	FT	/note= "Protein kinase C (PKC) site"
FT	484	XX	WO200031235-A2.
FT	Modified-site	PN	
FT	488	XX	02-JUN-2000.
FT	/note= "Protein kinase C (PKC) site"	PD	
FT	488	XX	05-NOV-1999; 99WO-US026160.
FT	/note= "Protein kinase C (PKC) site"	PF	
FT	502	XX	06-NOV-1998; 98US-0107446P.
FT	/note= "Casein kinase II site"	PR	
FT	Inhibitory-site	XX	(SCHW/) SCHWAB M B.
FT	542. .722	XX	(CHEN/) CHEN M S.
FT	Modified-site	XX	Schwab ME, Chen MS;
FT	623. .640	XX	WPI; 2000-400052/34.
FT	/note= "Used as immunogen to generate antibody AS 472"	DR	
FT	626	XX	Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons.
FT	/note= "Protein kinase C (PKC) site"	XX	Claim 3; Fig 13; 122pp; English.
FT	661	PS	
FT	Misc-difference	XX	The present sequence is an alternative version of rat Nogo A protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) myelin material with which it is native
FT	694. .696	CC	associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
FT	/note= "Asn is N-glycosylated"	CC	Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. Note: The present sequence is an alternative version of the Nogo A sequence shown in Fig. 2A (see AA71310). SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However the specification does not include sequences for these SEQ ID numbers
FT	715	CC	
FT	/note= "Casein kinase II site"	CC	
FT	762. .1163	CC	
FT	/note= "used as immunogen to generate antibody AS Bruna"	CC	
FT	784	CC	
FT	/note= "Protein kinase C (PKC) site"	CC	
FT	820	CC	
FT	/note= "There is Leu at this position in the sequence shown in AA71310"	CC	
FT	821	CC	
FT	Modified-site	CC	
FT	830	CC	
FT	/note= "Protein kinase C (PKC) site"	CC	
FT	855	CC	
FT	/note= "Protein kinase C (PKC) site"	CC	
FT	863	CC	
FT	/note= "Casein kinase II site"	CC	
FT	868	CC	
FT	/note= "Protein kinase C (PKC) site"	CC	
FT	893	CC	
FT	/note= "Protein kinase C (PKC) site"	CC	
FT	912. .914	CC	
FT	/note= "Asn is N-glycosylated"	CC	
FT	925. .927	CC	
FT	/note= "Asn is N-glycosylated"	XX	
FT	954	SQ	Sequence 1163 AA;
FT	Modified-site		
FT	956		Query Match 100.0%; Score 925; DB 3; Length 1163;
FT	/note= "PKC and casein kinase II sites"		Best Local Similarity 100.0%; Pred. NO. 4.4e-89;
FT	975. .1162		Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT	Region		



QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
 DB 975 SVVDLLYWRDIKKTGVVFGASLFLLLSLTFSIVSVTAYIALALLSVTISFRIYKGVIOA 1034  
 QY 61 IQKDEGHPPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVLSLKPAV 120  
 DB 1035 IQKDEGHPPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVLSLKPAV 1094  
 QY 121 LMWVFTYVYVGFALFNGLTLLILALISLFSIPVIYERHVOVDHYLGLANKSVKDMAKIOAK 180  
 DB 1095 LMWVFTYVYVGFALFNGLTLLILALISLFSIPVIYERHVOVDHYLGLANKSVKDMAKIOAK 1154  
 QY 181 IPGLKRRKAD 189  
 DB 1155 IPGLKRRKAD 1163

## RESULT 4

ID ABB81074 standard; protein; 1163 AA.

AC ABB81074;

DT 05-NOV-2002 (first entry)

DE Rat neurotransmitter receptor protein Nogo-A.

KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;  
 KW central nervous system; peripheral nervous system; tranquilizer; Nogo;  
 KW vulnary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;  
 KW neotropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;  
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;  
 KW neurotransmitter receptor; rat; receptor.

OS Rattus norvegicus.

PN US2002072493-A1.

PD 13-JUN-2002.

PF 28-JUN-2001; 2001US-00893348.

PR 19-MAY-1998; 98IL-00124500.

PR 21-JUL-1998; 98WO-US014715.

PR 22-DEC-1998; 98US-00218277.

PR 19-MAY-1999; 99US-00314161.

PA (YEDA ) YEDA RES & DEV CO LTD.

PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;

PI Moalem G;

XX WPI; 2002-607255/65.

DR N-PSDB; ABN86600.

XX Promoting nerve regeneration and preventing neuronal degeneration in the

PT central/peripheral nervous system from injury/disease comprises

PT administering nervous system-specific activated T cells/antigen, or

PT analogs/peptides.

PS Example 5; Page 44-47; 93pp; English.

XX The invention relates to promoting nerve regeneration or conferring  
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the  
 CC central/peripheral nervous system (NS). The method involves administering  
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its  
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or  
 CC combinations. The method is useful for promoting nerve regeneration and  
 CC preventing neuronal degeneration in central/peripheral nervous system  
 CC from injury/disease, where the injury is spinal cord injury, blunt  
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or  
 CC damages caused by surgery such as tumour excision. The disease is not an  
 CC autoimmune disease or neoplasm. The disease results in a degenerative

CC process occurring in either gray or white matter or both. The disease is  
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,  
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and  
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such  
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral  
 CC to uraemia, porphyria, hypoglycemia, Sjogren Larsson syndrome, acute  
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary  
 CC amyloidosis, obstructive lung diseases, acromegaly, maleabsorption  
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-  
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins  
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia  
 CC telangectasia, Friedreich's ataxia, amyloid polynuropathies,  
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's  
 CC disease, or lipoproteinemia. The present sequence represents the rat  
 CC neurotransmitter receptor protein Nogo-A, an example of NS-specific  
 CC antigen

XX Sequence 1163 AA;

Query Match 100.0%; Score 925; DB 5; Length 1163;

Best Local Similarity 100.0%; Pred. No. 4.4e-89;

Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTFSIVSVTAYIALALLSVTISFRIYKGVIOA 60

DB 975 SVVDLLYWRDIKKTGVVFGASLFLLLSLTFSIVSVTAYIALALLSVTISFRIYKGVIOA 1034

QY 61 IQKDEGHPPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVLSLKPAV 120

DB 1035 IQKDEGHPPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVLSLKPAV 1094

QY 121 LMWVFTYVYVGFALFNGLTLLILALISLFSIPVIYERHVOVDHYLGLANKSVKDMAKIOAK 180

DB 1095 LMWVFTYVYVGFALFNGLTLLILALISLFSIPVIYERHVOVDHYLGLANKSVKDMAKIOAK 1154

QY 181 IPGLKRRKAD 189

DB 1155 IPGLKRRKAD 1163

## RESULT 5

ADO26399 standard; protein; 1163 AA.

XX ADO26399 standard; protein; 1163 AA.

AC ADO26399;

DT 29-JUL-2004 (first entry)

DE Rat truncated Nogo-A protein.

XX rat; human; Nogo-A; truncated; affinity; membrane-bound protein.

XX Rattus sp.

PN WO2004039836-A1.

PD 13-MAY-2004.

PF 31-OCT-2002; 2002WO-EP012210.

PR 31-OCT-2002; 2002WO-EP012210.

PA (PIER-) PIERIS PROTEOLAB AG.

PI Skerra A, Fiedler M;

DR WPI; 2004-376159/35.

XX New isolated truncated Nogo-A polypeptide that corresponds to a truncated  
 PT form of the Nogo-A protein, useful for identifying a compound having  
 PT detectable affinity to a Nogo-A protein.

```

XX
XX
XX
CC Claim 1; Fig 6A; 80pp; English.
CC The present invention relates to an isolated truncated Nogo-A polypeptide
CC that corresponds to a truncated form of the Nogo-A protein from the rat
CC and from the human. The truncated polypeptide is useful for identifying a
CC compound having detectable affinity to a Nogo-A protein. The present
CC sequence is a Nogo-A polypeptide of the invention.
XX
XX
SQ Sequence 1163 AA;
    Query Match 100.0%; Score 925; DB 8; Length 1163;
    Best Local Similarity 100.0%; Pred. No. 4.4e-89;
    Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSPVSVTVTAYIALALLSVTISFRIYKGVIOA 60
Db 975 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSPVSVTVTAYIALALLSVTISFRIYKGVIOA 1034
    |||||
Qy 61 IQSDDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKPAV 120
Db 1035 IQSDDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKPAV 1094
    |||||
Qy 121 LMWFTYVVGALFENGLTLILLALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIOAK 180
Db 1095 LMWFTYVVGALFENGLTLILLALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIOAK 1154
    |||||
Qy 181 IPGLKRXAD 189
Db 1155 IPGLKRXAD 1163
    |||||
RESULT 6
ADP45572
ID ADP45572 standard; protein; 1163 AA.
XX
XX ADP45572;
XX
XX 09-SEP-2004 (first entry)
XX
XX Rat NogoA protein SEQ ID NO:26.
XX
XX binding molecule; human; NogoA; NiG; NiG-D20; NogoA_623-640;
XX KW nerve repair; neuroprotective; gene therapy;
XX KW central nervous system injury; CNS injury; neurodegenerative disorder;
XX KW rat.
XX
XX OS Rattus norvegicus.
XX
XX WO2004052932-A2.
XX
XX 24-JUN-2004.
XX
XX 09-DEC-2003; 2003WO-EP013960.
XX
XX 10-DEC-2002; 2002GB-00028832.
XX
XX (NOVS ) NOVARTIS AG.
XX PA (NOVS ) NOVARTIS PHARMA GMBH.
XX PA (UYZU-) UNIV ZUERICH.
XX
XX Barske C, Mir AK, Oertle T, Schnell L, Schwab ME, Vitaliti A;
XX PI Zurini M;
XX
XX WPI; 2004-468818/44.
XX DR N-PSDB; ADP45571.
XX
XX New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-
XX PT D20 or NogoA623-640, useful in preparing a composition for treating CNS
XX PT injury or neurodegenerative disorders.
XX
XX Example 1; SEQ ID NO 26; 121pp; English.
XX
XX

```

CC	The present invention describes a binding molecule which binds to human
CC	NogoA polypeptide, human NiG, human NiG-D20 or human NogoA 623-640 with a
CC	dissociation constant of less than 100nM. Also described: (1) a
CC	polynucleotide encoding the binding molecule; (2) an expression vector or
CC	system comprising the polynucleotide; (3) a host cell comprising the
CC	expression system; (4) a pharmaceutical composition comprising the
CC	binding molecule and a carrier or diluent; and (5) treating diseases
CC	associated with nerve repair. The binding molecule has neuroprotective
CC	activity, and can be used in gene therapy. The binding molecule is useful
CC	in preparing a composition for treating central nervous system (CNS)
CC	injury or neurodegenerative disorders. The present sequence represents
CC	rat NogoA, which is used in the exemplification of the present invention.
XX	
SQ	Sequence 1163 AA;
	Query Match 100.00%; Score 925; DB 8; Length 1163;
	Best Local Similarity 100.0%; Pred. No. 4.4e-89;
	Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 SVVDLLAYWRDIKKTGVVFGASLFLLLSLTVFSTVSVTATIALALLSVTISFRIYKGVIOA 60
DB	975 SVVDLLAYWRDIKKTGVVFGASLFLLLSLTVFSTVSVTATIALALLSVTISFRIYKGVIOA 1034
QY	61 IQKSDGHPFRAYLSEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 120
DB	1035 IQKSDGHPFRAYLSEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 1094
QY	121 LMWFTYVYGALFNLTLILLALISLESIPVIYERHOVIDHYGLANKSVKDMAKIOAK 180
DB	1095 LMWFTYVYGALFNLTLILLALISLESIPVIYERHOVIDHYGLANKSVKDMAKIOAK 1154
QY	181 IPLGKRRKAD 189
DB	1155 IPLGKRRKAD 1163
RESULT 7	
ADB85283	ID ID ADB85283 standard; protein; 379 AA.
XX	AC ADB85283;
XX	DT 04-DEC-2003 (first entry)
XX	DE Rat foocen-m2 reticulon SEQ ID NO:164.
XX	KW rat; streptozocin; kinase; phosphatase; ion channel protein; receptor;
XX	KW transporter; G-protein coupled receptor; GPCR; DNA-binding proteins;
XX	XX protease; enzyme; analgesic; gene therapy; pain; diabetes.
OS	Rattus norvegicus.
XX	EP1284297-A2.
XX	PD 19-FEB-2003.
XX	PF 26-JUL-2002; 2002EP-00255228.
XX	PR 27-JUL-2001; 2001GB-00018354.
XX	PR 07-FEB-2002; 2002GB-00002880.
XX	PA (WARN ) WARNER LAMBERT CO.
XX	PI Brooksbank RA, Dixon AK, Lee K, Pinnock RD;
XX	DR WPI; 2003-364994/35.
XX	XX N-PSDB; ADB85284.
PT	Use of gene sequence that is down-regulated in response to streptozocin-
PT	induced diabetes, vector, host cell, animal, polypeptide and antibody, in
PT	screening of compounds for treating or diagnosing pain.
XX	
PS	Disclosure; Page 239-240; 256pp; English.

XX The invention relates to a novel isolated gene sequence that is down-  
 CC regulated in the spinal cord in response to streptozocin-induced  
 CC diabetes, or comprising, hybridising or having at least 80% sequence  
 CC identity to a sequence whose expression products are kinases,  
 CC phosphatases, ion channel proteins, receptors, transporters, G-protein  
 CC coupled receptor proteins, DNA-binding proteins, proteases or enzymes,  
 CC given in the specification. A gene of the invention has analgesic  
 CC activity, and may have a use in gene therapy. The gene sequences, vector,  
 CC host cell, animal, polypeptide and antibody are useful for screening of  
 CC compounds for diagnosing or treating pain. The kits are useful for  
 CC simultaneous, separate or sequential detecting and/or quantifying down-  
 CC regulation of a gene sequence in the spinal cord of a mammal in response  
 CC to streptozocin-induced diabetes. The compound or pharmaceutical  
 CC composition is useful as a medicament for treating or diagnosing pain.  
 CC The present sequence represents a protein encoded by a gene of the  
 CC invention.

XX SQ Sequence 379 AA;

Query Match 99.7%; Score 922; DB 7; Length 379;  
 Best Local Similarity 99.5%; Pred. No. 2.1e-89;  
 Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVFGASIFLLSLTVFSIVSVTAYIALALSVTISFRIYKGVIOA 60  
 Db :|||||  
 191 AVVDLLYWRDIKKTGVFGASIFLLSLTVFSIVSVTAYIALALSVTISFRIYKGVIOA 250

Qy 61 IQKSDGHPFRAYLSEVAISEELVQKYSNKGALGHVNSTIKELRRLFLVDLVDLSKPAV 120  
 Db :|||||  
 251 IQKSDGHPFRAYLSEVAISEELVQKYSNKGALGHVNSTIKELRRLFLVDLVDLSKPAV 310

Qy 121 LMWFTYVYGALFNGLTLLILALISLFSIPVIYERHGVQIDHYLGLANKSVKDMAKIOAK 180  
 Db :|||||  
 311 LMWFTYVYGALFNGLTLLILALISLFSIPVIYERHGVQIDHYLGLANKSVKDMAKIOAK 370

Qy 181 IPGLKRRKAD 189  
 Db :|||||  
 371 IPGLKRRKAD 379

RESULT 8  
 ABB81077  
 ID ABB81077 standard; protein; 199 AA.  
 XX  
 AC ABB81077;  
 XX  
 XX 05-NOV-2002 (first entry)  
 DT  
 XX Rat neurotransmitter receptor protein Nogo-C.  
 DE  
 XX Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;  
 KW central nervous system; peripheral nervous system; tranquilizer; Nogo;  
 KW vulnary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;  
 KW neotropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;  
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;  
 KW neurotransmitter receptor; rat; receptor.

XX  
 OS Rattus norvegicus.  
 XX  
 XX US2002072493-A1.  
 XX  
 XX 13-JUN-2002.  
 PD  
 XX  
 XX 28-JUN-2001; 2001US-00893348.  
 PF  
 XX 19-MAY-1998; 98IL-00124500.  
 PR 21-JUL-1998; 98WO-US014715.  
 PR 22-DEC-1998; 98US-00218277.  
 PR 19-MAY-1999; 99US-00314161.  
 XX  
 XX (YEDA ) YEDA RES & DEV CO LTD.  
 PA  
 XX

PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;  
 PI Moalem G;  
 XX  
 DR WPI; 2002-607255/65.  
 DR N-PSDB; ABN86600.  
 XX  
 PS Promoting nerve regeneration and preventing neuronal degeneration in the  
 CC central/peripheral nervous system from injury/disease, comprises  
 CC administering nervous system-specific activated T cells/antigen, or  
 CC analogs/peptides.

XX Example 5; Page 48-49; 93pp; English.

XX The invention relates to promoting nerve regeneration or conferring  
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the  
 CC central/peripheral nervous system (NS). The method involves administering  
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its  
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or  
 CC combinations. The method is useful for promoting nerve regeneration and  
 CC preventing neuronal degeneration in central/peripheral nervous system  
 CC from injury/disease, where the injury is spinal cord injury, blunt  
 CC trauma, penetrating trauma, hemorrhagic stroke, ischemic stroke or  
 CC damages caused by surgery such as tumour excision. The disease is not an  
 CC autoimmune disease or neoplasm. The disease results in a degenerative  
 CC process occurring in either gray or white matter or both. The disease is  
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,  
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and  
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such  
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral  
 CC neuropathies associated with various diseases, including but not limited  
 CC to uraemia, porphyria, hypoglycemia, Sjogren Larsson syndrome, acute  
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary  
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption  
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-  
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins  
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia -  
 CC telangectasia, Friedreich's ataxia, amyloid polynuropathies,  
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's  
 CC disease, or lipoproteinemia. The present sequence represents the rat  
 CC neurotransmitter receptor protein Nogo-C, an example of NS-specific  
 CC antigen

XX SQ Sequence 199 AA;

Query Match 99.6%; Score 921; DB 5; Length 199;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-89;  
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVDLLYWRDIKKTGVFGASIFLLSLTVFSIVSVTAYIALALSVTISFRIYKGVIOAI 61  
 Db :|||||  
 12 VVDLLYWRDIKKTGVFGASIFLLSLTVFSIVSVTAYIALALSVTISFRIYKGVIOAI 71

Qy 62 QKSDGHPFRAYLSEVAISEELVQKYSNKGALGHVNSTIKELRRLFLVDLVDLSKPAVL 121  
 Db :|||||  
 72 QKSDGHPFRAYLSEVAISEELVQKYSNKGALGHVNSTIKELRRLFLVDLVDLSKPAVL 131

Qy 122 MWFTYVYGALFNGLTLLILALISLFSIPVIYERHGVQIDHYLGLANKSVKDMAKIOAKI 181  
 Db :|||||  
 132 MWFTYVYGALFNGLTLLILALISLFSIPVIYERHGVQIDHYLGLANKSVKDMAKIOAKI 191

Qy 182 PGLKRRKAD 189  
 Db :|||||  
 192 PGLKRRKAD 199

RESULT 9  
 AAY71383  
 ID AAY71383 standard; protein; 360 AA.  
 XX  
 AC AAY71383;  
 XX  
 XX 02-NOV-2000 (first entry)  
 DT

XX DE Rat neurite growth inhibitor Nogo B.

XX KW Rat; neurite growth inhibitor; Nogo B; neural cell; myelin; CNS;

XX KW central nervous system; neoplastic disease; antiproliferative; glioma;

XX KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;

XX KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;

XX KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;

XX KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;

XX KW structural plasticity; screening.

XX OS Rattus sp.

XX FH Key

XX FH Region

FT FT 1. .172 Location/Qualifiers

FT FT /note= "Corresponds to amino acids 1-172 of Nogo A

FT FT protein shown in AAY71310"

FT FT Inhibitory-site 1. .171

FT FT /note= "Inhibits NIH 3T3 fibroblast spreading"

FT FT Modified-site 30

FT FT /note= "Casein kinase II site"

FT FT Region 31. .58

FT FT /note= "Acidic region"

FT FT Region 173. .360

FT FT /note= "Corresponds to C-terminal 188 amino acids

FT FT (residues 976-1163) of Nogo A protein (AAY71310). This

FT FT region is common to Nogo A, B and C isoforms"

FT FT Domain 185. .220

FT FT /label= Transmembrane domain

FT FT /note= "C-terminal hydrophobic region"

FT FT Modified-site 221

FT FT /note= "Protein kinase C (PKC) site"

FT FT Modified-site 268. .270

FT FT /note= "Asn is N-glycosylated"

FT FT Modified-site 270

FT FT /note= "Protein kinase C (PKC) site"

FT FT Modified-site 286

FT FT /note= "Protein kinase C (PKC) site"

FT FT Domain 287. .322

FT FT /label= Transmembrane domain

FT FT /note= "C-terminal hydrophobic region"

FT FT Modified-site 338. .340

FT FT /note= "Asn is N-glycosylated"

FT FT Modified-site 340

FT FT /note= "Protein kinase C (PKC) site"

XX PN WO200031235-A2.

XX PN 02-JUN-2000.

XX PF 05-NOV-1999; 99WO-US026160.

XX PF 06-NOV-1998; 98US-0107446P.

XX PA (SCHW/) SCHWAB M E.

XX PA (CHEN/) CHEN M S.

XX PI Schwab ME, Chen MS;

XX XX WPI; 2000-400052/34.

XX XX

XX XX Nogo proteins and nucleic acids useful for treating neoplastic disorders

XX XX of the central nervous system and inducing regeneration of neurons.

XX XX Example; Page; 122pp; English.

XX XX

XX XX The present sequence is a rat Nogo B protein which is a potent neural

XX XX cell growth inhibitor and is free of all central nervous system (CNS)

XX XX myelin material with which it is native associated. The Nogo B

XX XX transcript arises as a result of alternative splicing of Nogo gene. Nogo

XX XX proteins and fragments displaying neurite growth inhibitory activity are

XX XX used in the treatment of neoplastic disease of the CNS e.g. glioma,

XX XX glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma,

CC haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma,

CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.

CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo

CC activity can be used to treat or prevent hyperproliferative or benign

CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.

CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit

CC production of Nogo protein to induce regeneration of neurons or to

CC promote structural plasticity of the CNS in disorders where neurite

CC growth, regeneration or maintenance are deficient or desired. The animal

CC models can be used in diagnostic and screening methods for predispotion

CC to disorders and to screen for or test molecules which can treat or

CC prevent disorders or diseases of the CNS. Note: The present sequence is

CC not given in the specification but is derived from Nogo A protein

CC sequence (AAY71310) and corresponds to residues 1-172 fused to 976-1163

CC of Nogo A. The specification claims an alternative version of this

CC sequence (see AAY71385.) which corresponds to residues 1-172 fused to 975

CC -1163 of Nogo A. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID

CC NO: 29 in disclosure of the specification. However the specification does

CC not include sequences for these SEQ ID numbers

XX XX

XX SQ Sequence 360 AA;

Query Match 99.6%; Score 921; DB 3; Length 360;

Best Local Similarity 100.0%; Pred. No. 2.6e-89;

Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYITALALLSVTISFRIYKGVIOAI 61

Db 173 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYITALALLSVTISFRIYKGVIOAI 232

QY 62 QKSDGHPFRAYLSEVAISELVOKYNSALGHVNSTIKELRLFLVDLVDLSLKFAVL 121

Db 233 QKSDGHPFRAYLSEVAISELVOKYNSALGHVNSTIKELRLFLVDLVDLSLKFAVL 292

QY 122 MVVFTYVGALFNGLTLLILALISLFSIPVIYERHQQVIDHYLGLANKSVKDAWAKIQAKI 181

Db 293 MVVFTYVGALFNGLTLLILALISLFSIPVIYERHQQVIDHYLGLANKSVKDAWAKIQAKI 352

QY 182 PGLKRRAD 189

Db 353 PGLKRRAD 360

RESULT 10

ABB81076

ID ABB81076 standard; protein; 360 AA.

XX ABB81076;

XX AC

XX DT 05-NOV-2002 (first entry)

XX DE Rat neurotransmitter receptor protein Nogo-B.

XX KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;

XX KW central nervous system; peripheral nervous system; tranquilizer; Nogo;

XX KW vulnary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;

XX KW neurotropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;

XX KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;

XX KW neurotransmitter receptor; rat; receptor.

XX OS Rattus norvegicus.

XX XX

XX XX US2002072493-A1.

XX XX

XX PD 13-JUN-2002.

XX XX

XX PF 28-JUN-2001; 2001US-00893348.

XX XX

XX PF 19-MAY-1998; 98IL-00124500.

XX PR 21-JUL-1998; 98WO-US014715.

XX PR 22-DEC-1998; 98US-00218277.

XX PR 19-MAY-1999; 99US-00314161.

XX XX

```
PA (YEDA ) YEDA RES & DEV CO LTD.
XX
XX
XX PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;
XX PI Moalem G;
XX
XX WPI: 2002-607255/65.
XX DR N-PSDB; ABN86600.
XX
XX Promoting nerve regeneration and preventing neuronal degeneration in the
XX central/peripheral nervous system from injury/disease, comprises
XX administering nervous system-specific activated T cells/antigen, or
XX analogs/peptides.
XX
XX Example 5; Page 47-48; 93pp: English.
XX
XX The invention relates to promoting nerve regeneration or conferring
XX neuroprotection and preventing or inhibiting neuronal degeneration in the
XX central/peripheral nervous system (NS). The method involves administering
XX NS-specific activated T cells, NS-specific antigen, its analogue or its
XX peptide, a nucleotide sequence the NS-specific antigen or its analogue or
XX combinations. The method is useful for promoting nerve regeneration and
XX preventing neuronal degeneration in central/peripheral nervous system
XX from injury/disease, where the injury is spinal cord injury, blunt
XX trauma, penetrating trauma, hemorrhagic stroke, ischemic stroke or
XX damages caused by surgery such as tumour excision. The disease is not an
XX autoimmune disease or neoplasm. The disease results in a degenerative
XX process occurring in either gray or white matter or both. The disease is
XX diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
XX disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
XX amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
XX vitamin deficiency, intervertebral disc herniation, prion diseases such
XX as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
XX neuropathies associated with various diseases, including but not limited
XX to uremia, porphyria, hypocalcemia, Sjogren Larsson syndrome, acute
XX sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
XX amyloidosis, obstructive lung diseases, acromegaly, malabsorption
XX syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
XX pathies, complications of various drugs (e.g., metronidazole) and toxins
XX (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
XX telangiectasia, Friedreich's ataxia, amyloid polynuropathies,
XX adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
XX disease, or lipoproteinemia. The present sequence represents the rat
XX neurotransmitter receptor protein Nogo-B, an example of NS-specific
XX antigen
XX
XX Sequence 360 AA;
XX
XX Query Match 99.6%; Score 921; DB 5; Length 360;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-89;
XX Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAIYALALLSVTISFRIYKGVIOAI 61
XX Db 173 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAIYALALLSVTISFRIYKGVIOAI 232
XX
XX QY 62 QKSDGHPFRAYLESEVAISELVQKYSNLSALGHVNSTIKELRRLFLVDDLVDLSLKPAVL 121
XX Db 233 QKSDGHPFRAYLESEVAISELVQKYSNLSALGHVNSTIKELRRLFLVDDLVDLSLKPAVL 292
XX
XX QY 122 MWVFTYVGLFNGLLTLLALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI 181
XX Db 293 MWVFTYVGLFNGLLTLLALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI 352
XX
XX QY 182 PGLKRRKAD 189
XX Db 353 PGLKRRKAD 360
XX
XX RESULT 11
XX ID AAY71312
XX AC AAY71312 standard; protein; 522 AA.
XX
XX AAY71312;
XX
```

```
XX
XX 02-NOV-2000 (first entry)
XX
XX DE Rat neurite growth inhibitor Nogo C.
XX
XX KW Rat; neurite growth inhibitor; Nogo C; neural cell; myelin; CNS;
XX KW central nervous system; neoplastic disease; antiproliferative; glioma;
XX KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
XX KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
XX KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
XX KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
XX KW structural plasticity; screening.
XX
XX OS Rattus sp.
XX
XX FH Key Location/Qualifiers
XX FT Region 1..39
XX FT /note= "Sequence upstream to the N-terminus of Nogo C
XX FT protein"
XX FT Misc-difference 3
XX FT /note= "Encoded by TAG"
XX FT Region 11..191
XX FT /note= "Region specifically described in claim 16"
XX FT Misc-difference 29
XX FT /note= "Encoded by TAA"
XX FT Protein 40..238
XX FT /label= Nogo_C_protein
XX FT Region 51..238
XX FT /note= "C-terminal common region found in Nogo A, B and C
XX FT isoforms"
XX FT Region 239..522
XX FT /note= "Sequence downstream to the C-terminus of Nogo C
XX FT protein"
XX FT Misc-difference 239
XX FT /note= "Encoded by TGA"
XX FT Misc-difference 263
XX FT /note= "Encoded by TGA"
XX FT Misc-difference 276
XX FT /note= "Encoded by TAG"
XX FT Misc-difference 281
XX FT /note= "Encoded by TGA"
XX FT Misc-difference 295
XX FT /note= "Encoded by TAA"
XX FT Misc-difference 298
XX FT /note= "Encoded by TAA"
XX FT Misc-difference 314
XX FT /note= "Encoded by TGA"
XX FT Misc-difference 318
XX FT /note= "Encoded by TGA"
XX FT Misc-difference 335
XX FT /note= "Encoded by TAG"
XX FT Misc-difference 371
XX FT /note= "Encoded by TGA"
XX FT Misc-difference 374
XX FT /note= "Encoded by TAG"
XX FT Misc-difference 380
XX FT /note= "Encoded by TAA"
XX FT Misc-difference 406
XX FT /note= "Encoded by TAA"
XX FT Misc-difference 408
XX FT /note= "Encoded by TAG"
XX FT Misc-difference 410
XX FT /note= "Encoded by TAA"
XX FT Misc-difference 422
XX FT /note= "Encoded by TAA"
XX FT Misc-difference 433
XX FT /note= "Encoded by TGA"
XX FT Misc-difference 440
XX FT /note= "Encoded by TAG"
XX FT Misc-difference 453
XX FT /note= "Encoded by TAG"
XX FT Misc-difference 465
XX FT /note= "Encoded by TAG"
XX
```



CC in claim 32 and SEQ ID NO: 29 in disclosure of the specification.  
CC However, the specification does not include sequences for these SEQ ID  
CC numbers  
XX  
SQ Sequence 199 AA;  
Query Match 99.4%; Score 919; DB 3; Length 199;  
Best Local Similarity 100.0%; Pred. No. 1.9e-89;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SVVDLLYWRDIKKTGVFGASLFLLSLTFTVSIVSTAYIALLSVTISPRYKGVIOA 60  
Db 12 SVVDLLYWRDIKKTGVFGASLFLLSLTFTVSIVSTAYIALLSVTISPRYKGVIOA 71  
Qy 61 IQKSDGHPFRAYLESEVAISELVQKYSNLSALGHVNSTIKELRRLFLVDDLVSLKFAV 120  
Db 72 IQKSDGHPFRAYLESEVAISELVQKYSNLSALGHVNSTIKELRRLFLVDDLVSLKFAV 131  
Qy 121 LMWFTYVVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 180  
Db 132 LMWFTYVVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 191  
Qy 181 IPGLKRKA 188  
Db 192 IPGLKRKA 199  
RESULT 13  
AA711558  
ID AAY71558 standard; protein; 359 AA.  
XX  
AC AAY71558;  
XX  
XX  
DT 02-NOV-2000 (first entry)  
XX  
DE Rat Nogo A protein fragment used in the construction of mutant Nogo-B.  
XX  
XX Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
KW central nervous system; neoplastic disease; antiproliferative; glioma;  
KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
KW structural plasticity; screening; mutant; mutein.  
XX  
OS Rattus sp.  
XX  
XX Key Location/Qualifiers  
FH 1.171  
FT Region /note= "Corresponds to residues 1-171 of rat Nogo A  
FT protein shown in AAY71310"  
FT 172..359  
FT Region /note= "Corresponds to residues 975-1162 of rat Nogo A  
FT protein shown in AAY71310"  
XX  
XX WO200031235-A2.  
XX  
XX PD 02-JUN-2000.  
XX  
XX PF 05-NOV-1999; 99WO-US026160.  
XX  
XX PF 06-NOV-1998; 98US-0107446P.  
XX  
XX (SCHW/) SCHWAB M E.  
XX (CHEN/) CHEN M S.  
XX  
XX PI Schwab ME, Chen MS;  
XX  
XX WPI; 2000-400052/34.  
XX  
XX Nogo proteins and nucleic acids useful for treating neoplastic disorders  
XX of the central nervous system and inducing regeneration of neurons.  
XX

PS  
XX  
CC The patent relates to neurite growth inhibitor Nogo which is free of all  
CC central nervous system (CNS) myelin material with which it is natively  
CC associated. Nogo proteins and fragments displaying neurite growth  
CC inhibitory activity are used in the treatment of neoplastic disease of  
CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,  
CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,  
CC oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and  
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.  
CC Therapeutics which promote Nogo activity can be used to treat or prevent  
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis  
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be  
CC used to inhibit production of Nogo protein to induce regeneration of  
CC neurons or to promote structural plasticity of the CNS in disorders where  
CC neurite growth, regeneration or maintenance are deficient or desired. The  
CC animal models can be used in diagnostic and screening methods for  
CC predisposition to disorders and to screen for or test molecules which can  
CC treat or prevent disorders or diseases of the CNS. The present sequence  
CC is derived by fusing two fragments of rat Nogo A protein shown in  
CC AAY71310. The fragment is used in the construction of mutant Nogo-B. The  
CC mutant is composed of His-tag/T7-tag/vector/Nogo-A sequence aa 1-171 +  
CC 975-1162. Nogo A deletion mutants were used for mapping the inhibitory  
CC sites of Nogo protein. Major inhibitory region was identified in the Nogo  
CC A sequence from amino acids 172-974, particularly amino acids 542-722. In  
CC addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3  
CC fibroblast spreading. Note: The present sequence is not given in the  
CC specification but is derived from rat Nogo A sequence shown in AAY71310.  
CC SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in  
CC disclosure of the specification. However, the specification does not  
CC include sequences for these SEQ ID numbers  
XX  
SQ Sequence 359 AA;  
Query Match 99.4%; Score 919; DB 3; Length 359;  
Best Local Similarity 100.0%; Pred. No. 4.2e-89;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SVVDLLYWRDIKKTGVFGASLFLLSLTFTVSIVSTAYIALLSVTISPRYKGVIOA 60  
Db 172 SVVDLLYWRDIKKTGVFGASLFLLSLTFTVSIVSTAYIALLSVTISPRYKGVIOA 231  
Qy 61 IQKSDGHPFRAYLESEVAISELVQKYSNLSALGHVNSTIKELRRLFLVDDLVSLKFAV 120  
Db 232 IQKSDGHPFRAYLESEVAISELVQKYSNLSALGHVNSTIKELRRLFLVDDLVSLKFAV 291  
Qy 121 LMWFTYVVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 180  
Db 292 LMWFTYVVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 351  
Qy 181 IPGLKRKA 188  
Db 352 IPGLKRKA 359  
RESULT 14  
AA711563  
ID AAY71563 standard; protein; 403 AA.  
XX  
AC AAY71563;  
XX  
DT 02-NOV-2000 (first entry)  
XX  
DE Rat Nogo A protein fragment used in the construction of mutant EST.  
XX  
XX Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
KW central nervous system; neoplastic disease; antiproliferative; glioma;  
KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
KW structural plasticity; screening; mutant; mutein.  
XX

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OS Rattus sp.
XX WO200031235-A2.
XX 02-JUN-2000.
XX 05-NOV-1999; 99WO-US026160.
XX 06-NOV-1998; 98US-0107446P.
XX (SCHW/) SCHWAB M E.
XX (CHEN/) CHEN M S.
XX Schwab ME, Chen MS;
XX WPI; 2000-400052/34.
XX Nogo proteins and nucleic acids useful for treating neoplastic disorders
XX of the central nervous system and inducing regeneration of neurons.
XX Example; Page; 122pp; English.
XX The patent relates to neurite growth inhibitor Nogo which is free of all
XX central nervous system (CNS) myelin material with which it is native
XX associated. Nogo proteins and fragments displaying neurite growth
XX inhibitory activity are used in the treatment of neoplastic disease of
XX the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
XX ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
XX oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and
XX degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
XX Therapeutics which promote Nogo activity can be used to treat or prevent
XX hyperproliferative or benign dysproliferative disorders e.g. psoriasis
XX and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
XX used to inhibit production of Nogo protein to induce regeneration of
XX neurons or to promote structural plasticity of the CNS in disorders where
XX neurite growth, regeneration or maintenance are deficient or desired. The
XX animal models can be used in diagnostic and screening methods for
XX predisposition to disorders and to screen for or test molecules which can
XX treat or prevent disorders or diseases of the CNS. The present sequence
XX is a fragment of rat Nogo A protein shown in AAY71310, which is used in
XX the construction of mutant EST. The mutant is composed of His-tag/TT-
XX tag/Nogo-A sequence aa 760-1162. Nogo A deletion mutants were used for
XX mapping the inhibitory sites of Nogo protein. Major inhibitory region was
XX identified in the Nogo A sequence from amino acids 172-974, particularly
XX amino acids 542-722. In addition, N-terminal region 1-171 was found to be
XX inhibitory to NIH 3T3 fibroblast spreading. Note: The present sequence is
XX not given in the specification but is derived from rat Nogo A sequence
XX shown in AAY71310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ
XX ID NO: 29 in disclosure of the specification. However, the specification
XX does not include sequences for these SEQ ID numbers
XX Sequence 403 AA;
XX
XX Query Match 99.4%; Score 919; DB 3; Length 403;
XX Best Local Similarity 100.0%; Pred. No. 4.8e-89;
XX Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SVVDLLYWRDIIKKTGVVFGASLFLLSLTVFSTVSVTAYIALALLSVTISFRIYKGVIOA 60
XX DB 216 SVVDLLYWRDIIKKTGVVFGASLFLLSLTVFSTVSVTAYIALALLSVTISFRIYKGVIOA 275
XX
XX QY 61 IQKSDGHPFRAYLSEVAISELVOKYNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
XX DB 276 IQKSDGHPFRAYLSEVAISELVOKYNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 335
XX
XX QY 121 LMWFTYVGFALFNGLLTLLIALLSLFSIPVIYERHQVQIDHYGLANKSVKQAMAKIOAK 180
XX DB 336 LMWFTYVGFALFNGLLTLLIALLSLFSIPVIYERHQVQIDHYGLANKSVKQAMAKIOAK 395
XX
XX QY 181 IPLGKRKA 188
XX DB 396 IPLGKRKA 403

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RESULT 15  
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 ID AAY71557 standard; protein; 1162 AA.  
 XX  
 AC AAY71557;  
 XX  
 DT 02-NOV-2000 (first entry)  
 XX  
 DE Rat Nogo A truncated protein used in the construction of mutant Nogo-A.  
 XX  
 KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
 KW central nervous system; neoplastic disease; antiproliferative; glioma;  
 KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
 KW structural plasticity; screening; mutant; mutein.  
 XX  
 OS Rattus sp.  
 XX  
 PS WO200031235-A2.  
 XX  
 PN 02-JUN-2000.  
 PD  
 PF 05-NOV-1999; 99WO-US026160.  
 XX  
 PR 06-NOV-1998; 98US-0107446P.  
 XX  
 PA (SCHW/) SCHWAB M E.  
 PA (CHEN/) CHEN M S.  
 PI Schwab ME, Chen MS;  
 DR WPI; 2000-400052/34.  
 XX  
 PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
 PT of the central nervous system and inducing regeneration of neurons.  
 XX  
 PS Example; Page; 122pp; English.  
 XX  
 CC The patent relates to neurite growth inhibitor Nogo which is free of all  
 CC central nervous system (CNS) myelin material with which it is native  
 CC associated. Nogo proteins and fragments displaying neurite growth  
 CC inhibitory activity are used in the treatment of neoplastic disease of  
 CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,  
 CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,  
 CC oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and  
 CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.  
 CC Therapeutics which promote Nogo activity can be used to treat or prevent  
 CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis  
 CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be  
 CC used to inhibit production of Nogo protein to induce regeneration of  
 CC neurons or to promote structural plasticity of the CNS in disorders where  
 CC neurite growth, regeneration or maintenance are deficient or desired. The  
 CC animal models can be used in diagnostic and screening methods for  
 CC predisposition to disorders and to screen for or test molecules which can  
 CC treat or prevent disorders or diseases of the CNS. The present sequence  
 CC is a fragment of rat Nogo A protein shown in AAY71310, which is used in  
 CC the construction of mutant EST. The mutant is composed of His-tag/TT-  
 CC tag/Nogo-A sequence aa 760-1162. Nogo A deletion mutants were used for  
 CC mapping the inhibitory sites of Nogo protein. Major inhibitory region was  
 CC identified in the Nogo A sequence from amino acids 172-974, particularly  
 CC amino acids 542-722. In addition, N-terminal region 1-171 was found to be  
 CC inhibitory to NIH 3T3 fibroblast spreading. Note: The present sequence is  
 CC not given in the specification but is derived from rat Nogo A sequence  
 CC shown in AAY71310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ  
 CC ID NO: 29 in disclosure of the specification. However, the specification  
 CC does not include sequences for these SEQ ID numbers  
 XX  
 XX Sequence 403 AA;  
 XX  
 XX Query Match 99.4%; Score 919; DB 3; Length 403;  
 XX Best Local Similarity 100.0%; Pred. No. 4.8e-89;  
 XX Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 SVVDLLYWRDIIKKTGVVFGASLFLLSLTVFSTVSVTAYIALALLSVTISFRIYKGVIOA 60  
 XX DB 216 SVVDLLYWRDIIKKTGVVFGASLFLLSLTVFSTVSVTAYIALALLSVTISFRIYKGVIOA 275  
 XX  
 XX QY 61 IQKSDGHPFRAYLSEVAISELVOKYNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120  
 XX DB 276 IQKSDGHPFRAYLSEVAISELVOKYNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 335  
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 XX QY 121 LMWFTYVGFALFNGLLTLLIALLSLFSIPVIYERHQVQIDHYGLANKSVKQAMAKIOAK 180  
 XX DB 336 LMWFTYVGFALFNGLLTLLIALLSLFSIPVIYERHQVQIDHYGLANKSVKQAMAKIOAK 395  
 XX  
 XX QY 181 IPLGKRKA 188  
 XX DB 396 IPLGKRKA 403





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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:19:00 ; Search time 7.13706 Seconds  
(without alignments)  
1976.818 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163  
Perfect score: 925  
Sequence: 1 SVVDLLYWRDIKKTGVFEA.....VKDAMKIQAKIPGLKRRAD 189

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	904	97.7	199	2	US-08-700-607-1
2	904	97.7	201	4	US-09-949-016-9124
3	679	73.4	208	2	US-08-700-607-7
4	679	73.4	356	2	US-08-700-607-6
5	679	73.4	439	4	US-09-949-016-9180
6	679	73.4	776	2	US-08-700-607-5
7	679	73.4	776	4	US-09-949-016-6998
8	665	71.9	262	2	US-08-700-607-8
9	625.5	67.6	192	4	US-09-949-016-8859
10	539.5	58.3	168	4	US-09-149-476-563
11	518	56.0	219	4	US-09-270-767-45132
12	516	55.8	241	2	US-08-700-607-3
13	475	51.4	588	4	US-09-949-016-7290
14	286	30.9	92	4	US-09-149-476-411
15	246	26.6	114	4	US-09-513-999C-7861
16	142	15.4	374	4	US-09-248-796A-16008
17	100	10.8	80	3	US-08-905-223-411
18	95	10.3	468	4	US-08-487-596-8
19	95	10.3	468	4	US-08-660-451A-8
20	94	10.2	382	4	US-09-949-016-11596
21	88.5	9.6	1278	4	US-09-462-136-2
22	88.5	9.6	1318	4	US-09-949-016-10152
23	86.5	9.4	592	4	US-09-134-000C-5477
24	86	9.3	414	4	US-08-956-171E-5246
25	86	9.3	414	4	US-08-781-986A-5246
26	85.5	9.2	1051	3	US-09-134-001C-5005
27	84.5	9.1	593	4	US-09-328-352-4866

Sequence 302, App  
Sequence 3963, Ap  
Sequence 5202, Ap  
Sequence 2858, Ap  
Sequence 6175, Ap  
Sequence 14833, A  
Sequence 1, Appli  
Sequence 3, Appli  
Sequence 4880, Ap  
Sequence 4818, Ap  
Sequence 53, Appl  
Sequence 2019, Ap  
Sequence 27968, A  
Sequence 8, Appli  
Sequence 19, Appl  
Sequence 52, Appl  
Sequence 419, App  
Sequence 3805, Ap

ALIGNMENTS

RESULT 1  
US-08-700-607-1  
; Sequence 1, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/700,607  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0114 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 199 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE: Consensus  
US-08-700-607-1

Query Match 97.7%; Score 904; DB 2; Length 199;  
Best Local Similarity 97.3%; Pred. No. 7.9e-89;  
Matches 183; Conservative 3; Mismatches 0; Gaps 0;

OY 2 VVDLLYWRDIKKTGVFEASIFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61

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Db 12 VDLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 71
QY 62 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDSLKFAYL 121
Db 72 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDSLKFAYL 131
QY 122 MVFTYVGFALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI 181
Db 132 MVFTYVGFALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI 191
QY 182 PGLKRRAD 189
Db 192 PGLKRAE 199

RESULT 2
US-09-949-016-9124
; Sequence 9124, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 9124
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9124

Query Match 97.7%; Score 904; DB 4; Length 201;
Best Local Similarity 97.3%; Pred. No. 8e-89; 2; Indels 0; Gaps 0;
Matches 183; Conservative 3; Mismatches 2;

QY 2 VDLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61
Db 14 VDLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 73
QY 62 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDSLKFAYL 121
Db 74 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDSLKFAYL 133
QY 122 MVFTYVGFALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI 181
Db 134 MVFTYVGFALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI 193
QY 182 PGLKRRAD 189
Db 194 PGLKRAE 201

RESULT 3
US-08-700-607-7
; Sequence 7, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-Seq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307311
US-08-700-607-7

Query Match 73.4%; Score 679; DB 2; Length 208;
Best Local Similarity 67.9%; Pred. No. 1e-64; 29; Indels 0; Gaps 0;
Matches 127; Conservative 31; Mismatches 29;

QY 3 VDLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 62
Db 22 IDLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVVAYLALAALSATISFRIYKSVLQAVQ 81
QY 63 KSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDSLKFAYL 122
Db 82 KTDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDSLKFAYL 141
QY 123 MVFTYVGFALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI 182
Db 142 WLLTYVGFALFNGLTLLMAVSMFTLPVVYVVKHQADQYGLVTRTHINAVVAKIOAKI 201
QY 183 GLKRRAD 189
Db 202 GAKRAE 208

RESULT 4
US-08-700-607-6
; Sequence 6, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0114 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 356 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 307309
US-08-700-607-6

Query Match 73.4%; Score 679; DB 2; Length 356;
Best Local Similarity 67.9%; Pred. No. 2.2e-64;
Matches 127; Conservative 31; Mismatches 29; Indels 0; Gaps 0;

QY 3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQ 62
DB 170 IDLLYWRDIKQTGIVFGSLFLLLSLTVFSIVSVVAYIALAALSATISFRIYKSVLQAVQ 229
QY 63 KSDGHPFRAYLSEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLM 122
DB 230 KTDGHPFRAYLEITLSQEQIKYTDCLQFYVNSTLKELRRLFLVQDLVDSLKFAVLM 289
QY 123 WVFTYVGALFNLGLTLLIALLSLFSIPVIYERHQVIDHYLGLANKSVKDMAKIOAKIP 182
DB 290 WLLTYVGALFNLGLTLLMAVVSMTPLPVVYVKHQAIQDQYLGVLVTRTHNAVVAKIOAKIP 349
QY 183 GLKRRAD 189
DB 350 GAKRHAE 356

RESULT 5
US-09-949-016-9180
; Sequence 9180, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9180
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9180
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Query Match 73.4%; Score 679; DB 4; Length 439;
Best Local Similarity 67.9%; Pred. No. 2.9e-64;
Matches 127; Conservative 31; Mismatches 29; Indels 0; Gaps 0;

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QY 63 KSDGHPFRAYLSEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLM 122
DB 313 KTDGHPFRAYLEITLSQEQIKYTDCLQFYVNSTLKELRRLFLVQDLVDSLKFAVLM 372
QY 123 WVFTYVGALFNLGLTLLIALLSLFSIPVIYERHQVIDHYLGLANKSVKDMAKIOAKIP 182
DB 373 WLLTYVGALFNLGLTLLMAVVSMTPLPVVYVKHQAIQDQYLGVLVTRTHNAVVAKIOAKIP 432
QY 183 GLKRRAD 189
DB 433 GAKRHAE 439

RESULT 6
US-08-700-607-5
; Sequence 5, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REFERENCE/DOCKET NUMBER: PP-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 776 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307307
; US-08-700-607-5

Query Match 73.4%; Score 679; DB 2; Length 776;
Best Local Similarity 67.9%; Pred. No. 6.5e-64;
Matches 127; Conservative 31; Mismatches 29; Indels 0; Gaps 0;

QY 3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQ 62
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QY 123 WFTYVYGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKIP 182
DB 710 WLLTYVYGALFNGLTLLMAVSMFTLPVVYVKHQVQIDQYGLVTRTHINAVVAKIOAKIP 769
QY 183 GLKRAK 189
DB 770 GAKRAE 776

RESULT 7
US-09-949-016-6998
; Sequence 6998, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6998
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6998

Query Match 73.4%; Score 679; DB 4; Length 776;
Best Local Similarity 67.9%; Pred. No. 6.5e-64;
Matches 127; Conservative 31; Mismatches 29; Indels 0; Gaps 0;

QY 3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIOAQ 62
DB 590 IDLLYWRDIKQTGIVFGSFLLLSLTQFSVSVWYALALALSATISPRIYKSVLQAVQ 649
QY 63 KSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 122
DB 650 KTDGHPFRAYLEITLSQEQIKYTDCLQFYVNSTKLRLFLVQDLVDSLKFAVL 709
QY 123 WFTYVYGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKIP 182
DB 710 WLLTYVYGALFNGLTLLMAVSMFTLPVVYVKHQVQIDQYGLVTRTHINAVVAKIOAKIP 769
QY 183 GLKRAK 189
DB 770 GAKRAE 776

RESULT 8
US-08-700-607-8
; Sequence 8, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
```

```
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0114 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 281046
US-08-700-607-8

Query Match 71.9%; Score 665; DB 2; Length 267;
Best Local Similarity 67.2%; Pred. No. 4.6e-63;
Matches 123; Conservative 32; Mismatches 28; Indels 0; Gaps 0;

QY 3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIOAQ 62
DB 13 IDLLYWRDIKQTGIVFGSFLLLSLTQFSVSVWYALALALSATISPRIYKSVLQAVQ 72
QY 63 KSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 122
DB 73 KTDGHPFRAYLEITLSQEQIKYTDCLQFYVNSTKLRLFLVQDLVDSLKFAVL 132
QY 123 WFTYVYGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKIP 182
DB 133 WLLTYVYGALFNGLTLLMAVSMFTLPVVYVKHQVQIDQYGLVTRTHINAVVAKIOAKIP 192
QY 183 GLK 185
DB 193 GAR 195

RESULT 9
US-09-949-016-8859
; Sequence 8859, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8859
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; LENGTH: 192
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8859

Query Match      67.6%; Score 625.5; DB 4; Length 192;
Best Local Similarity 60.0%; Pred. No. 5e-59;
Matches 114; Conservative 40; Mismatches 35; Indels 1; Gaps 1;

QY 1 SVVDLLYWRDIKKTGVVFCASIFLLLSLTIVFSIVTAIALLSVTSIPRIYKGVIOA 60
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 SVHDLIFWRDVKTKTGFVFTTLMLLSLAASFVSVSYLLIALLSVTSIPRIYKSVIOA 62
   :|||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 IQKSDGHPFRAYLSEVAISEBELVQKYSNSALGHVNSTIKELRFLVDDLVDLSLKFV 120
   :|||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 VQKSEGHFFKAYLDVDTLSEAFHYNNAAMVHINRAKLIIIRFLVEDLVDLSKLAV 122
   :|||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 LMWVTYVYCALPNGTLLILALISLFSPIVYERHQQVDHYGLANKSVKDMAKIOAK 180
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 123 FFWLMTYVCAVFNGITLLILAEILLFSPVYKVKYQIDHYVGIARDQTKSIVEKIOAK 182
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 181 IPGL-KRKAD 189
Db 183 LPGIARKKAE 192

RESULT 10
US-09-149-476-563
; Sequence 563, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
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1	EARLIER APPLICATION NUMBER: 60/056,879
2	EARLIER FILING DATE: 1997-08-22
3	EARLIER APPLICATION NUMBER: 60/056,880
4	EARLIER FILING DATE: 1997-08-22
5	EARLIER APPLICATION NUMBER: 60/056,884
6	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/056,911
8	EARLIER FILING DATE: 1997-08-22
9	EARLIER APPLICATION NUMBER: 60/056,636
10	EARLIER FILING DATE: 1997-08-22
11	EARLIER APPLICATION NUMBER: 60/056,874
12	EARLIER FILING DATE: 1997-08-22
13	EARLIER APPLICATION NUMBER: 60/056,910
14	EARLIER FILING DATE: 1997-08-22
15	EARLIER APPLICATION NUMBER: 60/056,864
16	EARLIER FILING DATE: 1997-08-22
17	EARLIER APPLICATION NUMBER: 60/056,631
18	EARLIER FILING DATE: 1997-08-22
19	EARLIER APPLICATION NUMBER: 60/056,845
20	EARLIER FILING DATE: 1997-08-22
21	EARLIER APPLICATION NUMBER: 60/056,892
22	EARLIER FILING DATE: 1997-08-22
23	EARLIER APPLICATION NUMBER: 60/057,761
24	EARLIER FILING DATE: 1997-08-22
25	EARLIER APPLICATION NUMBER: 60/047,595
26	EARLIER FILING DATE: 1997-05-23
27	EARLIER APPLICATION NUMBER: 60/047,599
28	EARLIER FILING DATE: 1997-05-23
29	EARLIER APPLICATION NUMBER: 60/047,588
30	EARLIER FILING DATE: 1997-05-23
31	EARLIER APPLICATION NUMBER: 60/047,585
32	EARLIER FILING DATE: 1997-05-23
33	EARLIER APPLICATION NUMBER: 60/047,586
34	EARLIER FILING DATE: 1997-05-23
35	EARLIER APPLICATION NUMBER: 60/047,590
36	EARLIER FILING DATE: 1997-05-23
37	EARLIER APPLICATION NUMBER: 60/047,594
38	EARLIER FILING DATE: 1997-05-23
39	EARLIER APPLICATION NUMBER: 60/047,589
40	EARLIER FILING DATE: 1997-05-23
41	EARLIER APPLICATION NUMBER: 60/047,593
42	EARLIER FILING DATE: 1997-05-23
43	EARLIER APPLICATION NUMBER: 60/047,614
44	EARLIER FILING DATE: 1997-05-23
45	EARLIER APPLICATION NUMBER: 60/043,578
46	EARLIER FILING DATE: 1997-04-11
47	EARLIER APPLICATION NUMBER: 60/043,576
48	EARLIER FILING DATE: 1997-04-11
49	EARLIER APPLICATION NUMBER: 60/047,501
50	EARLIER FILING DATE: 1997-05-23
51	EARLIER APPLICATION NUMBER: 60/043,670
52	EARLIER FILING DATE: 1997-04-11
53	EARLIER APPLICATION NUMBER: 60/056,632
54	EARLIER FILING DATE: 1997-08-22
55	EARLIER APPLICATION NUMBER: 60/056,664
56	EARLIER FILING DATE: 1997-08-22
57	EARLIER APPLICATION NUMBER: 60/056,876
58	EARLIER FILING DATE: 1997-08-22
59	EARLIER APPLICATION NUMBER: 60/056,881
60	EARLIER FILING DATE: 1997-08-22
61	EARLIER APPLICATION NUMBER: 60/056,909
62	EARLIER FILING DATE: 1997-08-22
63	EARLIER APPLICATION NUMBER: 60/056,875
64	EARLIER FILING DATE: 1997-08-22
65	EARLIER APPLICATION NUMBER: 60/056,862
66	EARLIER FILING DATE: 1997-08-22
67	EARLIER APPLICATION NUMBER: 60/056,887
68	EARLIER FILING DATE: 1997-08-22
69	EARLIER APPLICATION NUMBER: 60/056,908
70	EARLIER FILING DATE: 1997-08-22
71	EARLIER APPLICATION NUMBER: 60/048,964
72	EARLIER FILING DATE: 1997-06-06
73	EARLIER APPLICATION NUMBER: 60/057,650

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; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 58.3%; Score 539.5; DB 4; Length 168;
Best Local Similarity 59.3%; Pred. No. 6.7e-50;
Matches 99; Conservative 36; Mismatches 31; Indels 1; Gaps 1

Qy 24 LLSLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIOAIQKSDGHPFRAYLESEVAISEE 83
Db 1 MLLSLAAFSVTSVSVSYLIALLSVTISPRIYKSVIOAQVQKSEGHPPFRAYLDVDITLSSE 60
Qy 84 LVQKYSNALSCHVNSTIKELRRLFLVDDLVDLSKFAVLMMVFTYVYGALFNGTLTLIALI 143
Db 61 AFHYMAMAMVHINRAKLIIRLFLVEDVDLSKLAVFWMMLTYGVAFNGITLILIAEL 120
Qy 144 SLFSIPVIYERHQVIDHYLGLANKSVKDMAKIOAKIPGL-KRKAD 189
Db 121 LIFSVPVIYEKYQIDHYVGIARDQTKSVIEKIQAKLPGIAKKAAE 167

RESULT 11
US-09-270-767-45132
; Sequence 45132, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45132
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45132

Query Match 56.0%; Score 518; DB 4; Length 219;
Best Local Similarity 52.2%; Pred. No. 1.9e-47;
Matches 93; Conservative 41; Mismatches 44; Indels 0; Gaps 0

Qy 5 LLYWRDICKTVGFGASLFLLSLSTVTSIVSVTAYIALALLSVTISPRIYKGVIOAIQKS 64
Db 26 LIYWRDVKKSGIVFGAGLITLAAISFSFVISVFAVLSLTLFTGTAFRIYKSVTQAVQKT 85
Qy 65 DEGHPPFRAYLESEVAISEELVQKYSNALSCHVNSTIKELRRLFLVDDLVDLSKFAVLMMV 124
Db 86 NEGHPPFDYLEDLDTLSLSEKQNTAGVAHNGFISLRRRLFLVEDIIDSIFGVILMW 145
Qy 125 FTYVYGALFNGTLTLIALLSFSPVIYERHQVIDHYLGLANKSVKDMAKIOAKIP 182
Db 146 FTYVYGAWFNGMTLVILAFVSLFTLPKVYENNKQSIDTHLDLVRSLKLTETTDKIRVAIP 203

RESULT 12
US-08-700-607-3
; Sequence 3, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9

```



CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/700,607  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PP-0114 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: THPINOB01  
CLONE: 31870  
US-08-700-607-3

Query Match 55.8%; Score 516; DB 2; Length 241;  
Best Local Similarity 59.9%; Pred. No. 3.6e-47;  
Matches 94; Conservative 33; Mismatches 30; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVFGASIFLLSLTFTVFSIVSVTAIYALALLSVTISFRIYKGVIOA 60  
Db 47 AVHDLIXWRDVKTGFVGTTLMLSLAASFVSVSYLIALLSVTISFRIYKSVIOA 106  
Qy 61 IQKSDGHPFRAYLESEVAISELVQKYSNLSALGHVNSTIKELRRLFLVDDLVDSLKPAV 120  
Db 107 VQKSEGHFPFRAYLDVDTLTSSAPHNMYNAAMVHINRAKLIIRLFLVEDLVDSKLAV 166  
Qy 121 LMWFTYVGALENGTLTLLILALISLFSIPVIYERHQQV 157  
Db 167 FMWLTYYGAVFNGITLLILAELLIXSVPIYXKYKV 203

## RESULT 13

US-09-949-016-7290  
Sequence 7290, Application US/09949016  
Patent No. 6812339

GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7290  
LENGTH: 588  
TYPE: PRT

ORGANISM: Human  
US-09-949-016-7290

Query Match 51.4%; Score 475; DB 4; Length 588;  
Best Local Similarity 50.5%; Pred. No. 3.1e-42;  
Matches 92; Conservative 36; Mismatches 54; Indels 0; Gaps 0;

Qy 2 VVDLLYWRDIKKTGVFGASIFLLSLTFTVFSIVSVTAIYALALLSVTISFRIYKGVIOAI 61  
Db 388 VADLLYWKDTRTSGVFTGLVSLCLLHFFSVVAHALLLLCGTISLRVYKVLQAV 447  
Qy 62 QKSDGHPFRAYLESEVAISELVQKYSNLSALGHVNSTIKELRRLFLVDDLVDSLKPAV 121  
Db 448 HRGDCANPFQAYLDVDTLTREQTERLSHQITSRVVSAAATQLRHFFVEDLVSLKALL 507  
Qy 122 MWFTYVGALENGTLTLLILALISLFSIPVIYERHQQVTDHYVLGLANKSVKDMAKIOAKI 181  
Db 508 FYILTFVGAIFNGITLLILGLFTPLLYRQHQAIQDQVGLVTNQLSHIKAKIRAKI 567  
Qy 182 PG 183  
Db 568 PG 569

## RESULT 14

US-09-149-476-411  
Sequence 411, Application US/09149476  
Patent No. 6420526

GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: P2002P1  
CURRENT FILING DATE: 1998-09-08  
CURRENT APPLICATION NUMBER: US/09/149,476  
EARLIER APPLICATION NUMBER: PCT/US98/04493  
EARLIER FILING DATE: 1998-03-06  
EARLIER APPLICATION NUMBER: 60/040,162  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,333  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/038,621  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,626  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,334  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,336  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,163  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/047,600  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,615  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,597  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,502  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,633  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,583  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,617  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,618  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,503  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,592  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,581  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,584



Search completed: June 16, 2005, 12:33:38  
Job time : 9.13706 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:29:05 ; Search time 24.5171 Seconds  
(without alignments)  
2960.058 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163  
Perfect score: 925  
Sequence: 1 SWDLYWRDIKTGWFGA.....VKDAMAKIQAKIPGLKRAKAD 189

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1714042

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	925	100.0	1163	9 US-09-893-348-18	Sequence 18, Appl
2	925	100.0	1163	16 US-10-810-653-18	Sequence 18, Appl
3	922	99.7	379	14 US-10-205-194-164	Sequence 164, Appl
4	921	99.6	199	9 US-09-893-348-21	Sequence 21, Appl
5	921	99.6	199	16 US-10-810-653-21	Sequence 21, Appl
6	921	99.6	360	9 US-09-893-348-20	Sequence 20, Appl
7	921	99.6	360	16 US-10-810-653-20	Sequence 20, Appl
8	917	99.1	1162	16 US-10-633-423-10	Sequence 10, Appl
9	917	99.1	1162	16 US-10-427-741-10	Sequence 10, Appl
10	908	98.2	1192	9 US-09-789-386-2	Sequence 2, Appl
11	908	98.2	1192	9 US-09-758-140-6	Sequence 6, Appl

12	908	98.2	1192	9 US-09-893-348-23	Sequence 23, Appl
13	908	98.2	1192	9 US-09-972-599A-6	Sequence 6, Appl
14	908	98.2	1192	14 US-10-060-036-71	Sequence 71, Appl
15	908	98.2	1192	15 US-10-267-502-429	Sequence 429, Appl
16	908	98.2	1192	16 US-10-327-213-9	Sequence 9, Appl
17	908	98.2	1192	16 US-10-466-258-9	Sequence 9, Appl
18	908	98.2	1192	16 US-10-810-653-23	Sequence 23, Appl
19	908	98.2	1192	15 US-10-267-502-431	Sequence 431, Appl
20	904	97.7	199	9 US-09-893-348-25	Sequence 25, Appl
21	904	97.7	199	15 US-10-660-946-1	Sequence 1, Appl
22	904	97.7	199	16 US-10-810-653-25	Sequence 25, Appl
23	904	97.7	373	9 US-09-789-386-6	Sequence 6, Appl
24	904	97.7	373	9 US-09-765-205-6	Sequence 6, Appl
25	904	97.7	373	9 US-09-893-348-24	Sequence 24, Appl
26	904	97.7	373	14 US-10-060-036-72	Sequence 72, Appl
27	904	97.7	373	15 US-10-408-967-8	Sequence 8, Appl
28	904	97.7	373	16 US-10-466-258-4	Sequence 4, Appl
29	904	97.7	373	16 US-10-810-653-24	Sequence 24, Appl
30	904	97.7	373	17 US-10-347-669-6	Sequence 6, Appl
31	904	97.4	1192	15 US-10-408-967-7	Sequence 7, Appl
32	897	97.0	199	15 US-10-408-967-9	Sequence 9, Appl
33	895	96.8	199	11 US-09-978-360A-467	Sequence 467, Appl
34	864	93.4	199	16 US-10-466-258-11	Sequence 11, Appl
35	679	73.4	208	15 US-10-660-946-7	Sequence 7, Appl
36	679	73.4	356	15 US-10-660-946-6	Sequence 6, Appl
37	679	73.4	776	15 US-10-660-946-5	Sequence 5, Appl
38	679	73.4	776	15 US-10-267-502-430	Sequence 430, Appl
39	679	73.4	776	16 US-10-723-860-1481	Sequence 1481, Appl
40	678	73.3	777	14 US-10-205-219-93	Sequence 93, Appl
41	678	73.3	780	15 US-10-267-502-432	Sequence 432, Appl
42	665	71.9	267	14 US-10-205-194-127	Sequence 127, Appl
43	665	71.9	267	15 US-10-660-946-8	Sequence 8, Appl
44	622.5	67.3	236	9 US-09-729-674-20	Sequence 20, Appl
45	622.5	67.3	236	9 US-09-765-205-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1  
US-09-893-348-18  
; Sequence 18, Application US/09893348  
; Patent No. US20020072493A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN, Itun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SCHWARTZ=2A  
; CURRENT APPLICATION NUMBER: US/09/893,348  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 1163  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
; US-09-893-348-18

Query Match 100.0%; Score 925; DB 9; Length 1163;  
Best Local Similarity 100.0%; Pred. No. 4e-81;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Query Match 99.6%; Score 921; DB 9; Length 199;  
Best Local Similarity 100.0%; Pred. No. 1e-81;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61  
DB 12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 71

QY 62 QKSDGHPFRAYLESEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLDVSLKPAVL 121  
DB 72 QKSDGHPFRAYLESEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLDVSLKPAVL 131

QY 122 MWFTYVGCALFNGLLTLLILALISLFSIPVIYERHQQVDHYLGLANKSVKDMAKIOAKI 181  
DB 132 MWFTYVGCALFNGLLTLLILALISLFSIPVIYERHQQVDHYLGLANKSVKDMAKIOAKI 191

QY 182 PGLKRRKAD 189  
DB 192 PGLKRRKAD 199

RESULT 5  
US-10-810-653-21  
; Sequence 21, Application US/10810653  
; Publication No. US20040253218A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN, Irun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SCHWARTZ-2A  
; CURRENT APPLICATION NUMBER: US/10/810,653  
; CURRENT FILING DATE: 2004-03-29  
; PRIOR APPLICATION NUMBER: US/09/893,348  
; PRIOR FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 21  
; LENGTH: 199  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-10-810-653-21

Query Match 99.6%; Score 921; DB 16; Length 199;  
Best Local Similarity 100.0%; Pred. No. 1e-81;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 62 QKSDGHPFRAYLESEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLDVSLKPAVL 121  
DB 72 QKSDGHPFRAYLESEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLDVSLKPAVL 131

QY 122 MWFTYVGCALFNGLLTLLILALISLFSIPVIYERHQQVDHYLGLANKSVKDMAKIOAKI 181  
DB 132 MWFTYVGCALFNGLLTLLILALISLFSIPVIYERHQQVDHYLGLANKSVKDMAKIOAKI 191

QY 182 PGLKRRKAD 189  
DB 192 PGLKRRKAD 199

RESULT 6  
US-09-893-348-20  
; Sequence 20, Application US/09893348  
; Patent No. US20020072493A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN, Irun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SCHWARTZ-2A  
; CURRENT APPLICATION NUMBER: US/09/893,348  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-09-893-348-20

Query Match 99.6%; Score 921; DB 9; Length 360;  
Best Local Similarity 100.0%; Pred. No. 2.2e-81;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61  
DB 173 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 232

QY 62 QKSDGHPFRAYLESEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLDVSLKPAVL 121  
DB 233 QKSDGHPFRAYLESEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLDVSLKPAVL 292

QY 122 MWFTYVGCALFNGLLTLLILALISLFSIPVIYERHQQVDHYLGLANKSVKDMAKIOAKI 181  
DB 293 MWFTYVGCALFNGLLTLLILALISLFSIPVIYERHQQVDHYLGLANKSVKDMAKIOAKI 352

QY 182 PGLKRRKAD 189  
DB 353 PGLKRRKAD 360

RESULT 7  
US-10-810-653-20  
; Sequence 20, Application US/10810653  
; Publication No. US20040253218A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN, Irun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SCHWARTZ-2A  
; CURRENT APPLICATION NUMBER: US/10/810,653  
; CURRENT FILING DATE: 2004-03-29  
; PRIOR APPLICATION NUMBER: US/09/893,348  
; PRIOR FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-10-810-653-20

Query Match 99.6%; Score 921; DB 16; Length 360;  
Best Local Similarity 100.0%; Pred. No. 2.2e-81;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 173 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 232  
QY 62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVL 121  
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QY 122 LMWFTYVYGALFNGLTLLILALISLFSIPVIYERHQQIDHYGLANKSVKDMAKIOAKI 181  
DB 293 LMWFTYVYGALFNGLTLLILALISLFSIPVIYERHQQIDHYGLANKSVKDMAKIOAKI 352  
QY 182 PGLKRRKAD 189  
DB 353 PGLKRRKAD 360

RESULT 8  
US-10-633-423-10  
; Sequence 10, Application US/10633423  
; Publication No. US20040191240A1  
; GENERAL INFORMATION:  
; APPLICANT: Tohyama, Masaya  
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION  
; FILE REFERENCE: 59150-8023 US00  
; CURRENT APPLICATION NUMBER: US/10/633,423  
; CURRENT FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: US 10/427,741  
; PRIOR FILING DATE: 2003-04-30  
; PRIOR APPLICATION NUMBER: JP 2003-92923  
; PRIOR FILING DATE: 2003-03-28  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 1162  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-633-423-10

Query Match 99.1%; Score 917; DB 16; Length 1162;  
Best Local Similarity 98.9%; Pred. No. 2.4e-80;  
Matches 187; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
DB 974 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1033  
QY 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 120  
DB 1034 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 1093  
QY 121 LMWFTYVYGALFNGLTLLILALISLFSIPVIYERHQQIDHYGLANKSVKDMAKIOAK 180  
DB 1094 LMWFTYVYGALFNGLTLLILALISLFSIPVIYERHQQIDHYGLANKSVKDMAKIOAK 1153  
QY 181 IPGLKRRKAD 189

DB 1154 IPGLKRRKAE 1162  
RESULT 9  
US-10-427-741-10  
; Sequence 10, Application US/10427741  
; Publication No. US20040191291A1  
; GENERAL INFORMATION:  
; APPLICANT: Tohyama, Masaya  
; APPLICANT: Yamashita, Toshihide  
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION  
; FILE REFERENCE: 59150-8023  
; CURRENT APPLICATION NUMBER: US/10/427,741  
; CURRENT FILING DATE: 2003-04-30  
; PRIOR APPLICATION NUMBER: JP 2003-92923  
; PRIOR FILING DATE: 2003-03-28  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 1162  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-427-741-10

Query Match 99.1%; Score 917; DB 16; Length 1162;  
Best Local Similarity 98.9%; Pred. No. 2.4e-80;  
Matches 187; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
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DB 974 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1033  
QY 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 120  
DB 1034 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 1093  
QY 121 LMWFTYVYGALFNGLTLLILALISLFSIPVIYERHQQIDHYGLANKSVKDMAKIOAK 180  
DB 1094 LMWFTYVYGALFNGLTLLILALISLFSIPVIYERHQQIDHYGLANKSVKDMAKIOAK 1153  
QY 181 IPGLKRRKAD 189  
DB 1154 IPGLKRRKAE 1162

RESULT 10  
US-09-789-386-2  
; Sequence 2, Application US/09789386  
; Patent No. US20020010324A1  
; GENERAL INFORMATION:  
; APPLICANT: MICHALOVICH, DAVID  
; APPLICANT: PRINJHA, RABINDER KUMAR  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP-30165-C1  
; CURRENT APPLICATION NUMBER: US/09/789,386  
; CURRENT FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: U.K. 9916898.1  
; PRIOR FILING DATE: 1999-07-19  
; PRIOR APPLICATION NUMBER: U.K. 9816024.5  
; PRIOR FILING DATE: 1998-07-22  
; PRIOR APPLICATION NUMBER: US 09/359,208  
; PRIOR FILING DATE: 1999-07-22  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-789-386-2  
Query Match 98.2%; Score 908; DB 9; Length 1192;  
Best Local Similarity 97.4%; Pred. No. 1.9e-79;



Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1063

Qy 61 IQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120  
Db 1064 IQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123

Qy 121 LMWVFTYVYVGFALFNGTLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 180  
Db 1124 LMWVFTYVYVGFALFNGTLTLLILALISLFSVPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 1183

Qy 181 IPGLKRXKAD 189  
Db 1184 IPGLKRXKAE 1192

RESULT 11  
US-09-758-140-6  
; Sequence 6, Application US/09758140  
; Patent No. US20020012965A1  
; GENERAL INFORMATION:  
; APPLICANT: Strittmatter, Stephen M.  
; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth  
; FILE REFERENCE: 44574-5073-US  
; CURRENT APPLICATION NUMBER: US/09/758,140  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/175,707  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: US 60/207,366  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/236,378  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-758-140-6

Query Match 98.2%; Score 908; DB 9; Length 1192;  
Best Local Similarity 97.4%; Pred. No. 1.9e-79;  
Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1063

Qy 61 IQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120  
Db 1064 IQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123

Qy 121 LMWVFTYVYVGFALFNGTLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 180  
Db 1124 LMWVFTYVYVGFALFNGTLTLLILALISLFSVPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 1183

Qy 181 IPGLKRXKAD 189  
Db 1184 IPGLKRXKAE 1192

RESULT 12  
US-09-893-348-23  
; Sequence 23, Application US/09893348  
; Patent No. US20020072493A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN, Irun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR US  
; FILE REFERENCE: EIS-SCHWARTZ-2A  
; CURRENT APPLICATION NUMBER: US/09/893,348  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 23  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-893-348-23

Query Match 98.2%; Score 908; DB 9; Length 1192;  
Best Local Similarity 97.4%; Pred. No. 1.9e-79;  
Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1063

Qy 61 IQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120  
Db 1064 IQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123

Qy 121 LMWVFTYVYVGFALFNGTLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 180  
Db 1124 LMWVFTYVYVGFALFNGTLTLLILALISLFSVPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 1183

Qy 181 IPGLKRXKAD 189  
Db 1184 IPGLKRXKAE 1192

RESULT 13  
US-09-972-599A-6  
; Sequence 6, Application US/09972599A  
; Patent No. US20020077295A1  
; GENERAL INFORMATION:  
; APPLICANT: STRITTMATTER, STEPHEN M.  
; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH  
; FILE REFERENCE: C077 CIP US  
; CURRENT APPLICATION NUMBER: US/09/972,599A  
; CURRENT FILING DATE: 2001-10-06  
; PRIOR APPLICATION NUMBER: PCT/US01/01041  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 09/758,140  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 60/236,378  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/207,366  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/175,707  
; PRIOR FILING DATE: 2000-01-12  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-972-599A-6

Query Match 98.2%; Score 908; DB 9; Length 1192;  
Best Local Similarity 97.4%; Pred. No. 1.9e-79;  
Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60
Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1063
QY 61 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKPAV 120
Db 1064 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKPAV 1123
QY 121 LMWVFTYVGCALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 180
Db 1124 LMWVFTYVGCALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 1183
QY 181 IPGLKRRKAD 189
Db 1184 IPGLKRRKAE 1192
```

## RESULT 14

US-10-060-036-71

; Sequence 71, Application US/10060036

; Publication No. US20030073144A1

; GENERAL INFORMATION:

; APPLICANT: Benson, Darin R.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Persing, David H.

; APPLICANT: Hepler, William T.

; APPLICANT: Jiang, Yugu

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

; FILE REFERENCE: 210121.566

; CURRENT APPLICATION NUMBER: US/10/060,036

; CURRENT FILING DATE: 2002-01-30

; NUMBER OF SEQ ID NOS: 4560

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 71

; LENGTH: 1192

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-060-036-71

```
Query Match 98.2%; Score 908; DB 14; Length 1192;
Best Local Similarity 97.4%; Pred. No. 1.9e-79;
Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60
Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1063
QY 61 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKPAV 120
Db 1064 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKPAV 1123
QY 121 LMWVFTYVGCALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 180
Db 1124 LMWVFTYVGCALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 1183
QY 181 IPGLKRRKAD 189
Db 1184 IPGLKRRKAE 1192
```

## RESULT 15

US-10-267-502-429

; Sequence 429, Application US/10267502

; Publication No. US20040071700A1

; GENERAL INFORMATION:

; APPLICANT: Kim, Jaeseob

; APPLICANT: Galant, Ron

; TITLE OF INVENTION: Obesity Linked Genes

; FILE REFERENCE: LSD-07416

; CURRENT APPLICATION NUMBER: US/10/267,502

; CURRENT FILING DATE: 2003-01-27

; NUMBER OF SEQ ID NOS: 439

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 429

; LENGTH: 1192

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-267-502-429

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Query Match 98.2%; Score 908; DB 15; Length 1192;
Best Local Similarity 97.4%; Pred. No. 1.9e-79;
Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60
Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1063
QY 61 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKPAV 120
Db 1064 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKPAV 1123
QY 121 LMWVFTYVGCALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 180
Db 1124 LMWVFTYVGCALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 1183
QY 181 IPGLKRRKAD 189
Db 1184 IPGLKRRKAE 1192
```

Search completed: June 16, 2005, 13:03:58

Job time : 24.5171 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:33:51 ; Search time 25.6406 Seconds  
(without alignments)  
3774.604 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163

Perfect score: 925

Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRRKAD 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	925	100.0	1163	1 RTN4 RAT	Q9jkl1 rattus norv
2	917	99.1	578	2 Q80W95	Q80w95 mus musculu
3	917	99.1	639	2 Q8K230	Q8k230 mus musculu
4	917	99.1	1046	2 Q8BGK7	Q8bgk7 mus musculu
5	917	99.1	1162	2 Q8BGM9	Q8bgm9 mus musculu
6	914	98.8	375	2 Q8BH75	Q8bh75 mus musculu
7	913	98.7	199	1 RTN4 MOUSE	Q99p72 mus musculu
8	913	98.7	356	2 Q8BH78	Q8bh78 mus musculu
9	908	98.2	986	2 Q8IU84	Q8iua4 homo sapien
10	908	98.2	1192	1 RTN4 HUMAN	Q9nqc3 homo sapien
11	906.5	98.0	1163	2 Q8K3G8	Q8k3g8 mus musculu
12	905	97.8	392	2 Q96B16	Q96b16 homo sapien
13	904	97.7	199	2 Q7YRW9	Q7yrw9 bos taurus
14	904	97.7	343	2 Q6IPN0	Q6ipn0 homo sapien
15	902.5	97.6	357	2 Q8K3G7	Q8k3g7 mus musculu
16	900	97.3	199	2 Q6IM70	Q6im70 sus scrofa
17	896	96.9	187	2 Q6IG15	Q6ig15 sus scrofa
18	895	96.8	199	2 Q7PC77	Q7pcj7 macaca fasc
19	879	95.0	658	2 Q6RS58	Q6rsa8 gallus gall
20	872	94.3	199	2 Q7T224	Q7t224 gallus gall
21	844	91.2	179	2 Q9GM33	Q9gm33 macaca fasc
22	773	83.6	193	2 Q6IFY5	Q6ify5 xenopus tro
23	772	83.5	315	2 Q6IFY4	Q6ify4 xenopus tro
24	764	82.6	1024	2 Q6JRV2	Q6jrv2 xenopus lae
25	764	82.6	1043	2 Q6JRV0	Q6jrv0 xenopus lae
26	764	82.6	1055	2 Q6JRV1	Q6jrv1 xenopus lae
27	761	82.3	193	2 Q6JRV6	Q6jrv6 xenopus lae
28	761	82.3	330	2 Q6JRV4	Q6jrv4 xenopus lae
29	760	82.2	199	2 Q6PB23	Q6pb23 xenopus lae
30	760	82.2	311	2 Q6JRV3	Q6jrv3 xenopus lae
31	747	80.8	1013	2 Q6JRV9	Q6jrv9 xenopus lae

32	747	80.8	1032	2 Q6JRV7	Q6jrv7 xenopus lae
33	747	80.8	1044	2 Q6JRV8	Q6jrv8 xenopus lae
34	744	80.4	193	2 Q6JRW4	Q6jrw4 xenopus lae
35	744	80.4	323	2 Q6JRW1	Q6jrw1 xenopus lae
36	743	80.3	199	2 Q6JRW3	Q6jrw3 xenopus lae
37	743	80.3	304	2 Q6JRW0	Q6jrw0 xenopus lae
38	743	80.3	316	2 Q6JRW2	Q6jrw2 xenopus lae
39	733	79.2	214	2 Q7T222	Q7t222 carassius a
40	719	77.7	196	2 Q6IRI6	Q6iel6 cyprinus ca
41	711	76.9	193	2 Q6IEB4	Q6iel4 fugu rubrip
42	705	76.2	197	2 Q6EHZ3	Q6ehz3 brachydanio
43	697.5	75.4	209	2 Q6IEJ1	Q6iel1 oncorhynch
44	683	73.8	208	2 Q6IAX4	Q6iax4 homo sapien
45	679	73.4	199	2 Q9BQ59	Q9bq59 homo sapien

## ALIGNMENTS

RESULT 1  
RTN4 RAT  
ID RTN4 RAT STANDARD; PRT; 1163 AA.  
AC Q9UK11; Q9JK10; Q9ROD9; Q9WUE9; Q9WUF0;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foccen)  
DE (Glut4 vesicle 20 kDa protein).  
GN Name=Rtn4; Synonyms=Nogo;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.  
RC STRAIN=Sprague-Dawley; TISSUE=Adipocyte;  
RX MEDLINE=99249816; PubMed=10231557; DOI=10.1016/S0167-4889(99)00033-6;  
RA Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lienhard G.E.;  
RT "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an  
RT antigen for monoclonal antibody IN-1.";  
RT a new member of the reticulon family.";  
RL Blochim. Biophys. Acta 1450:68-76(1999).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RX MEDLINE=20129258; PubMed=10667796; DOI=10.1038/35000219;  
RA Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,  
RA Spillmann A.A., Christ F., Schwab M.E.;  
RT "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an  
RL Nature 403:434-439(2000).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).  
RC STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;  
RA Ito T., Schwartz S.M.;  
RT "Cloning of a member of the reticulon gene family in rat: one of two  
RT minor splice variants.";  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP FUNCTION.  
RX MEDLINE=22033691; PubMed=12037567; DOI=10.1038/417547a;  
RA GrandPre T., Li S., Strittmatter S.M.;  
RT "Nogo-66 receptor antagonist peptide promotes axonal regeneration.";  
RL Nature 417:547-551(2002).  
CC -/- FUNCTION: Potent neurite outgrowth inhibitor which may also help  
CC block the regeneration of the nervous central system in adults (By  
CC similarity).  
CC -/- SUBUNIT: Binds to RTN4R. Interacts with Bcl-x1 and Bcl-2 (By  
CC similarity).  
CC -/- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the  
CC membrane of the endoplasmic reticulum through 2 putative  
CC transmembrane domains (By similarity).  
CC -/- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=4;  
CC Name=1; Synonyms=Nogo-A, NI-220-250;

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CC      Isoid=Q9JK11-1; Sequence=Displayed;
CC      Name=2; Synonyms=Nogo-B, Foccn-M1;
CC      Isoid=Q9JK11-2; Sequences=VSP_005659;
CC      Name=3; Synonyms=Nogo-C, VP20;
CC      Isoid=Q9JK11-3; Sequences=VSP_005656, VSP_005657;
CC      Name=4; Synonyms=Foccn-M2;
CC      Isoid=Q9JK11-4; Sequence=VSP_005659;
CC      -!- TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in optic
CC      nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are
CC      present in dorsal root ganglion, sciatic nerve and PC12 cells
CC      after longer exposure. Isoforms 2 and 3 are detected in kidney,
CC      cartilage, skin, lung and spleen. Isoform 3 is expressed at high
CC      level in skeletal muscle. In adult animals isoform 1 is expressed
CC      mainly in the nervous system.
CC      -!- SIMILARITY: Contains 1 reticulin domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; AF051335; AAF01564.1; -
CC      EMBL; AJ242961; CAB71027.1; -
CC      EMBL; AJ242962; CAB71028.1; -
CC      EMBL; AJ242963; CAB71029.1; -
CC      EMBL; AF132045; AAD31019.1; -
CC      EMBL; AF132046; AAD31020.1; -
CC      GO; GO:0030176; C:integral to endoplasmic reticulum membrane; IDA.
CC      GO; GO:0005635; C:nuclear membrane; ISS.
CC      GO; GO:0005515; F:protein binding; ISS.
CC      GO; GO:0019987; P:negative regulation of axon extension; ISS.
CC      GO; GO:0030517; P:negative regulation of anti-apoptosis; ISS.
CC      InterPro; IPR003388; Reticulon.
CC      Pfam; PF02453; Reticulon.
CC      PROSITE; PS50845; Reticulon.
CC      Alternative splicing; Direct protein sequencing;
CC      Endoplasmic reticulum; Transmembrane.
CC      DOMAIN 1 989 Cytoplasmic (Potential).
CC      TRANSMEM 990 1010 Potential.
CC      DOMAIN 1011 1104 Lumenal (Potential).
CC      TRANSMEM 1105 1125 Potential.
CC      DOMAIN 1126 1163 Cytoplasmic (Potential).
CC      DOMAIN 976 1163 Reticulon.
CC      DOMAIN 33 46 Poly-Glu.
CC      DOMAIN 73 76 Poly-Ala.
CC      DOMAIN 140 145 Poly-Pro.
CC      VARSPLIC 1 564 Missing (in isoform 3).
CC      VARSPLIC 965 975 /FTID=VSP_005656.
CC      AVLSAELSKTS -> MDGQKHKWKD (in isoform
CC      3).
CC      /FTID=VSP_005657.
CC      VARSPLIC 173 975 Missing (in isoform 2).
CC      /FTID=VSP_005658.
CC      VARSPLIC 192 975 Missing (in isoform 4).
CC      /FTID=VSP_005659.
CC      CONFLICT 1130 1131 Missing (in Ref. 3; AAD31020).
CC      SEQUENCE 1163 AA; 126386 MW; 8CB94B09E94F0B6 CRC64;
Query Match 100.0%; Score 925; DB 1; Length 1163;
Best Local Similarity 100.0%; Pred. No. 3.le-68;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SVDDLRYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTSFRIYKGVIOA 60
Db 975 SVDDLRYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTSFRIYKGVIOA 1034
Qy 61 IQKSDGHPFRAYLSEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVLSLKFV 120
Db 1035 IQKSDGHPFRAYLSEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVLSLKFV 1094
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Qy 121 LMWFTYVYGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 180
Db 1095 LMWFTYVYGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 1154
Qy 181 IPGLKRRKAD 189
Db 1155 IPGLKRRKAD 1163
RESULT 2
Q80W95 PRELIMINARY; PRT; 578 AA.
AC Q80W95;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nogo-A (Fragment).
GN Name=Nogo-A;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tozaki H., Hirata T.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073672; BAC75974.1; -
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon.
DR PROSITE; PS50845; RETICULON.
FT NON TER 1
SQ SEQUENCE 578 AA; 63696 MW; 832670C171E4AC61 CRC64;
Query Match 99.1%; Score 917; DB 2; Length 578;
Best Local Similarity 98.9%; Pred. No. 7e-68;
Matches 187; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 SVDDLRYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTSFRIYKGVIOA 60
Db 390 SVDDLRYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTSFRIYKGVIOA 449
Qy 61 IQKSDGHPFRAYLSEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVLSLKFV 120
Db 450 IQKSDGHPFRAYLSEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVLSLKFV 509
Qy 121 LMWFTYVYGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 180
Db 510 LMWFTYVYGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 569
Qy 181 IPGLKRRKAD 189
Db 570 IPGLKRRKAE 578
RESULT 3
Q8K290 PRELIMINARY; PRT; 639 AA.
AC Q8K290;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Rtn4 protein.
GN Name=Rtn4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci F., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
 RA Strausberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC032192; AAH32192.1; -;  
 DR MGD; MGI:1915835; Rtn4.  
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 SQ SEQUENCE 639 AA; 70312 MW; 309A19DA37603F11 CRC64;

Query Match 99.1%; Score 917; DB 2; Length 639;  
 Best Local Similarity 98.9%; Pred. No. 7.8e-68;  
 Matches 187; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASFLLLSLTVPFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
 Db 451 SVVDLLYWRDIKKTGVVFGASFLLLSLTVPFSIVSVTAYIALALLSVTISFRIYKGVIOA 510

Qy 61 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVLSLKFV 120  
 Db 511 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVLSLKFV 570

Qy 121 LMWVTVVGVLFNGLTLLILALISLFSIPVYERHQVQIDHYLGLANKSVKDAWAKIOAK 180  
 Db 571 LMWVTVVGVLFNGLTLLILALISLFSIPVYERHQVQIDHYLGLANKSVKDAWAKIOAK 630

Qy 181 IPGLKRRKAD 189  
 Db 631 IPGLKRRKAE 639

RESULT 4  
 Q8BGK7 PRELIMINARY; PRT; 1046 AA.  
 AC Q8BGK7  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE RTN4.  
 GN Name=Rtn4;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=129/SvcJ7, and 129SvcJ7;  
 RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;  
 RA Oertle T., Huber C., van der Putten H., Schwab M.E.;  
 RT "Genomic structure and functional characterisation of the promoters of  
 human and mouse nogo/rtn4.";

RL J. Mol. Biol. 325:299-323 (2003).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=129/SvcJ7;  
 RA Van der Putten H.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=129SvcJ7;  
 RA Van der Putten H., Mir A.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY102280; AA073502.1; -;  
 DR MGD; AY102286; AA073507.1; -;  
 DR MGI:1915835; Rtn4.  
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.  
 DR GO; GO:0005515; F:protein binding; IPI.  
 DR GO; GO:0001525; P:angiogenesis; IMP.  
 DR GO; GO:0007399; P:neurogenesis; IDA.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 SQ SEQUENCE 1046 AA; 114221 MW; 8CE2E2238ED51222 CRC64;

Query Match 99.1%; Score 917; DB 2; Length 1046;  
 Best Local Similarity 98.9%; Pred. No. 1.3e-67;  
 Matches 187; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASFLLLSLTVPFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
 Db 858 SVVDLLYWRDIKKTGVVFGASFLLLSLTVPFSIVSVTAYIALALLSVTISFRIYKGVIOA 917

Qy 61 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVLSLKFV 120  
 Db 918 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVLSLKFV 977

Qy 121 LMWVTVVGVLFNGLTLLILALISLFSIPVYERHQVQIDHYLGLANKSVKDAWAKIOAK 180  
 Db 978 LMWVTVVGVLFNGLTLLILALISLFSIPVYERHQVQIDHYLGLANKSVKDAWAKIOAK 1037

Qy 181 IPGLKRRKAD 189  
 Db 1038 IPGLKRRKAE 1046

RESULT 5  
 Q8BGK9 PRELIMINARY; PRT; 1162 AA.  
 AC Q8BGK9  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE RTN4.  
 GN Name=Rtn4;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=129/SvcJ7, and 129SvcJ7;  
 RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;  
 RA Oertle T., Huber C., van der Putten H., Schwab M.E.;  
 RT "Genomic structure and functional characterisation of the promoters of  
 human and mouse nogo/rtn4.";

RA Van der Putten H., Mir A.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; AY102284; AAM73506.1; --  
DR EMBL; AY102286; AAM73511.1; --  
DR MGD; MGI:1915835; Rtn4.  
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0001525; P:angiogenesis; IMP.  
DR GO; GO:0007399; P:neurogenesis; IDA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS0845; Reticulon; 1.  
SQ SEQUENCE 1162 AA; 126612 MW; 855697FPBEE11781F CRC64;  
  
Query Match 99.1%; Score 917; DB 2; Length 1162;  
Best Local Similarity 98.9%; Pred. No. 1.4e-67;  
Matches 187; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 60  
DB 974 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 1033  
  
QY 61 IQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNSTIKELRRLFLVDLVDLSLKFAV 120  
DB 1034 IQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNSTIKELRRLFLVDLVDLSLKFAV 1093  
  
QY 121 LMWFTYVYVGALENGTLILALISLFSIPVIYERHQQVQIDHYLGLANKSVKDMAKIQAK 180  
DB 1094 LMWFTYVYVGALENGTLILALISLFSIPVIYERHQQVQIDHYLGLANKSVKDMAKIQAK 1153  
  
QY 181 IPGLKRRKAD 189  
DB 1154 IPGLKRRKAE 1162  
  
RESULT 6  
Q8BHF5 PRELIMINARY; PRT; 375 AA.  
AC Q8BHF5;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE RTN4.  
GN Name=Rtn4;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7, and 129SvcJ7;  
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;  
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;  
RT "Genomic structure and functional characterisation of the promoters of  
human and mouse nogo/rtn4";  
RL J. Mol. Biol. 325:299-323 (2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7;  
RX STRAIN=129/SvcJ7;  
RA Van der Putten H.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBSJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129SVCJ7;  
RX STRAIN=129SVCJ7;  
RA Van der Putten H., Mir A.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; AY102282; AAM73504.1; --  
DR EMBL; AY102286; AAM73509.1; --  
DR MGD; MGI:1915835; Rtn4.  
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0001525; P:angiogenesis; IMP.  
DR GO; GO:0007399; P:neurogenesis; IDA.

DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS0845; Reticulon; 1.  
SQ SEQUENCE 375 AA; 40300 MW; 23D9EB19BE671AE6 CRC64;  
  
Query Match 98.8%; Score 914; DB 2; Length 375;  
Best Local Similarity 98.4%; Pred. No. 8e-68;  
Matches 186; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 60  
DB 187 AVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 246  
  
QY 61 IQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNSTIKELRRLFLVDLVDLSLKFAV 120  
DB 247 IQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNSTIKELRRLFLVDLVDLSLKFAV 306  
  
QY 121 LMWFTYVYVGALENGTLILALISLFSIPVIYERHQQVQIDHYLGLANKSVKDMAKIQAK 180  
DB 307 LMWFTYVYVGALENGTLILALISLFSIPVIYERHQQVQIDHYLGLANKSVKDMAKIQAK 366  
  
QY 181 IPGLKRRKAD 189  
DB 367 IPGLKRRKAE 375  
  
RESULT 7  
RTN4 MOUSE  
ID RTN4 MOUSE STANDARD; PRT; 199 AA.  
AC Q99P72; OSCTE3;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein).  
GN Name=Rtn4; Synonyms=Nogo;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=3T3-L1; TISSUE=Adipocyte;  
RA Coulson A.C., Craggs P.D., Morris N.J.;  
RT "Mouse vp20/RTN4C cDNA";  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBSJ databases.  
RN [2]  
RP SEQUENCE OF 170-199 FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Embryo;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaide I., Oeato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Bruscia V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perce G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Sempole C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yangisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.,  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs."  
RL Nature 420:563-573 (2002).  
CC -1- FUNCTION: Potent neurite outgrowth inhibitor which may also help  
CC block the regeneration of the nervous central system in adults (By  
CC similarity).  
CC -1- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By  
CC similarity).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the  
CC membrane of the endoplasmic reticulum through 2 putative  
CC transmembrane domains (By similarity).  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=1;  
CC Comment=A number of isoforms may be produced;  
CC Name=s1;  
CC IsoId=Q99P72-1; Sequence=Displayed;  
CC -1- SIMILARITY: Contains 1 reticulon domain.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC -----  
DR EMBL; AFJ26337; AAK08076.1; -;  
DR EMBL; AK003859; -; NOT ANNOTATED\_CDS.  
DR MGD; MGI:1915835; Rtn4.  
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; ISS.  
DR GO; GO:0005635; F:nuclear membrane; ISS.  
DR GO; GO:0005515; F:protein binding; ISS.  
DR GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.  
DR GO; GO:0030517; P:negative regulation of axon extension; ISS.  
DR GO; GO:0007399; P:neurogenesis; IDA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
DR KW Alternative splicing; Endoplasmic reticulum; Transmembrane.  
FT DOMAIN 1 25 Cytoplasmic (Potential).  
FT TRANSMEM 26 50 Potential.  
FT DOMAIN 51 137 Luminal (Potential).  
FT TRANSMEM 138 162 Potential.  
FT DOMAIN 163 199 Cytoplasmic (Potential).  
FT DOMAIN 12 199 Reticulon.  
SQ SEQUENCE 199 AA; 22466 MW; 07BESD58059ED9C CRC64;  
  
Query Match 98.78; Score 913; DB 1; Length 199;  
Best Local Similarity 98.94; Pred. No. 5.1e-68;  
Matches 186; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 VDVLVYRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIOAI 61  
DB 12 VDVLVYRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIOAI 71  
  
QY 62 QKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDLVDSLKPAVL 121  
DB 72 QKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDLVDSLKPAVL 131  
  
QY 122 MVVFTYVGVLFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI 181  
DB 132 MVVFTYVGVLFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI 191  
  
QY 182 PGLKRAKAD 189  
DB 192 PGLKRAE 199  
  
RESULT 8  
Q8BH78

ID Q8BH78 PRELIMINARY; PRT; 356 AA.  
AC Q8BH78;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE RTN4.  
GN Names=Rtn4;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7, and 129SVCJ7;  
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;  
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;  
RT "Genomic structure and functional characterisation of the promoters of  
RT human and mouse nogo/rtn4.";  
RL J. Mol. Biol. 325:299-323(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7;  
RA Van der Putten H.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129SVCJ7;  
RA Van der Putten H., Mir A.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY102281; AAM73503.1; -;  
DR EMBL; AY102286; AAM73508.1; -;  
DR MGD; MGI:1915835; Rtn4.  
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0005152; P:angiogenesis; IMP.  
DR GO; GO:0007399; P:neurogenesis; IDA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
SQ SEQUENCE 356 AA; 38403 MW; 4366C03BA9630B56 CRC64;  
  
Query Match 98.78; Score 913; DB 2; Length 356;  
Best Local Similarity 98.94; Pred. No. 9.2e-68;  
Matches 186; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 VDVLVYRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIOAI 61  
DB 169 VDVLVYRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIOAI 228  
  
QY 62 QKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDLVDSLKPAVL 121  
DB 229 QKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDLVDSLKPAVL 288  
  
QY 122 MVVFTYVGVLFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI 181  
DB 289 MVVFTYVGVLFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOAKI 348  
  
QY 182 PGLKRAKAD 189  
DB 349 PGLKRAE 356  
  
RESULT 9  
Q8IU04  
ID Q8IU04 PRELIMINARY; PRT; 986 AA.  
AC Q8IU04;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE RTN4 (RTN4 isoform AB) (RTN4 isoform D) (RTN4 isoform E) (RTN4 isoform  
DE F) (RTN4 isoform G) (RTN4 isoform Aa).  
GN Names=Rtn4;  
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT "Genomic structure and functional characterisation of the promoters of
RT human and mouse nogo/rtn4";
RL J. Mol. Biol. 325:299-323(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Oertle T., Schwab M.E.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102285; AAM64244.1; -
DR EMBL; AY123246; AAM64250.1; -
DR EMBL; AY123247; AAM64251.1; -
DR EMBL; AY123248; AAM64252.1; -
DR EMBL; AY123249; AAM64253.1; -
DR EMBL; AY123250; AAM64254.1; -
DR EMBL; AY123245; AAM64249.1; -
DR GO; GO:0005783; C:Endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS0845; RETICULON; 1.
DR SEQUENCE 986 AA; 108449 MW; 0CDE8F647036415A CRC64;

Query Match          98.2%; Score 908; DB 2; Length 986;
Best Local Similarity 97.4%; Pred. No. 6.8e-67;
Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVVDLLYWRDIKKTGVFGASLFLLLSLTVSVTVAYIALALLSVTFRYKGVIOA 60
DB 798 SVVDLLYWRDIKKTGVFGASLFLLLSLTVSVTVAYIALALLSVTFRYKGVIOA 857

QY 61 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRFLVLDVLSKPAV 120
DB 858 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVLDVLSKPAV 917

QY 121 LMWFTYVYGFALFNGLTLLILALISLFSVPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 180
DB 918 LMWFTYVYGFALFNGLTLLILALISLFSVPVIYERHQVQIDHYLGLANKSVKDMAKIOAK 977

QY 181 IPGLKRRKAD 189
DB 978 IPGLKRRKAE 986

RESULT 10
RTN4 HUMAN
ID RTN4 HUMAN STANDARD; PRT; 1192 AA.
AC Q9NQC3; Q9A962; Q9BXG5; Q9H212; Q9H3I3; Q9UQ42; Q9Y293; Q9Y2Y7;
AT Q9Y5U6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Focosen)
DE (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific
DE protein C homolog) (RTN-x) (Reticulon 5) (My043 protein).
GN Name=RTN4; Synonyms=ASY, KIAA0886, NOGO;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
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RX MEDLINE=20129242; PubMed=10667780; DOI=10.1038/35000287;
RA Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G.,
RA Michalovich D., Simmons D.L., Walsh F.S.;
RT "Inhibitor of neurite outgrowth in humans.";
RL Nature 403:383-384(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Brain;
RX MEDLINE=21010696; PubMed=11126360; DOI=10.1038/sj.onc.1203948;
RA Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;
RT "A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on
RT endoplasmic reticulum and reduces their anti-apoptotic activity.";
RL Oncogene 19:5736-5746(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=20237542; PubMed=10773680;
RA Yang J., Yu L., Bi A.D., Zhao S.-Y.;
RT "Assignment of the human reticulon 4 gene (RTN4) to chromosome
RT 2p14-->2p13 by radiation hybrid mapping.";
RL Cytogenet. Cell Genet. 88:101-102(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 4).
RA Jin W.-L., Ju G.;
RT "Developmentally-regulated alternative splicing in a novel Nogo-A.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
RC TISSUE=Placenta, and Skeletal muscle;
RA Ito T., Schwartz S.M.;
RT "Cloning of a member of the reticulon gene family in human.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Fibroblast;
RA Yutsudo M.;
RT "Isolation of a cell death-inducing gene.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Pituitary;
RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,
RA Luo B., Hu R., Chen J.;
RT "Human neuroendocrine-specific protein C (NSP) homolog gene.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
RA Yu J., Han L.H.;
RT "Novel human cDNA clones with function of inhibiting cancer cell
RT growth.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=99156230; PubMed=10048485;
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosewa M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 5:355-364(1998).
RN [10]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
RC TISSUE=Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,  
 RA Pheby J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [11]  
 RN SEQUENCE FROM N.A. (ISOFORM 3).  
 RC TISSUE=Umbilical cord blood;  
 RX MEDLINE=20499367; Pubmed=11042152; DOI=10.1101/gr.140200;  
 RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,  
 RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,  
 RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;  
 RT "Cloning and functional analysis of cDNAs with open reading frames for  
 RT 300 previously undefined genes expressed in CD34+ hematopoietic  
 RT stem/progenitor cells.";  
 RL Genome Res. 10:1546-1560(2000).  
 RN [12]  
 RN SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).  
 RC TISSUE=Brain;  
 RX TISSUE=Brain;  
 RA Mao Y.M., Xie Y., Zheng Z.H.;  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 RN [13]  
 RN SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1).  
 RC TISSUE=Testis;  
 RA Sha J.H., Zhou Z.M., Li J.M.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 RN [14]  
 RN TOPOLOGY.  
 RC TISSUE=Brain;  
 RX MEDLINE=20129259; Pubmed=10667797; DOI=10.1038/35000226;  
 RA Grandpre T., Nakamura F., Vartanian T., Strittmatter S.M.;  
 RT "Identification of the Nogo inhibitor of axon regeneration as a  
 RT Reticulon protein.";  
 RL Nature 403:439-444(2000).  
 RN [15]  
 RN FUNCTION.  
 RC TISSUE=Brain;  
 RX MEDLINE=21089055; Pubmed=11201742; DOI=10.1038/35053072;  
 RA Fournier A.E., Grandpre T., Strittmatter S.M.;  
 RT "Identification of a receptor mediating Nogo-66 inhibition of axonal  
 RT regeneration.";  
 RL Nature 409:341-346(2001).  
 RN [16]  
 RN REVIEW.  
 RX MEDLINE=21888956; Pubmed=11891768; DOI=10.1002/jnr.10134;  
 RA Ng C.B.L., Tang B.L.;  
 RT "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron  
 RT regeneration.";  
 RL J. Neurosci. Res. 67:559-565(2002).  
 CC -1- FUNCTION: Potent neurite outgrowth inhibitor which may also help  
 CC block the regeneration of the nervous central system in adults.  
 CC Isoform 2 reduces the anti-apoptotic activity of Bcl-x1 and Bcl-2.  
 CC This is likely consecutive to their change in subcellular  
 CC location, from the mitochondria to the endoplasmic reticulum,  
 CC after binding and sequestration.  
 CC -1- SUBUNIT: Binds to RTNAR. Interacts with Bcl-x1 and Bcl-2.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic  
 CC reticulum. Anchored to the membrane of the endoplasmic reticulum  
 CC through 2 putative transmembrane domains.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=1; Synonyms=RTN 4A, Nogo-A, RTN-XL;  
 CC IsoId=Q9NQC3-1; Sequence=Displayed;  
 CC Name=2; Synonyms=RTN 4B, Nogo-B, RTN-XS, Foccen-M;  
 CC IsoId=Q9NQC3-2; Sequence=VSP\_005655;

CC Name=3; Synonyms=RTN 4C, Nogo-C, Foccen-S;  
 CC IsoId=Q9NQC3-3; Sequence=VSP\_005652, VSP\_005653;  
 CC Name=4;  
 CC IsoId=Q9NQC3-4; Sequence=VSP\_005654;  
 CC -1- TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain  
 CC and testis and weakly in heart and skeletal muscle. Isoform 2 is  
 CC widely expressed excepted for the liver. Isoform 3 is expressed in  
 CC brain, skeletal muscle and adipocytes. Isoform 4 is testis-  
 CC specific.  
 CC -1- SIMILARITY: Contains 1 reticulon domain.  
 CC -1- CAUTION: Ref.11 sequence differs from that shown due to  
 CC frameshifts in positions 1149 and 1156.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk).  
 CC -----  
 CC EMBL; AJ251383; CAB99248.1; -  
 CC EMBL; AJ251384; CAB99249.1; -  
 CC EMBL; AJ251385; CAB99250.1; -  
 CC EMBL; AB040462; BAB18927.1; -  
 CC EMBL; AB040463; BAB18928.1; -  
 CC EMBL; AF148517; AAG12176.1; -  
 CC EMBL; AF148538; AAG12177.1; -  
 CC EMBL; AF087901; AAG12205.1; -  
 CC EMBL; AF320999; AAG40878.1; -  
 CC EMBL; AF132047; AAD31021.1; -  
 CC EMBL; AF132048; AAD31022.1; -  
 CC EMBL; AB015639; BAA83712.1; -  
 CC EMBL; AF077050; AAD27783.1; -  
 CC EMBL; AF177332; AAG17976.1; -  
 CC EMBL; AB020693; BAA74909.2; ALT\_INIT.  
 CC EMBL; BC001035; AAH01035.1; -  
 CC EMBL; BC007109; AAH07109.1; -  
 CC -----  
 CC Query Match 98.2%; Score 908; DB 1; Length 1192;  
 CC Best Local Similarity 97.4%; Pred. No. 8.3e-67;  
 CC Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 CC -----  
 CC QY 1 SVVDLLYWRDKTKTGVVFGASLFLSLTVFSVSVTAYIALALLSVTIFRIYKGVIOA 60  
 CC DB 1004 SVVDLLYWRDKTKTGVVFGASLFLSLTVFSVSVTAYIALALLSVTIFRIYKGVIOA 1063  
 CC QY 61 IQKSDGHPFRAYLESEVAISELQKYSNLSALGHVNSTIKELRLPLVDLVDLSLKFV 120  
 CC DB 1064 IQKSDGHPFRAYLESEVAISELQKYSNLSALGHVNSTIKELRLPLVDLVDLSLKFV 1123  
 CC QY 121 LMMVFTVVGALFNLTLILALISLPSIPVYERHQVIDHYLGLANKSVKDAWAKIOAK 180  
 CC DB 1124 LMMVFTVVGALFNLTLILALISLPSIPVYERHQVIDHYLGLANKSVKDAWAKIOAK 1183  
 CC QY 181 IPLGLKRAKAD 189  
 CC DB 1184 IPLGLKRAKAE 1192  
 CC -----  
 CC RESULT 11  
 CC Q8K3G8 PRELIMINARY; PRT; 1163 AA.  
 CC AC Q8K3G8 (T-EMBLrel. 22, Created)  
 CC DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)  
 CC DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)  
 CC DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
 CC DE Nogo-A.  
 CC GN Name=RTn4;  
 CC OS Mus musculus (Mouse).  
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC OX NCBI\_TaxID=10090;

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RN RP SEQUENCE FROM N.A.
RC STRAIN=BALE/c;
RA Jin W., Long M., Li R., Ju G.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY114152; AAM77068.1; -.
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 1163 AA; 126690 MW; 6B5F362799417EA4 CRC64;

Query Match 98.0%; Score 906.5; DB 2; Length 1163;
Best Local Similarity 98.4%; Pred. No. 1.1e-66;
Matches 187; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 SVVDLLYWRDIKKTGVVFGASLFLLSITVFSIVSVTAYIALALLSVTISFRIYKGVQ 59
Db 974 SVVDLLYWRDIKKTGVVFGASLFLLSITVFSIVSVTAYIALALLSVTISFRIYKGVQ 1033
QY 60 AIQSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDLVDLSKFA 119
Db 1034 AIQSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDLVDLSKFA 1093
QY 120 VLMVFTYVVGALFNGLTLLILALISLFSIPVIYERHQQIDHYLGLANKSVKDAKIQ 179
Db 1094 VLMVFTYVVGALFNGLTLLILALISLFSIPVIYERHQQIDHYLGLANKSVKDAKIQ 1153
QY 180 KIPGLKRRKAD 189
Db 1154 KIPGLKRRKAE 1163

RESULT 12
ID Q96B16 PRELIMINARY; PRT; 392 AA.
AC Q96B16;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Reticulon 4, isoform D (RTN4 isoform B2).
GN Name=RTN4;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.

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RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT "Genomic structure and functional characterisation of the promoters of
human and mouse nogo/rtn4.";
RL J. Mol. Biol. 325:299-323(2003).
RN [4]
RP SEQUENCE FROM N.A.
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016165; AAH16165.1; -.
DR EMBL; AY102278; AAM64247.1; -.
DR EMBL; AY102285; AAM64242.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 392 AA; 42274 MW; D7B2AA5E839E58AD CRC64;

Query Match 97.8%; Score 905; DB 2; Length 392;
Best Local Similarity 96.8%; Pred. No. 4.7e-67;
Matches 183; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVVDLLYWRDIKKTGVVFGASLFLLSITVFSIVSVTAYIALALLSVTISFRIYKGVQ 60
Db 204 AVDLLYWRDIKKTGVVFGASLFLLSITVFSIVSVTAYIALALLSVTISFRIYKGVQ 263
QY 61 IQSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDLVDLSKPAV 120
Db 264 IQSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDLVDLSKPAV 323
QY 121 LMVFTYVVGALFNGLTLLILALISLFSIPVIYERHQQIDHYLGLANKSVKDAKIQ 180
Db 324 LMVFTYVVGALFNGLTLLILALISLFSIPVIYERHQQIDHYLGLANKSVKDAKIQ 383
QY 181 IPGLKRRKAD 189
Db 384 IPGLKRRKAE 392

RESULT 13
ID Q7YRW9 PRELIMINARY; PRT; 199 AA.
AC Q7YRW9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DB RTN4-C.
GN Name=RTN4;
OS Bos taurus (Bovine);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22715887; PubMed=12832288;
RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT "A reticular rhapsody: phylogenetic evolution and nomenclature of the
RTN/Nogo gene family.";
RL FASEB J. 17:1238-1247(2003).
DR EMBL; AY164744; AAP47319.2; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 199 AA; 22395 MW; C60161DF3FB34D80 CRC64;

Query Match 97.7%; Score 904; DB 2; Length 199;

```

Best Local Similarity 97.3%; Pred. No. 2.8e-67;  
Matches 183; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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QY 2 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61
Db 12 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 71
QY 62 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
Db 72 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 131
QY 122 MWVFTYVGVLFNGTLTLLILALISLFSIPVYERHVOQIDHYLGLANKSVKDMAKIOAKI 181
Db 132 MWVFTYVGVLFNGTLTLLILALISLFSIPVYERHVOQIDHYLGLANKSVKDMAKIOAKI 191
QY 182 PGLKRRKAD 189
Db 192 PGLKRRKAE 199

RESULT 14
Q6IPNO PRELIMINARY; PRT; 343 AA.
AC Q6IPNO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE RIN4 protein.
GN Name=RIN4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heih F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC071848; AAH71848.1; -.
DR GO: GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro: IPR003388; Reticulon.
DR Pfam: PF02453; Reticulon; 1.
DR PROSITE: PS50845; RETICULON; 1.
SQ SEQUENCE 343 AA; 36918 MW; 813207C29AB15BA4 CRC64;

Query Match 97.7%; Score 904; DB 2; Length 343;
Best Local Similarity 97.3%; Pred. No. 5e-67;
Matches 183; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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QY 2 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61
Db 156 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 215
QY 62 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
Db 216 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 275
QY 122 MWVFTYVGVLFNGTLTLLILALISLFSIPVYERHVOQIDHYLGLANKSVKDMAKIOAKI 181
Db 276 MWVFTYVGVLFNGTLTLLILALISLFSIPVYERHVOQIDHYLGLANKSVKDMAKIOAKI 335
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Db 336 PGLKRRKAE 343

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AC Q8K3G7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nogo-B.
GN Name=Rtn4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Jin W., Li R., Long M., Shen J., Ju G.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY114153; AAM77069.1; -.
DR MGD; MGI:1915835; Rtn4.
DR GO: GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro: IPR003388; Reticulon.
DR Pfam: PF02453; Reticulon; 1.
DR PROSITE: PS50845; RETICULON; 1.
SQ SEQUENCE 357 AA; 38566 MW; 73BB3D17DFDBDF15 CRC64;

Query Match 97.6%; Score 902.5; DB 2; Length 357;
Best Local Similarity 98.4%; Pred. No. 6.9e-67;
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Search completed: June 16, 2005, 13:17:34
Job time : 26.6406 secs

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GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 19, 2005, 05:38:22 ; Search time 2737.5 Seconds  
(without alignments)  
3345.401 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163

Perfect score: 925

Sequence: 1 SVVDLLYWRDKTKGWFGA.....VKDAMAKIQAKIPGLKRRAD 189

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

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2: gb\_hgt.\*

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4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

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12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	925	100.0	3489	6	AX766046 Sequence
2	925	100.0	3492	6	CQ829507 Sequence
3	925	100.0	4684	10	AJ242961 Rattus no
4	922	99.7	2782	6	AX700396 Sequence

5	922	99.7	2782	10	AY164741	AY164741 Rattus no
6	922	99.7	2782	10	AF132045	AF132045 Rattus no
7	921	99.6	764	10	AF051335	AF051335 Rattus no
8	921	99.6	1568	10	RNO242963	AJ242963 Rattus no
9	921	99.6	2156	10	AY164740	AY164740 Rattus no
10	921	99.6	2156	10	RNO242962	AJ242962 Rattus no
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12	917	99.1	1738	10	AB073672	AB073672 Mus muscu
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35	908	98.2	4109	9	AY123248	AY123248 Homo sapi
36	908	98.2	4123	9	AY123247	AY123247 Homo sapi
37	908	98.2	4160	9	AY123246	AY123246 Homo sapi
38	908	98.2	4166	9	AB040462	AB040462 Homo sapi
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ALIGNMENTS

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LOCUS	AX766046				
DEFINITION	AX766046				
ACCESSION	AX766046.1	GI:32260128			
VERSION					
KEYWORDS					
SOURCE	Rattus norvegicus (Norway rat)				
ORGANISM	Rattus norvegicus				
REFERENCE	1	Eisenbach-Schwartz,M. and Hauben,E.			
AUTHORS		Nogo and nogo receptor derived peptides for t-cell mediated			
TITLE		neuroprotection			
JOURNAL		Patent: WO 03002602-A 1 09-JAN-2003;			
FEATURES		YEDA RESEARCH AND DEVELOPMENT CO. LTD. (IL)			
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exon					
ORIGIN					
Alignment Scores:		2.82e-85	Length:		3489
Pred. No.:					

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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 2983 AGCTTATTCTCTGCTCTGCTGACAGTGTTCAGCAATGTTCAGTGTAAACGGCTACAT 3042
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
DB 3043 GCCTTGGCCCTGCTCTCGTGACTATCAGCTTTAGGATATATAGGGCGGTGATCCAGGT 3102
QY 61 IleGlnLysSerAspGluGlyHisPropheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 3103 ATCCAGAAATCAGATGAAGCCACCCATTCAGGGCATAATTAGAAATCTCAAGTTGCTATA 3162
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
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QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaVal 120
DB 3223 AAAGAACTAGAGCGGCTTCTTCTAGTTGATGATTTAGTTGATTCCTCGAAGTTGCAGTG 3282
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
DB 3283 TTGATGGGTGTTTACTTATGTTGGTGGCTTGTTCATGGTCTGACACTACTGATTTTA 3342
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QY 181 IleProGlyLeuLysArgLysAlaAsp 189
DB 3463 ATCCCTGGATTGAAGGCCAAAGCAGAT 3489

RESULT 2
CQ829507
LOCUS CQ829507 3492 bp DNA linear PAT 05-JUL-2004
DEFINITION Sequence 25 from Patent WO2004052932.
ACCESSION CQ829507
VERSION CQ829507.1 GI:49732820
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
REFERENCE 1. .3492
AUTHORS Barske,C., Mir,A.K., Oertle,T., Schnell,L., Schwab,M.E., Vitaliti,A. and Zurini,M.
TITLE Nogo a binding molecules and pharmaceutical use thereof
JOURNAL Patent: WO 2004052932-A 25 24-JUN-2004; Novartis AG (CH)
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LABFSELYSEMGSSFKGSPKGSALIVENTKEEVIRSKOKEDILVCSAALHPOESP
VKGDRVVSPEKTMDFINEMQMSVAVPREYADFKPEQAVEWEDTTEGSRDLVAAR
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VIOAQKSGDEGHPFRAYLESAVISELVQYSNLSALGHVNSTIKELRRLFLVDDLV
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ORIGIN
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Score: 925.00 Matches: 189
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x CQ829507 (1-3492)

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QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 2983 AGCTTATTCTCTGCTCTGCTGACAGTGTTCAGCAATGTTCAGTGTAAACGGCTACAT 3042
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
DB 3043 GCCTTGGCCCTGCTCTCGTGACTATCAGCTTTAGGATATATAGGGCGGTGATCCAGGT 3102
QY 61 IleGlnLysSerAspGluGlyHisPropheArgAlaTyrLeuGluSerGluValAlaIle 80
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QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
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QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaVal 120
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QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
DB 3283 TTGATGGGTGTTTACTTATGTTGGTGGCTTGTTCATGGTCTGACACTACTGATTTTA 3342
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
DB 3343 GCTCTGATCTCACTCTTCAGTATTCCTGTTATTATTAAGACGGCATCAGGTGCAGATAGAT 3402
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
DB 3403 CATTATCTAGGACTTGCAACACAGAGTGTTAAGATGCCATGCCAAATCCAGCAAAA 3462
QY 181 IleProGlyLeuLysArgLysAlaAsp 189
DB 3463 ATCCCTGGATTGAAGGCCAAAGCAGAT 3489
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QY	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
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QY	81	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle	100
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QY	121	IleGlnLysSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp	140
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QY	161	HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys	180
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QY	181	IleProGlyLeuLysArgLysAlaAsp	189
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DB	1331	AGCTTATCTCGTCTGCTCTGACAGTTCAGCATTTAGTATTAAGCGCTACAT	1390
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DB	1391	GCCTTGGCCCTGCTCTCGGTAGCATATCAGCTTTAGGATATATAAGGCGTGATCCAGGCT	1450
QY	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleuGluSerGluValAlaIle	80
DB	1451	ATCCAGAAATCAGATGAAGCGCCACCATTCAGGGCATATTTAGAATCTGAAGTTCATATA	1510
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DB	1511	TCAGAGAAATGCTTCAGAAATACAGTAATTCCTCTCTGTCATGTGAACAGCACATA	1570
QY	101	LysGluLeuArgGluPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal	120
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QY	141	AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp	160
DB	1691	GCTCTGATCTCACTCTCTAGTATTTCTGTTATTTATGAACGCATCAGGTGCAGATAGAT	1750
QY	161	HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys	180
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DEFINITION	Rattus norvegicus RTN4-B2 (Rtn4) mRNA, complete cds; alternatively spliced.		
ACCESSION	AV164741		
VERSION	AV164741.1	GI:32331282	
KEYWORDS	Rattus norvegicus (Norway rat)		
SOURCE	Rattus norvegicus		
ORGANISM	Rattus norvegicus		
REFERENCE	1 (bases 1 to 2782)		
AUTHORS	Certle, T., Klinger, M., Stuermer, C.A. and Schwab, M.E.		
TITLE	A reticular rhapsody: phylogenetic evolution and nomenclature of the RTN/Nogo gene family		
JOURNAL	FASEB J. 17 (10), 1238-1247 (2003)		
PUBMED	12832288		
REFERENCE	2 (bases 1 to 2782)		
AUTHORS	Certle, T. and Schwab, M.E.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-OCT-2002) Brain Research Institute and Department Biology, University of Zurich and ETH Zurich, Winterthurerstr.190, Zurich 8057, Switzerland		
FEATURES	Location/Qualifiers		



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Db      1811 ATCCCTGGATTGAAGCGCAAGCAGAT 1837
|||||
RESULT 6
AF132045      2782 bp mRNA linear ROD 18-MAY-1999
LOCUS      Rattus norvegicus foocen-m2 mRNA, alternate splice product,
DEFINITION complete cds.
ACCESSION AF132045
VERSION AF132045.1 GI:4838512
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 2782)
AUTHORS Ito,T. and Schwartz,S.M.
TITLE Cloning of a member of the reticulon gene family in rat: One of two
JOURNAL minor splice variants
AUTHORS Unpublished
REFERENCE 2 (bases 1 to 2782)
AUTHORS Ito,T. and Schwartz,S.M.
JOURNAL Direct Submission
TITLE Submitted (27-FEB-1999) Pathology, University of Washington, 1959
JOURNAL Pacific NE, Seattle, WA 98195, USA
FEATURES
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1. 2782
/organism="Rattus norvegicus"
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/db_xref="taxon:10116"
/sex="male"
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/dev_stage="3 months old"
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product"
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/db_xref="GI:4838513"
/translation="MEDIDQSLVSSSTDSPPRPAPFYQVTEPEDEDEDEDEDE
BEDDLELEVLERKPAAGLSAAAPPAALPLDFSDSDSVPPAPRGLPAPAPAP
EAPQWSPAPAPLPPAAALPKLPEDDEPPARPPPPAGASPLAPAPAPST
PAAPKRGSGVDTLPLPAASEPVISSAVDLLYWRDIKKTGVFGASLFLILSL
TVFSIVSTAYIALALLSVTSFRIYKGVIAIQKSDGHPFRAYLESEVALSELVQ
KYSNALGHVNSTIKELRLFLVDLVDLSKFAVLMWVFTYVGLFNGLTLLILALIS
LFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD"

CDS
|||||
US-09-830-972-2_COPY_975_1163 (1-189) x AF132045 (1-2782)

Alignment Scores:
Pred. No.: 4,318-85 Length: 2782
Score: 922.00 Matches: 188
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.47% Mismatches: 0
Query Match: 99.68% Indels: 0
DB: 10 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x AF132045 (1-2782)

Qy      1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db      1271 GCAGTTGTGTGACTCTCTACTGGAGACATTAGAGACTGGAGTGGTGTGGTCC 1330
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Qy      21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db      1331 AGCTTATTCTCTGCTGCTCTGACAGTGTTCAGCAITGTTCAGTGAACGGCTTACATT 1390
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Qy      41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db      1391 GCCTTTGGCCCTCTCTCGTGACTATACGCTTTAGGATATATAAGGGCGGTATCCAGGCT 1450
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Qy      61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db      1451 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATTTAGATCTGAAGTTGCTATA 1510
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Qy      81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db      1511 TCAGAGGAATTTGGTTTCAGAAATACAGTAATTTCTGCTCTTGGTTCATGTGAACACGCAATA 1570
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Qy      101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db      1571 AAAGAACTGAGCGGCGCTTTCTTAGTGATGATTTAGTTGATTCCTCCTCGAAGTTGCGATG 1630
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Qy      121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db      1631 TTGATGTGGGTGTTTACTTTATGTTGTGCTTGTTCATGTTGCTGACACTACTGATTTTA 1690
|||||
Qy      141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db      1691 GCTCTGATCTCCTCTTCAGTATTTCTCTGTTATTTATGAACGGCATCAGGTGCAGATAGAT 1750
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Qy      161 HistyLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db      1751 CATTATCTAGACTTGCACAAAGAGTGTTAAGGATGCGCATGCCCAAAATCCAGCAAAA 1810
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Qy      181 IleProGlyLeuLysArgLysAlaAsp 189
Db      1811 ATCCCTGGATTGAAGCGCAAGCAGAT 1837
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RESULT 7
AF051335      764 bp mRNA linear ROD 19-JAN-2000
LOCUS      Rattus norvegicus GLUT4 vesicle 20kDa protein mRNA, complete cds.
DEFINITION
ACCESSION AF051335
VERSION AF051335.1 GI:6016998
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 764)
AUTHORS Morris,N.J., Ross,S.A., Neveu,J.M., Lane,W.S. and Lienhard,G.E.
TITLE Cloning and characterization of a 22 kDa protein from rat
JOURNAL adipocytes: a new member of the reticulon family
MEDLINE Biochim. Biophys. Acta 1450 (1), 68-76 (1999)
PUBMED 99249816
REFERENCE 2 (bases 1 to 764)
AUTHORS Morris,N.J.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1998) Biochemistry, Dartmouth Medical School,
Hanover, NH 03755, USA
FEATURES
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/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/tissue_type="adipocyte"
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Accession Number U17605, to rat Rex encoded by GenBank
Accession Number U17603, and to human
neuroendocrine-specific protein C encoded by GenBank
Accession Number L10335"
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IYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD"

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Db      391 GAGGAATGGTTTCAGAAATACAGTAATTCCTGCTTGGTCATGTGACAGCACATAAAAA 450
Qy      102 GluLeuArgLeuPheLeuValAspLeuValAspLeuValAspLeuValPheAlaValLeu 121
Db      451 GAACGTAGCGGCTTTCTTAGTTCATGATTTAGTTGATTCCTCGAAGTTTCAGTGTTG 510
Qy      122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
Db      511 ATGTGGGTGTTTACTATGTTGGTGCCTTGTTCATGTTGACACTACTGATTTAGCT 570
Qy      142 LeuLeuSerLeuPheSerLeuProValLeuTyrGluArgHisGlnValGlnLeuAspHis 161
Db      571 CTGATCTCAGTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCAT 630
Qy      162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysLeuGlnAlaLysIle 181
Db      631 TATCTAGACTTGCACCAAGAGTGTTAAGGATGCGATGCGCCAAATCCAGCAAAAAATC 690
Qy      182 ProGlyLeuLysArgLysAlaAsp 189
Db      691 CCTGGATTGAAGCGCAAGCAGAT 714

RESULT 9
AY164740
LOCUS
DEFINITION
Rattus norvegicus RTN4-B1 (Rtn4) mRNA, complete cds; alternatively
spliced.
ACCESSION
AY164740
VERSION
AY164740.1 GI:32331280
KEYWORDS
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
1 (bases 1 to 2156)
Oertle,T., Klinger,M., Stuermer,C.A. and Schwab,M.E.
A reticular rhapsody: phylogenetic evolution and nomenclature of the
RTN/Nogo gene family
FASEB J. 17 (10), 1238-1247 (2003)
12832288
PUBMED
2 (bases 1 to 2156)
Oertle,T. and Schwab,M.E.
Direct Submission
Submitted (16-OCT-2002) Brain Research Institute and Department
Biology, University of Zurich and ETH Zurich, Winterthurerstr.190,
Zurich 8057, Switzerland
Location/Qualifiers
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/organism="Rattus norvegicus"
/mol_type="mRNA"
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1..2156
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PAAKRRGSGVVDLLYRDIKKTGVVFGASLFLLSLTFTVSIVTAYTALALLSV
TISPRYKGVQAIQKSDGHPFRAYLESEVALISELVQKYSNLSALGHVNSTIKELR
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3' UTR
ORIGIN

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Alignment Scores:
Pred. No.: 3,94e-85 Length: 2156
Score: 921.00 Matches: 188
Percent Similarity: 100.00% Conservations: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.57% Indels: 0
DB: 10 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x AY164740 (1-2156)

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Db      705 GTTGTGTGACCTCCTCTACTCGAGAGACATTAAAGAAGACTCGAGTGGTGTGTTGGTCCGACG 764
Qy      22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db      765 TTATTCCTGCTGCTGCTCTCTGACAGTGTTCAGCATTTGTCAGTGTAAACGGCTTACATGCC 824
Qy      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db      825 TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAGGGCGTGTATCCAGGCTATC 884
Qy      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db      885 CAGAAATCAGATGAAGGCCACCCATTTCAGGCATATTTAGAATCTGAAAGTTGCTATATCA 944
Qy      82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db      945 GAGGAATTTGGTTTCAGAAATACAGTAATTCCTCTTGTGTCATGTGAACAGCACATAAAA 1004
Qy      102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db      1005 GAACGTAGCGGCTTTCTTAGTTGATTTAGTTAGTTAGTTCCCTGNAAGTTTGCAGTGTG 1064
Qy      122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
Db      1065 ATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCATGCTGTCGACACTACTGATTTAGCT 1124
Qy      142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db      1125 CTGATCTCAGCTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGTGCAGATAGATCAT 1184
Qy      162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      1185 TATCTAGACTTGCACCAAGAGTGTTAAGGATGCCATGCCATGCCAAATCCAGCAAAAAATC 1244
Qy      182 ProGlyLeuLysArgLysAlaAsp 189
Db      1245 CCTGGATTGAAGCGCAAGCAGAT 1268

RESULT 10
RNO242962
LOCUS
DEFINITION
Rattus norvegicus mRNA for Nogo-B protein.
ACCESSION
AJ242962
VERSION
AJ242962.1 GI:6822248
KEYWORDS
Nogo-B protein.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
1
Chen,M.S., Huber,A.B., van der Haar,M.E., Frank,M., Schnell,L.,
Spillmann,A.A., Christ,F. and Schwab,M.E.
Nogo-A is a myelin-associated neurite outgrowth inhibitor and an
antigen for monoclonal antibody IN-1
Nature 403 (5768), 434-439 (2000)
20129258
JOURNAL
MEDLINE
PUBMED
10667796
REFERENCE
2 (bases 1 to 2156)
AUTHORS
Van der Haar,M.E.

```

TITLE Direct Submission  
JOURNAL Submitted (14-JUN-1999) Van der Haar M.E., Department of Neuromorphology, Brain Research Institute, University of Zurich, Winterthurerstrasse 190, Zurich, CH-8057, SWITZERLAND  
COMMENT Related sequence: AJ242961.  
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ORIGIN  
Alignment Scores:  
Pred. No.: 3,94e-85 Length: 2156  
Score: 921.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 10 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x RNO242962 (1-2156)

Qy 2 ValValAspLeuLeuThrTrpArgAspIleLeValThrGlyValValPheGlyAlaSer 21  
Db 705 GTTGTGACCTCTCTACTGGAGACATTAAAGACATGGAGTGTGTGGTGGCCAGC 764  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTrilleAla 41  
Db 765 TTATTCCTGCTGCTCTGACAGTGTTCAGCATTTGTCAGTGAACGGCTACATGTC 824  
Qy 42 LeuAlaLeuSerValThrIleSerPheArgIleTrpIleGlyValIleGlnAlaIle 61  
Db 825 TTGGCCCTGCTGCTGGTGATATACAGTCTTAGGATATATAAGGCGGTGATCCAGGCTATC 884  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTrpLeuGluSerGluValAlaIleSer 81  
Db 885 CAGAAATCAGATGAAGCCACCCATTTCAGGCGCATATTTAGAAATCTGAAGTTGCTATCA 944  
Qy 82 GluGluLeuValGlnLysTrpSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
Db 945 GAGGAATTGGTTCAGAAATACAGTAATTCCTGCTCTGTCATGTCAGACACCAATAAAA 1004  
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 1005 GAACCTGAGGCGGCTTTCTTAGTTAGTATGATTTTAGTTAGTTCCCTGAGTTGCGAGTTG 1064  
Qy 122 MetTrpValPheThrTrpValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
Db 1065 ATGTGGGTGTTTACTTANGTTGGTCTGTTCTGTTCAATGCTCTGACACTGATGATTTAGCT 1124  
Qy 142 LeuIleSerLeuPheSerIleProValIleTrpGluArgHisGlnValGlnIleAspHis 161  
Db 1125 CTGATCTCACTCTTCAGTATTCCTGTTATTTATGTAACGGCATCAGGTGCAGATGATCAT 1184

Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 1185 TATCTAGGACTTGCACAAAGAGTGTTAAGGATGCTGCGCCAAATATCCAGCAAAATC 1244  
Qy 182 ProGlyLeuLysArgLysAlaAsp 189  
Db 1245 CTGTGATTGAGCGCAAGCAGAT 1268

RESULT 11  
BC070879 2410 bp mRNA linear ROD 01-JUN-2004  
LOCUS Rattus norvegicus reticulon 4, mRNA (cdna clone IMAGE:7096609), complete cds.  
BC070879  
BC070879.1 GI:47477874  
Rattus norvegicus (Norway rat)  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
1 (bases 1 to 2410)  
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altshul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Small, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 2410)  
Straussberg, R.  
Direct Submission  
Submitted (17-MAY-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)  
Tissue Procurement: Howard Jacobs  
CDNA Library Preparation: Express Genomics  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Sequencing Center (NISC), Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc\\_mgc@nigr.nih.gov](mailto:nisc_mgc@nigr.nih.gov)  
Akhre, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgou, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 175 Row: a Column: 9  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13929187  
This clone has the following problem: The cds is short compared to the longest cds in the locus.

## FEATURES

Location/Qualifiers  
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/db\_xref="taxon:10116"  
/clone="IMAGE:7096609"  
/tissue\_type="lung, rat (Brown Norway)"  
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/note="Vector: pExpress1"

## gene

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PAAKRGSGSVVDLLVWDIKTKTVGVFGASFLLLSLTVFSVTVATALLSV  
TISPIYKGVTOAKQSDGHPFRAYLESEVAISEELVOKYSNALGHVNSTIKELRR  
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## ORIGIN

Alignment Scores:  
Pred. No.: 4,54e-85 Length: 2410  
Score: 921.00 Matches: 188  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 10 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BC070879 (1-2410)

QY 2 ValValAspLeuLeuTyrTriPargAspIleLysThrGlyValValPheGlyAlaSer 21  
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DB 890 GTTGTGACCTCCTCTACTGGAGACATTAAAGAGACTGGAGTGGTGTGGTCCAGC 949  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
|||||  
DB 950 TTATTCTCGTCTCTCTGACAGTGTTCAGCATGTTCAGTGAACGGCTTACATGCC 1009  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
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DB 1010 TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGGCTGATCCAGGCTATC 1069  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
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DB 1070 CAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATTTAGAACTTGAAGTGTCTATATCA 1129  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
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DB 1130 GAGGAATTTGGTTTCAGAAATACAGTAATTTCTGCTCTTGTGTCATGTGAACAGCACATAAAA 1189  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
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## RESULT 12

AB073672 1738 bp mRNA linear ROD 03-JUN-2003  
LOCUS AB073672 Mus musculus mRNA for Nogo-A, partial cds.  
DEFINITION AB073672  
ACCESSION AB073672  
VERSION AB073672.1 GI:30268592

## KEYWORDS

Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 Tozaki, H. and Hirata, T.  
The partial sequence of mouse nogo-A cDNA clone#4109  
AUTHORS  
JOURNAL  
REFERENCE  
2 (bases 1 to 1738)  
Tozaki, H. and Hirata, T.  
AUTHORS  
JOURNAL  
TITLE  
Direct Submission  
Submitted (29-OCT-2001) Hirokazu Tozaki, Division of Brain  
Function, National Institute of Genetice; Yata 1111, Mishima,  
Shizuoka 411-8540, Japan [E-mail:htozaki@lab.nig.ac.jp],  
URL: http://www.nig.ac.jp/home-j.html, Tel: 81-55-981-6721 (ex. 6721),  
Fax: 81-55-981-6722)

## FEATURES

## Location/Qualifiers

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## gene

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## CDS

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## ORIGIN

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Percent Similarity: 99.47% Conservatives: 1  
Best Local Similarity: 98.94% Mismatches: 1  
Query Match: 99.14% Indels: 0  
DB: 10 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AB073672 (1-1738)

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LOCUS Mus musculus reticulon 4, mRNA (cDNA clone MGC:38204
DEFINITION IMAGE:5323152), complete cds.
ACCESSION BC032192
VERSION BC032192.1 GI:21618980
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2958)
AUTHORS Strausberg R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S.,
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Bouffard, G.C., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallos, D.E.,
Scherer, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
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JOURNAL JOURNAL
MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 2958)
AUTHORS Strausberg, R.
DIRECT SUBMISSION Direct Submission
SUBMITTED (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
REMARK COMMENT
Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
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Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
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Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
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## ORIGIN

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Score: 917.00 Matches: 187  
Percent Similarity: 99.47% Conservatives: 1  
Best Local Similarity: 98.94% Mismatches: 0  
Query Match: 99.14% Indels: 1  
DB: 10 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BC032192 (1-2958)

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## RESULT 14

## BC032272

LOCUS BC032272 3815 bp mRNA linear ROD 16-APR-2003  
DEFINITION Mus musculus reticulon 4, mRNA (cdna clone IMAGE:5366860), partial cds.

## ACCESSION BC032272

## VERSION BC032272.1 GI:22749634

## KEYWORDS Mus musculus (house mouse)

## SOURCE Mus musculus

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3815)  
REFERENCE Strausberg,R.B., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REMARK

## COMMENT

Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.F., Rubin,G.M., Hong,L., Statleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Pahey,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.  
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 3815)  
Strausberg,R.  
Direct Submission  
Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)  
Tissue Procurement: The Cepko Laboratory  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc\\_mgc@hgrl.nih.gov](mailto:nisc_mgc@hgrl.nih.gov)  
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Green,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Latic,P., Legaspi,R., Madu,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAC Plate: 65 Row: f Column: 11  
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## ORIGIN

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Score: 917.00 Matches: 187  
Percent Similarity: 99.47% Conservatives: 1  
Best Local Similarity: 98.94% Mismatches: 1  
Query Match: 99.14% Indels: 0  
DB: 10 Gaps: 0

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VERSION AY102280.1 GI:23379808	
KEYWORDS	
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ORGANISM	
REFERENCE 1	
AUTHORS Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.	
TITLE Genomic Structure and Functional Characterisation of the Promoters of Human and Mouse nogo/rtn4	
JOURNAL J. Mol. Biol. 325 (2), 299-323 (2003)	
MEDLINE 22376540	
PUBMED 12488097	
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AUTHORS Oertle,T. and Schwab,M.E.	
TITLE Direct Submission	
JOURNAL Submitted (07-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057, Switzerland	
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AUTHORS Van der Putten,H.	
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Best Local Similarity: 98.94% Mismatches: 1	
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QY	41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
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Qy      141 AlaLeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAse 160
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LOCUS      Mus musculus cDNA clone MGC:73436 IMAGE:6847916, complete cds.
ACCESSION      BC056373
VERSION      BC056373.1 GI:33604147
KEYWORDS      MGC.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 4518)
Klausner,R.D., Collins,F.S., Wagner,L., Sherman,C.M., Schuler,G.D.,
Altechul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heileh,P.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
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Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalusz,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 4518)
Strausberg,R.
Direct Submission
Submitted (11-AUG-2003) National Institutes of Health, Mammalian
Genome Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
Thomas L. Casavant.
Web site: http://genome.uiowa.edu
Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,
Fiehler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,

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Casavant,T., Soares,M.B.
Clone distribution: MGC clone distribution information can be found
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Query Match: 99.14% Indels: 0
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Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
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Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 2266)  
Oertle, T., Huber, C., van der Putten, H. and Schwab, M.E.  
Genomic Structure and Functional Characterisation of the Promoters  
of Human and Mouse nogo/rtn4  
J. Mol. Biol. 325 (2), 299-323 (2003)  
22376540  
12488097

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

2 (bases 1 to 2266)  
Oertle, T. and Schwab, M.E.  
Direct Submission  
Submitted (07-MAY-2002) Brain Research Institute, University of  
Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,  
Switzerland

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

3 (bases 1 to 2266)  
Van der Putten, H.  
Direct Submission  
Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma  
Inc., Basel, Switzerland  
Location/Qualifiers

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DEFINITION Mus musculus vp20/RTN4C protein mRNA, complete cds.

ACCESSION AF326337

VERSION AF326337.1 GI:12802729

KEYWORDS Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 734)

AUTHORS Coulson, A.C., Craggs, P.D. and Morris, N.J.

TITLE Mouse vp20/RTN4C CDNA

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 734)

AUTHORS Morris, N.J.

TITLE Direct Submission

JOURNAL Submitted (05-DEC-2000) School of Biochemistry and Genetics, The

Medical School, Newcastle University, Newcastle upon Tyne, Tyne and

Wear NE2 4HH, UK

FEATURES Location/Qualifiers

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VERSION AY102283.1 GI:23379814
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SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1 (bases 1 to 1769)
AUTHORS Certle,T., Huber,C., van der Putten,H. and Schwab,M.E.
TITLE Genomic Structure and Functional Characterisation of the Promoters
of Human and Mouse nogo/rtn4
JOURNAL J. Mol. Biol. 325 (2), 299-323 (2003)
MEDLINE 22376540
PUBMED 12498097
REFERENCE 2 (bases 1 to 1769)
AUTHORS Certle,T. and Schwab,M.E.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Brain Research Institute, University of
Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
Switzerland
REFERENCE 3 (bases 1 to 1769)
AUTHORS Van der Putten,H.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basel, Switzerland
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Db      793 TATCTAGGACTTGCACAAACAGAGCGTTAAGATGCCATGCCAAATCCAGCAAAATC 852
QY      182 ProGlyLeuLysArgLysAlaAsp 189
Db      640 CCTGGATTGAAGCGCAACAGAGAA 663
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LOCUS   AY102281
DEFINITION Mus musculus RTN4 (Rtn4) mRNA, linear ROD 29-JAN-2003
ACCESSION AY102281
VERSION   AY102281.1 GI:23379810
KEYWORDS Mus musculus (house mouse)
SOURCE   Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 2209)
AUTHORS Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.
TITLE Genomic Structure and Functional Characterisation of the Promoters
of Human and Mouse nogo/rtn4
JOURNAL J. Mol. Biol. 325 (2), 299-323 (2003)
MEDLINE 22376540
PUBMED 12488097
REFERENCE 2 (bases 1 to 2209)
AUTHORS Oertle,T. and Schwab,M.E.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Brain Research Institute, University of
Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
Switzerland
REFERENCE 3 (bases 1 to 2209)
AUTHORS Van der Putten,H.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basel, Switzerland
FEATURES
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Score: 913.00 Matches: 186
Percent Similarity: 99.47% Conservative: 1
Best Local Similarity: 98.94% Mismatches: 1
Query Match: 98.70% Indels: 0
Gaps: 10
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DEFINITION Homo sapiens brain my043 protein mRNA, complete cds.
ACCESSION AF063601
VERSION   AF063601.1 GI:12002033
KEYWORDS Homo sapiens (human)
SOURCE   Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2481)
AUTHORS Mao,Y.M., Xie,Y. and Zheng,Z.H.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-1998) Institute of Genetics, School of Life
Science, Fudan University, 220 Handan Rd., Shanghai 200433,
P.R.China
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Qy 161 HistYrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
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Db 2854 ATCCCTGGATTGAAGCGCAAAAGCTGAA 2880

RESULT 24
LOCUS AF333336 3491 bp mRNA linear PRI 27-MAY-2003
DEFINITION Homo sapiens testis specific reticulon 5 protein mRNA, complete
cds.
ACCESSION AF333336
VERSION AF333336.1 GI:13377627
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 3491)
AUTHORS Zhou, Z.M., Sha, J.H., Li, J.M., Lin, M., Zhu, H., Zhou, Y.D., Wang, L.R.,
Zhu, H., Wang, Y.Q. and Zhou, K.Y.
TITLE Expression of a novel reticulon-like gene in human testis
JOURNAL Reproduction 123 (2), 227-234 (2002)
MEDLINE 21857060
PUBMED 11866689
REFERENCE 2 (bases 1 to 3491)
AUTHORS Sha, J.H., Zhou, Z.M. and Li, J.M.
TITLE Direct Submission
JOURNAL Submitted (04-JAN-2001) Key Lab of Reproductive Medicine, Nanjing
Medical University, Han Zhong Road 140, Nanjing, Jiangsu 210029,
China
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ORIGIN

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Alignment Scores:
Pred. No.: 1.6e-83 Length: 3491
Score: 908.00 Matches: 184
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.35% Mismatches: 2
Query Match: 98.16% Indels: 0
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US-09-830-972-2_COPY_975_1163 (1-189) x AF333336 (1-3491)

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Db 2630 AGCTATTCTCTGCTGCTTTCATTGACAGTATTGACATTTGAGCGTGAACGCCATACATT 2689
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 2690 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAAGCT 2749
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
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Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 2810 TCTGAGGAGTTGGTTTCAGAGTACAGTAAATTTCTGCTCTTGGTCATGTGAAGTGCAGATA 2869
Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
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Qy 161 HistYrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
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Qy 181 IleProGlyLeuLysArgLysAlaAsp 189
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RESULT 25
LOCUS AX766050 3576 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 5 from Patent WO03002602.
ACCESSION AX766050
VERSION AX766050.1 GI:32260129
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Eisenbach-Schwartz, M. and Hauben, E.
TITLE Nogo and nogo receptor derived peptides for t-cell mediated
neuroprotection
JOURNAL Patent: WO 03002602-A 5 09-JAN-2003;
YEDA RESEARCH AND DEVELOPMENT CO. LTD. (IL)
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Query Match: 98.16% Indels: 0  
DB: Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AX766050 (1-3576)

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## RESULT 26

BD249446 3579 bp DNA linear PAT 17-JUL-2003  
LOCUS Protein similar to neuroendocrine-specific protein, and encoding

## DEFINITION

CDNA.

## ACCESSION

BD249446

## VERSION

BD249446.1 GI:33059216

## KEYWORDS

JP 2002522016-A/1.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

## REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## AUTHORS

1 (bases 1 to 3579)

## TITLE

Protein similar to neuroendocrine-specific protein, and encoding

## JOURNAL

Patent: JP 2002522016-A 1 23-JUL-2002;

## COMMENT

SMITHKLINE BEECHAM PLC

OS Homo sapiens (human)

PN JP 2002522016-A/1

PD 23-JUL-2002

PF 21-JUL-1999 JP 2000561310

PR 22-JUL-1998 GB 9816024.5, 19-JUL-1999 GB 9916898.1 PI  
DAVID MICHALOVICH, RABINDER KUMAR PRINJHA  
PC  
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC  
10, C12P21/02, C12Q1/02, C12Q1/68, G01N33/15, G01N33/53, PC  
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PC C12P21/08, C12N15/00, C12N5/00  
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CC Protein similar to neuroendocrine-specific protein, and CC  
encoding cDNA

PH Key Location/Qualifiers  
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FEATURES  
source

Location/Qualifiers  
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Alignment Scores: 1.65e-83 Length: 3579  
Pred. No.: 908.00 Matches: 184  
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Percent Similarity: 98.94% Conservatives: 3  
Best Local Similarity: 97.35% Mismatches: 2  
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US-09-830-972-2\_COPY\_975\_1163 (1-189) x BD249446 (1-3579)

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Db 3070 AGCCTATTCTGCTGCTTTCATTGACAGATTCAGCATTTGTGAGCGTAACAGCTACAT 3129

QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAla 60

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QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleuSerGluValAlaIle 80

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QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100

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Db 3430 GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTAAGACGCATCAGCGGAGATAGAT 3489

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QY 181 IleProGlyLeuLysArgLysAlaAsp 189

Db 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

RESULT 27

HSA251383 3579 bp mRNA linear PRI 22-JUL-2000

LOCUS HSA251383





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DEFINITION Sequence 5 from Patent WO0151520.  
ACCESSION AX195249  
VERSION AX195249.1 GI:15385809  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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Nogo receptor-mediated blockade of axonal growth  
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YALE UNIVERSITY (US)  
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CDS

ORIGIN

Alignment Scores:  
Pred. No.: 1.94e-83 Length: 4053  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
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QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 3204 AGCCTATTCTGCTGCTTTCATGACAGTATTACAGATTTGAGCGTACAGCTACAT 3263  
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AB020693

LOCUS Homo sapiens mRNA for KIAA0886 protein, partial cds. PRI 10-JAN-2004

ACCESSION AB020693

VERSION AB020693.1 GI:4240260

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

AUTHORS Nagase,T., Ishikawa,K., Suyama,M., Kikuno,R., Hirose,M., Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.

TITLE Prediction of the coding sequences of unidentified human genes. XII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro

JOURNAL DNA Res. 5 (6), 355-364 (1998)

MEDLINE 99156230

REFERENCE 10048485

AUTHORS Ohara,O., Suyama,M., Kikuno,R., Nagase,T. and Ishikawa,K.

TITLE Direct Submission

JOURNAL Submitted (02-DEC-1998) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology, Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913, Fax:+81-438-52-3914)

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gene

CDS

## ORIGIN

Alignment Scores:

Pred. No.: 1.94e-83 Length: 4053

Score: 908.00 Matches: 184

Percent Similarity: 98.94% Conservative: 3

Best Local Similarity: 97.35% Mismatches: 2

Query Match: 98.16% Indels: 0

DB: 9 Gaps: 0

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Db 3684 ATCCCTGGATTGAAGCGCAAGCTGAA 3710

RESULT 31

AY123250

LOCUS Homo sapiens RTN4 isoform G (RTN4) mRNA, complete cds; alternatively spliced. PRI 23-SEP-2003

DEFINITION

ACCESSION AY123250

VERSION AY123250.1 GI:26800589

KEYWORDS

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AUTHORS	Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.	Db	2585	AGCCATTCTCTGCTCTTTCATTGACAGTATTTCAGATTGTGAGCGTAAACACCTACATT	2644
TITLE	Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4	QY	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
JOURNAL	J. Mol. Biol. 325 (2), 299-323 (2003)	Db	2645	GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATATCAAGGGTGTGATCCAAGCT	2704
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AUTHORS	Van der Putten,H.	Db	2765	TTGATGGAGTGGTTGTTGAGAAGTACAGTAATCTCTCTTGGTCATGTGAACTGCACGATA	2824
TITLE	Direct Submission	QY	101	LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal	120
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TITLE	Submitted (17-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057, Switzerland	QY	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuLeu	140
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		TITLE	Direct Submission	JOURNAL	Submitted (17-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057, Switzerland
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Query Match: 98.16% Indels: 0
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RESULT 33
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DEFINITION Secreted proteins and polynucleotides encoding them.
ACCESSION BD270070
VERSION BD270070.1 GI:33079838
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4093)
AUTHORS Valenzuela, D., Yuan, O., Hoffman, H., Hall, J., and Rapiejko, P.
TITLE Secreted proteins and polynucleotides encoding them
JOURNAL Patent: JP 2002537757-A 32 12-NOV-2002;
ALPHABET INC
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09-SEP-1998 US 60/109978, 23-DEC-1998 US 60/113645 PR
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ORIGIN
Alignment Scores:
Pred. No.: Length: 4093
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Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.35% Mismatches: 2
Query Match: 98.16% Indels: 0
DB: 9 Gaps: 0

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QY	161	HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys	180
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ORGANISM		Homo sapiens	
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AUTHORS		Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.	
TITLE		Genomic structure and functional characterisation of the promoters of human and mouse rttn4	
JOURNAL		J. Mol. Biol. 325 (2), 299-323 (2003)	
MEDLINE		22376540	
PUBMED		12488097	
REFERENCE		2 (bases 1 to 4102)	
AUTHORS		Van der Putten,H.	
TITLE		Direct Submission	
JOURNAL		Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma Inc., Basel, Switzerland	
REFERENCE		3 (bases 1 to 4102)	
AUTHORS		Oertle,T. and Schwab,M.E.	
TITLE		Direct Submission	
JOURNAL		Submitted (17-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057, Switzerland	
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REFERENCE
AUTHORS Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.
TITLE Genomic structure and functional characterisation of the promoters
of human and mouse nogo/rtn4
J. Mol. Biol. 325 (2), 299-323 (2003)
JOURNAL
MEDLINE 22376540
PUBMED 12488097
REFERENCE
AUTHORS Van der Putten,H.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
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REFERENCE
AUTHORS Oertle,T. and Schwab,M.E.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-2002) Brain Research Institute, University of
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4160)
AUTHORS Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.
TITLE Genomic structure and functional characterisation of the promoters
of human and mouse nogo/rtn4
J. Mol. Biol. 325 (2), 299-323 (2003)
MEDLINE 22376540
PUBMED 12488097
REFERENCE 2 (bases 1 to 4160)
AUTHORS Van der Putten,H.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basel, Switzerland
REFERENCE 3 (bases 1 to 4160)
AUTHORS Oertle,T. and Schwab,M.E.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-2002) Brain Research Institute, University of
Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
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AUTHORS Taira,K. and Kawasaki,H.  
TITLE Regulation of mammalian cells  
JOURNAL Patent: WO 2004076622-A 436 10-SEP-2004;  
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VERSION AY102279.1 GI:26800572  
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SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Oertle,T. and Schwab,M.E.  
TITLE Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4  
JOURNAL J. Mol. Biol. 325 (2), 299-323 (2003)  
MEDLINE 22376540  
PUBMED 12488097

REFERENCE 2 (bases 1 to 4789)  
Oertle,T. and Schwab,M.E.  
Direct Submission  
TITLE Submitted (07-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,  
Switzerland  
REFERENCE 3 (bases 1 to 4789)  
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Direct Submission  
TITLE Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma Inc., Basel, Switzerland  
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/protein\_id="AA064248.1"  
/db\_xref="GI:26800573"  
/translation="MEDLDQSLVSSSDSPRPQAPKYQFVREPEDEEBEERED  
EDLELEVLERKPAAGLAAVPPTAPAAAGPLMDFGNDVFPAPRGPAPAAPVAP  
ERQPSWDPSPVSVTPAPSPLSAAAVSPSKLPEDDEPPARPPPPASVSPQASPVMT

PPAPAPAPPSTPAAPKRRGSSGVDETLFALPAASEPVIRSSAENMDLKEOPGNTIS  
ACQEDFFSVLLTAAASLSLSAASFKEHEYLGNLSTVTEGTQLQENVSEAKV  
SENAKTLLDRLDTSELEYEMSGSFVSFPAESAVIVANPREIIVKNKDEEKL  
VNNILHNOQELPTALTLLKVEDVVSSEKADSFNEKRVAVEAPMBREYADFKPFR  
VNEVDKSDSMLAAGCKIENLESKVDKCFADSLEOTHEKDSGSDNDTSPST  
PGIKDRSGAYITCAPPNAAATESIATNIFPLIGDPTSENKDEKKIENKKAQIVTEK  
NTSTKTSNPLVAQDSEDTYVTDNLTKVTEEVANMPGLTPDLVBQACSELSNEV  
TGTKATYKMDLVOTSEVMQBSLYPAAQPCFSESEATPSVLPDIIVMEAPLNSAV  
PBKASVIVQSSPLEASVNYESI KHEPNPPYEAMSVLSKKVSGIKERIKEPEN  
INAAQDETPAISIACDLIKETLSAEPADPSDYSEMAKVEQVPVPHSELVEDSSP  
DSEPDLRDSDSIPOVPOKODETVMVKESLTSTFSMI EYENKEKLSALPEGGKP  
YLESFKLSLNDTKLLPDEVSTLSKKEKIPLOMBELSAVYNDDLRTSKQAQIRET  
ETFSUSSPIEIDEPPLISSKTDSPKLAERYTDLVSHKSEIANAPDAGSGLPCTE  
LPHDSLKNQKVEKISFSDDFKNGSATS KVLPPDPVSALATQABIESIVKPKV  
LVKAEKPLSPSTEDERSPSAIFSAELSKTSVNDLLYWRDIKKTGVVFGASLIFLLS  
LTVFISVTVATIALALASVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISELV  
OKYSNALSAGVNTICKELRRLFLVDDLVDLSPKFAVLMVFTVVGALENGLTLLILALI  
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3824..4789  
/gene="RTN4"

## 3' UTR

## ORIGIN

Alignment Scores:  
Pred. No.: 2,4e-83 Length: 4789  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AY102279 (1-4789)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
DB 3254 TCAGTTGTTGACCTCTGTACTGGAGACATTAAGACACTGGAGTGGTGTGGTGC 3313  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 3314 AGCCTATTCTGCTGCTTTTCATTGACAGTATTTCAGCATTTGTGAGCGTAAACAGCTACATT 3373  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
DB 3374 GCCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCT 3433  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
DB 3434 ATCCAGAAATCAGATGAAGCCACCATTTCAGGCATATCTGGAATCTGAAGTTGCTATA 3493  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
DB 3494 TCTGAGGAGTTGGTTTCAGAAAGTACAGATAATCTCTGCTTCTGGTCATGTGAACCTGCACGATA 3553  
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
DB 3554 AAGAACTCAGGCGCTCTCTTAGTTGATGATTTAGTTGATCTCTGAGTTGAGTG 3613  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
DB 3614 TTGATGGGTATTTACCTATGTTGGTGGCTTTTAAATGCTGTGACACTACTGATTTTG 3673  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
DB 3674 GCTCTCATTTCACTCTTCAGTGTTCCTGTTTATTTATGAACGGCATCAGGCACAGATAGAT 3733  
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
DB 3734 CATTATCTAGGACTTGCNAATAGATGTTTAAAGATGCTTAAATCCAGGCAAAA 3793  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
DB 3794 ATCCCTGGATTGAAGCGCAAGCTGAA 3820

RESULT 42

## AR220865

LOCUS AR220865 4822 bp DNA linear PAT 26-SEP-2002  
DEFINITION Sequence 106 from patent US 6426186.  
ACCESSION AR220865  
VERSION AR220865.1 GI:23327742  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 4822)  
AUTHORS Jones,K.A., Volkmut,W. and Walker,M.G.  
TITLE Bone remodeling genes  
JOURNAL Patent: US 6426186-A 106 30-JUL-2002;  
FEATURES  
source location/Qualifiers  
1..4822  
/organism="unknown"  
/mol\_type="genomic DNA"

## ORIGIN

Alignment Scores:  
Pred. No.: 2,42e-83 Length: 4822  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AR220865 (1-4822)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
DB 3265 TCAGTTGTTGACCTCTGTACTGGAGACATTAAGACACTGGAGTGGTGTGGTGC 3324  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 3325 AGCCTATTCTGCTGCTTTTCATTGACAGTATTTCAGCATTTGTGAGCGTAAACAGCTACATT 3384  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
DB 3385 GCCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCT 3444  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
DB 3445 ATCCAGAAATCAGATGAAGCCACCATTTCAGGCATATCTGGAATCTGAAGTTGCTATA 3504  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
DB 3505 TCTGAGGAGTTGGTTTCAGAAAGTACAGATAATCTCTGCTTCTGGTCATGTGAACCTGCACGATA 3564  
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
DB 3565 AAGGAACTCAGGCGCTCTCTTAGTTGATGATTTAGTTGATCTCTGAGTTGAGTG 3624  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
DB 3625 TTGATGGGTATTTACCTATGTTGGTGGCTTTTAAATGCTGTGACACTACTGATTTTG 3684  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
DB 3685 GCTCTCATTTCACTCTTCAGTGTTCCTGTTTATTTATGAACGGCATCAGGCACAGATAGAT 3744  
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
DB 3745 CATTATCTAGGACTTGCNAATAGATGTTTAAAGATGCTTAAATCCAGGCAAAA 3804  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
DB 3805 ATCCCTGGATTGAAGCGCAAGCTGAA 3831

## RESULT 43

AY114152 3821 bp mRNA linear ROD 17-JUL-2002  
LOCUS AY114152  
DEFINITION Mus musculus nogo-A mRNA, complete cds.





## CDS

245. .1423  
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 /note="RTN4-B2; alternatively spliced"  
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 /product="RTN4 isoform B2"  
 /protein\_id="AA064247.1"  
 /db\_xref="GI:26800569"  
 /translation="MEDLDQPLVSSDSPRPQAPKQYQVREDEDEEEED  
 EDEDLEELVLERKPAAGLPAAPVTPAAGAPLMDFGNDFVPPAPRGLPAAPVAP  
 EROPSWDSPVSVTPAPSPLSAAAVSPKLPEDDEPPARPPPPASVSPAEPVMT  
 PPAPAPAPPSTPAAPKRGSGVSDTLFALPAASEPVISSAVVDLLYWRDICKTG  
 VVFGASLELLSLTVFSIVSTAYIALALLSVTISFRIYKGVIAIQKSDSGHPFRAY  
 LVEVAISEELVQVNSALGHVNCITKELRLFLVDLVDLSLKFVILMWFTVYVYAL  
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 1424. .2389  
 /gene="RTN4"

## 3'UTR

## ORIGIN

## Alignment Scores:

Pred. No.: 2,01e-83 Length: 2389  
 Score: 905.00 Matches: 183  
 Percent Similarity: 98.94% Conservativeness: 4  
 Best Local Similarity: 96.83% Mismatches: 2  
 Query Match: 97.84% Indels: 0  
 DB: 9 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AY102278 (1-2389)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 ::  
 Db 854 GCAGTTGTTGACCTCTGCTACTGAGAGACATTAAGAGACTGGAGTGTGTTGGTGCC 913  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThraLaTyrlle 40  
 ::  
 Db 914 AGCCTATTCTCTGCTCTTCATGACAGTATTACGATTGTGAGCGTAACAGCCTACATT 973  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 ::  
 Db 974 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCT 1033  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 ::  
 Db 1034 ATCCAGAAATCAGATGAAGGCCACCATTCAGGCGCATATCTGGAATCTGAAGTTGCTATA 1093  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 ::  
 Db 1094 TCTGAGGAGTTGGTTTCAGAAAGTACAGTAATCTCTGCTCTTGGTCATGTGAACGTGACGATA 1153  
 QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 ::  
 Db 1154 AAGGAACCTCAGCGGCTCTCTTAGTGTAGTATTAGTATTCTCTGAAGTTGCAATG 1213  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuLeu 140  
 ::  
 Db 1214 TTGATGTGGTATTTACCTATGTTGGTGGCTTGTGTTTAAATGGTCTGACACTACTGATTTTG 1273  
 QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 ::  
 Db 1274 GCTCTCATTTCTACTCTGCTGTTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 1333  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 ::  
 Db 1334 CATTATCTAGGACTTGCAATTAAGATGTTAAAGATGCTATGGCTAAATCCACAGCAAA 1393  
 QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
 ::  
 Db 1394 ATCCCTGGATTGAAGCGCAAGCTGAA 1420

## RESULT 46

HSA251385

LOCUS

DEFINITION Homo sapiens mRNA for Nogo-C protein (Nogo gene).

linear

PRI 22-JUL-2000

## ACCESSION

AJ251385

## VERSION

AJ251385.1 GI:9408099

## KEYWORDS

Nogo gene; Nogo-C protein.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

## REFERENCE

1 Prinjha, R., Moore, S.E., Vinson, M., Blake, S., Morrow, R.,

Christie, G., Michalovich, D., Simmons, D.L. and Walsh, F.S.

Inhibitor of neurite outgrowth in humans

## JOURNAL

Nature 403 (6768), 383-384 (2000)

## MEDLINE

20129242

## PUBMED

10667780

## REFERENCE

2 (bases 1 to 600)

## AUTHORS

Michalovich, D.

## TITLE

Submitted (29-NOV-1999)

## JOURNAL

Beecham, Third Avenue, Harlow, Essex, CM19 5AW, BOSNIA AND

## FEATURES

Location/Qualifiers

1..600

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

1..600

/gene="Nogo"

1..600

/gene="Nogo"

/codon\_start=1

/evidence=experimental

/product="Nogo-C protein"

/protein\_id="CAB99250.1"

/db\_xref="GI:9408100"

/db\_xref="GOA:Q9NQC3"

/translation="MDGQKNKDKVLDLYRDIKKTGVVFGASLFLLLSLTVFSIV

SVTAYIALALLSVTISFRIYKGVIAIQKSDSGHPFRAYLSEVAISELWQKYSNA

LGHVNCITKELRLFLVDLVDLSLKFVILMWFTVYVYALFNGLLTLLIALISLSPVP

IYERHQAIQIDHYLGLANKNVKDMAKIQIKPLKRAE"

## ORIGIN

## Alignment Scores:

Pred. No.: 4.32e-84 Length: 600  
 Score: 904.00 Matches: 183  
 Percent Similarity: 98.94% Conservativeness: 3  
 Best Local Similarity: 97.34% Mismatches: 2  
 Query Match: 97.73% Indels: 0  
 DB: 9 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x HSA251385 (1-600)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 ::  
 Db 34 GTTGTGACCTCCTGCTACTGGAGACATTAAGAGACTGGAGTGTGTTGGTGCCAGC 93  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrlleAla 41  
 ::  
 Db 94 CTATTCTGCTGCTTTCATTGACAGTATTACGATTGTGAGCGTAACAGCCTACATTGCC 153  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 ::  
 Db 154 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 213  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 ::  
 Db 214 CAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGAATCTGAAGTTGCTATATCT 273  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 ::  
 Db 274 GAGGAGTTGGTTCAGAAATCAGTAATTTCTGCTCTTGGTTCATGTGAATCTGCACGATAAG 333  
 QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121

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|||||
334 GAACCTCAGCGCCTCTCTTAGTGTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 393
|||||
122 MetTrrPValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
|||||
394 NGTGGGTATTTACCTATGTTGGTGGCTTTGTTTAAATGGTCTGCACACTACTGATTTGGCT 453
|||||
142 LeuileSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
|||||
454 CTCAATTCACCTCTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 513
|||||
162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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514 TATCTAGGACTTGCATAATGAATGTTAAAGATGCTATGGCTAAATCCACGAAAAATC 573
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182 ProGlyLeuLysArgLysAlaAsp 189
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574 CTGGATTGAGCGCAAGCTGAA 597
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RESULT 47
AR028522
LOCUS
DEFINITION
Sequence 2 from patent US 5858708.
ACCESSION
AR028522
VERSION
AR028522.1 GI:5940495
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 799)
AUTHORS
Bandman,O., Au-Young,J., Goli,S.K. and Hillman,J.L.
TITLE
Polynucleotides encoding two novel human neuroendocrine-specific
JOURNAL
Patent: US 5858708-A 2 12-JAN-1999;
FEATURES
source
1. .799
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 6,24e-84 Length: 799
Score: 904.00 Matches: 183
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.73% Indels: 0
DB: 6 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x AR028522 (1-799)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 108 GTTGTGACCTCTGTTACTGGAGACATTAAGACACTGGAGTGGTGTGGTGGCCAGC 167
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 168 CTATTCCTCTGCTTTTCATTTGACAGTATTGACATTTGAGCGGTAAACGCCCTACATGTC 227
QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 228 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGATATACAGGGTGTGATCCAGCTATC 287
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 288 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTCGAAGTTGCTATATCT 347
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 348 GAGGAGTGGTTCAGAAAGTACAGTAATTCCTGCTCTTGGTCATGTTGAACGACGATAAAG 407
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 408 GAACCTCAGCGCCTCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 467

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QY 122 MetTrrPValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
Db 468 ATGTGGGTATTTACCTATGTTGGTGGCTTTGTTTAAATGGTCTGCACACTACTGATTTGGCT 527
QY 142 LeuileSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 528 CTCATTTCACTCTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 587
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 588 TATCTAGGACTTGCATAATGAATGTTAAAGATGCTATGGCTAAATCCACGAAAAATC 647
QY 182 ProGlyLeuLysArgLysAlaAsp 189
Db 648 CTGGATTGAGCGCAAGCTGAA 671
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RESULT 48
BC007109
LOCUS
DEFINITION
Homo sapiens reticulon 4, transcript variant 3, mRNA (cDNA clone
IMAGE:4291127), complete cds.
ACCESSION
BC007109
VERSION
BC007109.1 GI:13937989
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1079)
AUTHORS
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.P., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalley,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
REFERENCE
2 (bases 1 to 1079)
AUTHORS
Strausberg,R.
TITLE
Direct Submission
JOURNAL
Submitted (30-APR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK
NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT
Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found

```



through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAL Plate: 21 Row: h Column: 12  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: Similarity but not  
 identity to protein  
 This clone has the following problem: The cds is short compared to  
 the longest cds in the locus.

## FEATURES

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 /lab\_host="DH10B"  
 /note="Vector: pDNR-LIB"  
 1..1079  
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 /note="synonyms: NSP-CL, NOGO, ASY, NI220/250, NSP, RTN-X"  
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 /db\_xref="MIM:604475"  
 112..711  
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 /db\_xref="GI:13937990"  
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## gene

## CDS

QY 142 LeuileSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
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 Db 565 CTCATTTCACCTCTTCAGTGTCTCTGTTATTATGAACGGCATCAGGCACAGATGATCAT 624  
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 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 |||||  
 Db 625 TATCTAGGACTTGCAATAAGAAATGTTAAAGATGCTATGGCTAAATCCCAAGCAAAATC 684  
 |||||  
 QY 182 ProGlyLeuLysArgLysAlaAsp 189  
 |||||  
 Db 685 CTGGATTGAAGCGCAAGCTGAA 708  
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## RESULT 49

BD249448 1122 bp DNA linear PAT 17-JUL-2003  
 Locus similar to neuroendocrine-specific protein, and encoding  
 DEFINITION CDNA.

## ACCESSION

BD249448

VERSION BD249448.1 GI:33059218

KEYWORDS JP 2002522016-A/3.

SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 1122)

Michalovich D. and Prinjha, R.K.

Protein similar to neuroendocrine-specific protein, and encoding

## TITLE

Patient: JP 2002522016-A 3 23-JUL-2002;

## JOURNAL

SMITHKLINE BEECHAM PLC

## COMMENT

OS Homo sapiens (human)

PN JP 2002522016-A/3

PD 23-JUL-2002

PF 21-JUL-1999 JP 2000561310

PR 22-JUL-1998 GB 9816024.5,19-JUL-1999 GB 9916898.1 PI

PC DAVID MICHALOVICH,RABINDER KUMAR PRINJHA

PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC

10, C12P21/02,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53, PC

G01N33/566//

PC C12P21/08,C12N15/00,C12N5/00

CC Protein similar to neuroendocrine-specific protein, and CC

encoding CDNA

FH Key Location/Qualifiers

FT source 1..1122

/organism="Homo sapiens (human)"

Location/Qualifiers

1..1122

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.: 9.65e-84 Length: 1122

Score: 904.00 Matches: 183

Percent Similarity: 98.94% Conservatives: 3

Best Local Similarity: 97.34% Mismatches: 2

Query Match: 97.73% Indels: 0

DB: 6 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BD249448 (1-1122)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21

Db 556 GTTGTGACCTCTCTGACGACATTAAGAACTGGAGTGGTGTGGTGGCCAGC 615

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

Db 616 CTATTCTCGCTGCTTTTCATTGACAGTATTCAGCATTTGACGCGTAACAGCCTACATGCC 675

QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

## Alignment Scores:

Pred. No.: 9.18e-84 Length: 1079

Score: 904.00 Matches: 183

Percent Similarity: 98.94% Conservatives: 3

Best Local Similarity: 97.34% Mismatches: 2

Query Match: 97.73% Indels: 0

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QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

Db 205 CTATTCTCGCTGCTTTTCATTGACAGTATTCAGCATTTGAGCGTAACAGCCTACATGCC 264

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

Db 265 TTGGCCCTGCTCTGTGACCATCAGCTTAGGATATACAGGGTGTGATCCAGCTATC 324

QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81

Db 325 CAGAAATCAGATGAAGGCCACCAATTCAGGCGCATATCTGGAATCTGGAAGTTCGTATATCT 384

QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101

Db 385 GAGGAGTGGTTCAGAGTACAGTAAATTCCTGCTTGTGTCATGTGAACCTGACCGATAAG 444

QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121

Db 445 GAACCTCAGCGCGCTCTCTTAGTTCATGATTAGTTGATTCTCTGAAGTTGTCAGTGTG 504

QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141

Db 505 ATGTGGGTATTACCTATGTTGGTGGCTTGTAAATGGTCTGACACTACTGATTTGGCT 564

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Db      676 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 735
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Db      736 CAGAAATCAGATCAGAGCCACCATTCAGGCGCATATCTGGAATCTGGAATCTGCTATATCT 795
Qy      82  GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db      796 GAGGAGTTGGTTTTCAGAAAGTACAGTAATCTCTGCTTTGGTCACTGGAAGTGCACGATAAG 855
Qy      102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db      856 GAACCTCAGCGGCTCTCTCTAGTATGATTTAGTATGATCTCTGAGTTGAGTTG 915
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Qy      142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
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Qy      162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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RESULT 50
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LOCUS          Homo sapiens mRNA for Nogo-B protein (Nogo gene).
DEFINITION
ACCESSION     AJ251384
VERSION       AJ251384.1 GI:9408097
KEYWORDS      Nogo gene; Nogo-B protein.
SOURCE        Homo sapiens
ORGANISM      Homo sapiens
REFERENCE     1.
AUTHORS       Prinjha, R., Moore, S.E., Vinson, M., Blake, S., Morrow, R.,
              Christie, G., Michalovich, D., Simmons, D.L. and Walsh, P.S.
              Inhibitor of neurite outgrowth in humans
              Nature 403 (6768), 383-384 (2000)
MEDLINE       20129242
PUBMED        10667780
REFERENCE     2 (bases 1 to 1122)
AUTHORS       Michalovich, D.
TITLE         Direct Submission
JOURNAL       Submitted (29-NOV-1999) Michalovich D., Bioinformatics, Smithkline
              Beecham, Third Avenue, Harlow, Essex, CM19 5AW, BOSNIA AND
              HERZEGOVINA
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## ORIGIN

## Alignment Scores:

Pred. No.: 9,658-84 Length: 1122  
 Score: 904.00 Matches: 183  
 Percent Similarity: 98.94% Conservative: 3  
 Best Local Similarity: 97.34% Mismatches: 2  
 Query Match: 97.73% Indels: 0  
 DB: Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x HSA251384 (1-1122)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 Db 556 GTTGTGTGACCTCTCTACTGGAGAGACATTAAAGAGACTGGAGTGTGTTGGTGCCAGC 615  
 Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 616 CTATTCTCTGCTCTTTCATTCAGACTATTTCAGCATTTGTGAGCGTAAACAGCCTACATTC 675  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 676 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 735  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
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 Db 1036 TATCTAGGACTTGCAAATAGAAATGTTAAAGATGCTATGCTGCTAAATCCAGCAAAATC 1095  
 Qy 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 1096 CCTGGATTGAAGCGCAAAAGCTGAA 1119

## RESULT 51

BC001035  
 LOCUS Homo sapiens reticulon 4, transcript variant 3, mRNA (cdna clone  
 DEFINITION IMAGE:3139770), complete cds.

ACCESSION BC001035

VERSION BC001035.2 GI:33875905

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1151)

Klausner, R.D., Collins, F.S., Wagner, L., Shemen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,



**TITLE**  
**JOURNAL**  
**COMMENT**

86 human secreted proteins  
 Patent: JP 2002514090-A 78 14-MAY-2002;  
 HUMAN GENOME SCIENCES INC  
 OS Unidentified  
 PN JP 2002514090-A/78  
 PD 14-MAY-2002  
 PF 11-JUN-1998 JP 1999503203  
 PR 13-JUN-1997 US 60/049547,13-JUN-1997 US 60/049548 PR  
 13-JUN-1997 US 60/049549,13-JUN-1997 US 60/049550 PR  
 13-JUN-1997 US 60/050566,13-JUN-1997 US 60/049606 PR  
 13-JUN-1997 US 60/049607,13-JUN-1997 US 60/049608 PR  
 13-JUN-1997 US 60/049609,13-JUN-1997 US 60/049610 PR  
 13-JUN-1997 US 60/049611,13-JUN-1997 US 60/050901 PR  
 13-JUN-1997 US 60/052989,08-JUL-1997 US 60/051919 PR  
 18-AUG-1997 US 60/055984,12-SEP-1997 US 60/058665 PR  
 12-SEP-1997 US 60/058668,12-SEP-1997 US 60/058669 PR  
 12-SEP-1997 US 60/058750,12-SEP-1997 US 60/058971 PR  
 12-SEP-1997 US 60/058972,12-SEP-1997 US 60/058975 PR  
 02-OCT-1997 US 60/060834,02-OCT-1997 US 60/060841 PR  
 02-OCT-1997 US 60/060844,02-OCT-1997 US 60/060865 PR  
 02-OCT-1997 US 60/061059,02-OCT-1997 US 60/061060 PI PAUL A  
 MOORE,YANGGU SHI,CRAIG A ROSEN,STEVEN M RUBEN,DAVID W PI  
 LAFLEUR,  
 PI HENRIK S OLSEN,REINHARD EBNER,LAURIE A BREWER,PAUL YOUNG,JOHN  
 PI M GREENE,  
 PI ANN M FERRIE,GUO LIANG YU JIAN NI,PING FENG  
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RESULT 54  
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 VERSION BC071848.1 GI:47939581  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1466)  
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uedin, T.B., Toehiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullen, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalek, U., Smalilus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 PUBMED 12477932  
 REFERENCE 2 (bases 1 to 1466)  
 AUTHORS Strausberg, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-JUN-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 COMMENT Contact: MGC help desk  
 Email: [cgapsb-remail.nih.gov](mailto:cgapsb-remail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www-shgc.stanford.edu>  
 Contact: (Dickson, Mark) [mcdopaxil.stanford.edu](mailto:mcdopaxil.stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAL Plate: 58 Row: d Column: 23  
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24431932  
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#### FEATURES

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#### gene

#### CDS

#### ORIGIN

Alignment Scores:  
 Pred. No.: 1.36e-83 Length: 1466  
 Score: 904.00 Matches: 183  
 Percent Similarity: 98.94% Conservative: 3  
 Best Local Similarity: 97.34% Mismatches: 2  
 Query Match: 97.73% Indels: 0  
 DB: 9 Gaps: 0  
 US-09-830-972-2\_COPY\_975\_1163 (1-189) x BC071848 (1-1466)

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Score:	904.00	Matches:	183
Percent Similarity:	98.94%	Conservative:	3
Best Local Similarity:	97.34%	Mismatches:	2
Query Match:	97.73%	Indels:	0
DB:	6	Gaps:	0

US-09-830-972-2 COPY 975 1163 (1-189) x CQ769577 (1-1599)

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Qy	82	GluGluLeuValGlnIysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys	101
Db	911	GAGGAGTGGTTCAGAAGTACAGTAATTCGTCTTCTGGTCATGTGAACCTGCACGATAAAG	970
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Db	971	GAACCTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCCTCTGAAAGTTTGACGTCTG	1030
Qy	122	MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla	141
Db	1031	ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAAATGGTCTGCACACTACTGATTTTGGCT	1090
Qy	142	LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis	161
Db	1091	CTCATTTTCACCTCTTCAGTGTTCCTGTTATTATTATGAACGGCATCAGGCACAGATAGATCAT	1150
Qy	162	TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle	181
Db	1151	TATCTAGACTTGCAAATAGAAATGTTTAAGATGCTATGGCTAAATCCCAAGCAAAATC	1210
Qy	182	ProGlyLeuLysArgLysAlaAsp	189
Db	1211	CCTGGATTGAAGCGCAAGCTGAA	1234

RESULT	58
BD231889	
LOCUS	BD231889      Bone marrow secreted proteins and polynucleotides.
DEFINITION	linear DNA
ACCESSION	BD231889      1610 bp
VERSION	BD231889.1    GI:33041659
KEYWORDS	JP 2002511231-A/3.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
Eukaryota; Metazoa;	Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria;	Primates; Catarrhini; Hominidae; Homo.

PC	C12N15/00.A61K37/02.C12N5/00
CC	Bone marrow secreted proteins and polynucleotides FH Key
FT	Location/Qualifiers
FT	source 1..1610 /organism='Homo sapiens (human)'. Location/Qualifiers 1..1610 /organism='Homo sapiens' /mol_type='genomic DNA' /db_xref='taxon:9606'
ORIGIN	
Alignment Scores:	
Pred. No.:	1,538-83 Length: 1610
Score:	904.00 Matches: 183
Percent Similarity:	98.94% Conservative: 3
Best Local Similarity:	97.34% Mismatches: 2
Query Match:	97.73% Indels: 0
DB:	Gaps: 0
US-09-830-972-2_COPY_975_1163 (1-189) x BD231889 (1-1610)	
Qy	2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Dd	687 GTTGTTGACCTCCTGACTGAGAGACATTAAAGAAGCTGGAGTGTGTTGGTCGCAGC 746
Qy	22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Dd	747 CTATTCCTGCTGCTTCATTGACAGTATTGACGATTTGTGAGCGTAACAGCTACATTGCC 806
Qy	42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAlaIle 61
Dd	807 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGCTGTGATCCAAGCTATC 866
Qy	62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Dd	867 CAGAAATCATGATGAAGGCCACCCATTGAGGGCATATCTGGAATCTGAAGTTGCTATATCT 926
Qy	82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Dd	927 GAGGAGTTGGTTCAGAAGTACAGTAATTCGTCTTGTGTCATCTCAACTGCACGATAAAG 986
Qy	102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Dd	987 GAATCTCAGGCGCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGAGTGTG 1046
Qy	122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlnLysLeuThrLeuLeuAla 141
Dd	1047 ATGTGGGTATTACCTATGTTGGTGCCTGTTTAATGGTCTGACACTACTGATTTTGGCT 1106
Qy	142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Dd	1107 CTCATTTCACCTCTTCAGTGTCTCTGTTATTATTGAACGGCATCATCGGCACAGATAGATCAT 1166
Qy	162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Dd	1167 TATCTAGGACTTGCAANAATGAATGTTAAAGATGCTATGGCTAAAATCCAGCAAATATC 1226
Qy	182 ProGlyLeuLysArgLysAlaAsp 189
Dd	1227 CCTGGATTGAAGCGCAAAGCTGAA 1250

RESULT 59						PRI 09-SEP-2000
AF087901						
LOCUS	AF087901	1617 bp	mRNA	linear		
DEFINITION	Homo sapiens reticulon 4c mRNA, complete cds.					
ACCESSION	AF087901					
VERSION	AF087901.1	GI:10039642				
KEYWORDS	.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					



```

REFERENCE 1 (bases 1 to 1617)
AUTHORS Yang,J., Yu,L., Bi,A.D. and Zhao,S.Y.
TITLE Assignment of the human reticulon 4 gene (RTN4) to chromosome
2p14--2p13 by radiation hybrid mapping
JOURNAL Cytogenet. Cell Genet. 88 (1-2), 101-102 (2000)
MEDLINE 20237542
PUBMED 10773680
REFERENCE 2 (bases 1 to 1617)
AUTHORS Yang,J., Yu,L., Dai,P.Y., Cui,W.C., Zheng,L.H. and Zhao,S.Y.
TITLE Direct Submission
JOURNAL Submitted (27-AUG-1998) Lab of Human Gene Research, Institute of
Genetics, Fudan University, No. 220 Handan Rd., Shanghai 200433,
P.R.China
FEATURES
source
1. .1617
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106. .705
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polyA_signal 1590. .1595
polyA_site 1608
ORIGIN
Alignment Scores:
Pred. No.: 1,548-83 Length: 1617
Score: 904.00 Matches: 183
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.73% Indels: 0
Gaps: 0
DB: 9
US-09-830-972-2_COPY_975_1163 (1-189) x AF087901 (1-1617)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 139 GTTGTGACCTCTCTACTGGAGACATTAAGAGACTGGAGTGGTGTGGTGCCAGC 198
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 199 CTATTCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 258
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 259 TTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 318
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 319 CAGAAATCAGATGAGGCCACCCATTCAGGCATATCTGGAATCTGGAATCTGATATCT 378
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 379 GAGGAGTTGGTTTCAGAGTACAGTAAATCTGCTCTTGTGTCATGTGAACTGCACGATAAG 438
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 439 GAATCAGCGCGCTCTCTTAGTGTGATTTAGTTAGTTATCTCTGAAAGTTGCGAGTGTG 498
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeuAla 141
Db 499 ATGTGGGTATTTACCTATGTTGGTCCCTGTTTATGCTCTGACACTACTGATTTGGCT 558
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 559 CTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATGATCAT 618

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QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 619 TATCTAGACCTTGCAATTAAGATGTTAAGATGCTATGGCTTAATTCAGCAAAATC 678
QY 182 ProGlyLeuLysArgLysAlaAsp 189
Db 679 CCTGATTGAAGCGCAAGCTGAA 702
RESULT 60
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LOCUS Homo sapiens cDNA FLJ26295 fis, clone DMC07157.
ACCESSION AKI29806
VERSION AKI29806.1 GI:34526422
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
REFERENCE 1
AUTHORS Ota,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H., Suzuki,Y.,
Hata,H., Nakagawa,K., Mizuno,S., Morinaga,M., Kawamura,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Nishikawa,T.,
Sugiyama,A., Kawakami,B., Nagai,K., Isogai,T. and Sugano,S.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1619)
AUTHORS Sugano,S. and Suzuki,Y.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome
Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail: fclabna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction and 5'-end one pass sequencing: Institute of Medical
Science, University of Tokyo, Laboratory of Genome Structure, Human
Genome Center; 3'-end one pass sequencing: RAB; clone selection for
full insert sequencing: RAB and Helix Research Institute.
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/db_xref="taxon:9606"
/clone="DMC07157"
/tissue type="dermoid tumor"
/clone_lib="DMC"
/note="Cloning vector: pME18SFL3"
ORIGIN
Alignment Scores:
Pred. No.: 1,548-83 Length: 1619
Score: 904.00 Matches: 183
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.73% Indels: 0
Gaps: 0
DB: 9
US-09-830-972-2_COPY_975_1163 (1-189) x AKI29806 (1-1619)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 713 GTTGTGACCTCTCTACTGGAGACATTAAGAGACTGGAGTGGTGTGGTGCCAGC 772
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 773 CTATTCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 832
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

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QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaLysSer 81
Db 922 CAGAAATCAGATGAGGCCACCAATTCAGGCGCATATCTCGAATCTGGAATGCTATATCT 981
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 982 GAGGAGTTGGTCAGAGTACAGTAATCTGCTCTGGTCATGTGAGTGCACGATAAG 1041
QY 102 GluLeuArgGluPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 1042 GAACTCAGCGGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAGTTGCGAGTTG 1101
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
Db 1102 ATGTGGGTATTTACCTATGTTGGTCTGCTTTGTAATGGTCTGACACTACTGATTTGGCT 1161
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 1162 CTCATTTCACTCTTCAGTGTCTGTTATTTATGACGCGCATCAGGCACAGATAGATCAT 1221
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 1222 TATCAGGACTTGCAATTAAGAATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAATC 1281
QY 182 ProGlyLeuLysArgLysAlaAsp 189
Db 1282 CTGGGATTGAGCGCAAGCTGAA 1305

RESULT 63
AF132048 1691 bp mRNA linear PRI 18-MAY-1999
LOCUS Homo sapiens foocen-s mRNA, complete cds.
DEFINITION AF132048
VERSION AF132048.1 GI:4838518
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1691)
AUTHORS Ito, T. and Schwartz, S.M.
TITLE Cloning of a member of the reticulon gene family in human: skeletal
muscle type
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1691)
AUTHORS Ito, T. and Schwartz, S.M.
TITLE Direct Submission
JOURNAL Submitted (27-FEB-1999) Pathology, University of Washington, 1959
Pacific NE, Seattle, WA 98195, USA
FEATURES
Location/Qualifiers
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121..720
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SVTAYTALLSLRTTSIFRIYKGVQIAQSDGHPFVYALVEVAISELWKNYNSA
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ORIGIN
Alignment Scores: 1.63e-83 Length: 1691
Pred. No.: 904.00 Matches: 183
Score: 98.94% Conservative: 3
Percent Similarity: 97.34%
Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.73% Indels: 0

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DB: 9 Gaps: 0
US-09-830-972-2_COPY_975_1163 (1-189) x AF132048 (1-1691)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 154 GTTGTGGACCTCTCTACTCGGAGACATTAAGAGAGCTGGAGTGGTGTGTTGGTGCCAGC 213
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThAlaTyrIleAla 41
Db 214 CTATTCCTGCTGCTTTTCATTCAGCATTTGTGAGCGTAAACAGCCTACATTCGCC 273
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 274 TTGGGCCCTGCTCTCTGTGACCAATCAGCTTTAGGATATACAGGGGTGTGATCCAGCTATC 333
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaLysSer 81
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QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 394 GAGGAGTTGGTTCAGAGTACAGTAATCTGCTCTGGTCATGTGAACTGCACGATAAG 453
QY 102 GluLeuArgGluPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 454 GAACTCAGCGGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAGTTGCGAGTTGCTG 513
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
Db 514 ATGTGGGTATTTACCTATGTTGGTCTGCTTTGTAATGGTCTGACACTACTGATTTGGCT 573
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 574 CTCATTTCACTCTTCAGTGTCTGCTTTATTTATGACGCGCATCAGGCACAGATAGATCAT 633
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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RESULT 64
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DEFINITION IMAGE:3933041), complete cds.
ACCESSION BC014366
VERSION BC014366.1 GI:15680080
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1698)
AUTHORS
Klausner, R.D., Collins, F.S., Wagner, L.H., Derge, J.G.,
Krausberg, R.L., Feingold, E.A., Grouse, L.H., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.P., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schaefer, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

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Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,  
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 1698)  
Strausberg, R.  
Direct Submission  
Submitted (17-SEP-2001) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: CLONTECH  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbio.org>  
Contact: [amadansystemsbiology.org](mailto:amadansystemsbiology.org)  
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha  
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting  
Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 31 Row: 9 Column: 2  
This clone has the following problem: The cds is short compared to  
the longest cds in the locus.  
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IYERHQIDHYLGANKNVKDAKIQAKIPGLKRAE"  
ORIGIN  
Alignment Scores:  
Pred. No.: 1.64E-83 Length: 1698  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: 9 Gaps: 0  
US-09-830-972-2\_COPY\_975\_1163 (1-169) x BC014366 (1-1698)  
Qy 2 ValValAspLeuLeuTyTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 145 GTTGTTCACCTCCTGACTGGAGACATTAAAGAGACTGGAGTGGTGTGTTGGTCCAGC 204

22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrlleAla 41  
Db CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATGGC 264  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrlLysGlyValIleGlnAla 61  
Db TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGCTGTGATCCAAGCTATC 324  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrlLeuGluSerGluValAlaIleSer 81  
Db CAGAAATCAGATGAAGGCCACCCATTAGGGCATATCTGGAATCTGGAAGTTGCTATATCT 384  
Qy 82 GluGluLeuValGlnLysTyrlSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
Db GAGGAGTTGGTTTCAGAGTACAGTAATTCCTGCTCTGTGTCATGTGAACTGCACGATAAG 444  
Qy 102 GluLeuArgArgLeuPheLeuValAspSerLeuValAspSerLeuLysPheAlaValLeu 121  
Db GAACCTCAGGCGCCTCTTCTTAGTTGATGATTAGTTGATTCTCTGAGGTTTGCAGTGTG 504  
Qy 122 MetTrpValPheThrTyrlValGlyValAlaLeuPheGlnGlyLeuThrLeuLeuLeuAla 141  
Db ATGTGGGTATTACTATGTTGGTGGCTGTGTTTATGTCCTGACACTACTGATTTGGCT 564  
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrlGluArgHisGlnValGlnIleAspHis 161  
Db CTCATTTTCATCTTCAGTGTTCCTGTTATTATGAACGGCATCAGGCACAGATAGATCAT 624  
Qy 162 TyrlGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db TATCTAGGACTTGCAAAATAGAAATGTTAAAGATGCTATGGCTAAATCAAGCAAAATC 684  
Qy 182 ProGlyLeuLysArgLysAlaAsp 189  
Db CCTGGATTGAAGCGCAAGCTGAA 708  
RESULT 65  
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ACCESSION AF177332  
VERSION AF177332.1 GI:10503960  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Gu, J.R., Wan, D.F., Zhao, X.T., Zhou, X.M., Jiang, H.Q., Zhang, P.P.,  
Qin, W.X., Huang, Y., Qiu, X.K., Qian, L.F., He, L.P., Li, H.N., Yu, Y.,  
Yu, J. and Han, L.H.  
TITLE Novel human cDNA clone with function of inhibiting cancer cell  
Growth  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1700)  
AUTHORS Gu, J.R., Wan, D.F., Zhao, X.T., Zhou, X.M., Jiang, H.Q., Zhang, P.P.,  
Qin, W.X., Huang, Y., Qiu, X.K., Qian, L.F., He, L.P., Li, H.N., Yu, Y.,  
Yu, J. and Han, L.H.  
TITLE Direct Submission  
JOURNAL Submitted (06-AUG-1999) National Laboratory For Oncogenes & Related  
Genes, Shanghai Cancer Institute, 25/Ln 2200 Xie Tu Road, Shanghai  
200032, P.R. China  
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## ORIGIN

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Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
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US-09-830-972-2\_COPY\_975\_1163 (1-189) x AF177332 (1-1700)

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REFERENCE  
1  
AUTHORS Tagami,S., Eguchi,Y., Kinoshita,M., Takeda,M. and Tsujimoto,Y.  
TITLE A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on  
endoplasmic reticulum and reduces their anti-apoptotic activity  
JOURNAL Oncogene 19 (50), 5736-5746 (2000)  
MEDLINE 21010696

11126360

PUBMED  
REFERENCE

2 (bases 1 to 1709)  
Eguchi,Y., Tagami,S. and Tsujimoto,Y.  
AUTHORS Direct Submission  
TITLE Submitted (22-MAR-2000) Yutaka Eguchi, Osaka University Graduate  
JOURNAL School of Medicine, Biomedical Research Center, Department of  
Medical Genetics, Yamadaoka 2-2, Suita, Osaka 565-0871, Japan  
(E-mail:eguchi@gen.med.osaka-u.ac.jp, tel: +81-6-6879-3363,  
Fax: +81-6-6879-3369)

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## ORIGIN

## Alignment Scores:

Pred. No.: 1.66e-83 Length: 1709  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AB040463 (1-1709)

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JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 1728)  
Straussberg, R.  
Direct Submission  
Submitted (05-APR-2004) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabos@mail.nih.gov](mailto:cgabos@mail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: Ruben Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
BC Sequencing by: Genome Sequence Centre,  
BC Cancer Agency, Vancouver, BC, Canada  
[info@bcgsc.bc.ca](mailto:info@bcgsc.bc.ca)  
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,  
Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth  
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,  
Kim Macdonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,  
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Lilesa Prahbu,  
Parvaneh Saeedi, JR Santos, Angeli Schnerch, Ursula Skalska,  
Duane Smalius, Jeff Scott, Miranda Tsai, George Yang, Jacques  
Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found  
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ORIGIN  
Alignment Scores:  
Pred. No.: 1.68e-83 Length: 1728  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0

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CDS

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REFERENCE 1 (bases 1 to 1800)  
AUTHORS Oertle, T., Huber, C., van der Putten, H. and Schwab, M.E.  
TITLE Genomic structure and functional characterization of the promoters  
of human and mouse nogo/rtn4  
J. Mol. Biol. 325 (2), 299-323 (2003)  
MEDLINE 22376540  
PUBMED 12488097  
REFERENCE 2 (bases 1 to 1800)  
AUTHORS Oertle, T. and Schwab, M.E.  
TITLE Direct Submission  
JOURNAL Submitted (07-MAY-2002) Brain Research Institute, University of  
Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,  
Switzerland  
REFERENCE 3 (bases 1 to 1800)  
AUTHORS Van der Putten, H.  
TITLE Direct Submission  
JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma



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 1 (bases 1 to 2052)  
 Yutsudo, M.  
 Isolation of a cell death-inducing gene  
 Published Only in Database (1999)  
 REFERENCE 2 (bases 1 to 2052)  
 Yutsudo, M.  
 Direct Submission  
 Submitted (17-JUN-1998) Masuo Yutsudo, Osaka University, Dept. of  
 Tumor Virol., Res. Inst. Microb. Dis.; 3-1 Yamadaoka, Suita, Osaka  
 565-0871, Japan (E-mail: yutsudo@biken.osaka-u.ac.jp,  
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 Percent Similarity: 98.94% Conservative: 3  
 Best Local Similarity: 97.34% Mismatches: 2  
 Query Match: 97.73% Indels: 0  
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 US-09-830-972-2\_COPY\_975\_1163 (1-189) x AB015639 (1-2052)  
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REFERENCE      1 (bases 1 to 2235)
AUTHORS      Yang, J., Yu, L., Bi, A.D. and Zhao, S.Y.
TITLE      Assignment of the human reticulon 4 gene (RTN4) to chromosome
2p14-->p13 by radiation hybrid mapping
JOURNAL      Cytogenet. Cell Genet. 88 (1-2), 101-102. (2000)
MEDLINE      20237542
PUBMED      10773680
REFERENCE      2 (bases 1 to 2235)
AUTHORS      Zhou, Y., Yu, L. and Zhao, S.Y.
TITLE      Direct Submission
JOURNAL      Submitted (05-MAY-1999) Lab of Human Gene Research, Institute of
Genetics, Fudan University, No. 220 Handan Rd., Shanghai 200433,
P.R.China

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QY      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db      757 CTATTCCTGCTGCTCTTCAATGACAGTATTGACCAITGTGAGCGTAACAGCCTACATTCGC 816
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QY      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
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QY      82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db      937 GAGGAGTTGGTTCAGAGTACAGTAATCTGCTCTTGGTCACTGTGAACTGCACGATAAG 996
QY      102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
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QY      122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
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QY      142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
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QY      162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      1177 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAAGAAATC 1236
QY      182 ProGlyLeuLysArgLysAlaAsp 189
Db      1237 CTGGATTGAAGCGCAAGCTGAA 1260

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DEFINITION      AF132047
ACCESSION      AF132047
VERSION      AF132047.1 GI:4838516
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 2276)
AUTHORS      Ito, T. and Schwartz, S.M.
TITLE      Cloning of a member of the reticulon gene family in human:
ubiquitous type
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 2276)
AUTHORS      Ito, T. and Schwartz, S.M.
TITLE      Direct Submission
JOURNAL      Submitted (27-FEB-1999) Pathology, University of Washington, 1959
Pacific NE, Seattle, WA 98195, USA
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source      1..2276
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 Best Local Similarity: 97.34% Mismatches: 2  
 Query Match: 97.73% Indels: 0  
 DB: 9 Gaps: 0

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 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 795 CTATTCTCGCTCTTCAATGACGATTAACGATTTGAGCGTGAACGCTACATTCGCC 854  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
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 Db 915 CAGAAATCAGATGAAGCCACCAATTCAGGCGATATCTGGAATCTGAAGTTGCTATATCT 974  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
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 QY 102 GluLeuArgGluLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
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 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
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 QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
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 Db 1275 CTGCGATTGAAGCGCAAGCTGAA 1298  
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 LOCUS  
 DEFINITION Homo sapiens RTN4 isoform B1 (RTN4) mRNA, linear PRI 23-SEP-2003

alternatively spliced.  
 ACCESSION AY102277  
 VERSION AY102277.1 GI:26800561  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Carnathini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 2332)  
 AUTHORS Oertle, F., Huber, C., van der Putten, H. and Schwab, M.E.  
 TITLE Genomic structure and functional characterisation of the promoters  
 of human and mouse nogo/rtn4  
 J. Mol. Biol. 325 (2), 299-323 (2003)  
 JOURNAL 22376540  
 MEDLINE 1248097  
 PUBMED  
 REFERENCE 2 (bases 1 to 2332)  
 AUTHORS Oertle, T. and Schwab, M.E.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-MAY-2002) Brain Research Institute, University of  
 Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,  
 Switzerland  
 REFERENCE 3 (bases 1 to 2332)  
 AUTHORS Van der Putten, H.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma  
 Inc., Basel, Switzerland  
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 DB: 9 Gaps: 0  
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 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

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Db      860 CTATTCTCTGCTCTTTCATTGACAGTATTTCAGCAATTGTGAGCGTAACAGCCTACATTGCC 919
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Db      920 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAAGGTGTGATCCAAAGCTATC 979
Qy      62  GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db      980 CAGAAATCAGATGAGCGCCACCCATTTCAGGCATATCTGGAATCTCGAAGTTGCTATATCT 1039
Qy      82  GluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAenSerThrIleLys 101
Db      1040 GAGGAGTTGGTTCAGAAAGTACAGTAATCTGCTCTTGGTCATGTGAACTGCGACGATAAG 1099
Qy      102  GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
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Qy      142  LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
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Db      1280 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAATC 1339
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LOCUS      Mus musculus nogo-B mRNA linear ROD 17-JUL-2002
DEFINITION Mus musculus nogo-B mRNA, complete cds.
ACCESSION AY114153
VERSION    AY114153.1 GI:21898578
KEYWORDS   Mus musculus (house mouse)
SOURCE     Mus musculus
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 1276)
AUTHORS    Jin,W., Li,R., Long,M., Shen,J. and Ju,G.
TITLE      Cloning and expression of the mouse Nogo-B protein
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 1276)
AUTHORS    Jin,W., Li,R., Long,M., Shen,J. and Ju,G.
TITLE      Direct Submission
JOURNAL    Submitted (17-MAY-2002) Institute of Neurosciences, 17 Chang Le Xi
            Road, Xi'an, Shaanxi 710032, China

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Best Local Similarity: 97.57% Indels: 1
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Qy      21  SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
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Qy      41  AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
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Qy      81  SerGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAenSerThrIle 100
Db      864 TCAGAGGAATTTGGTTCAGAAATATAGTAATCTCTCTCTGTCATGTGAACAGCAATA 923
Qy      101  LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
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Qy      141  AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
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Qy      161  HisTyrLeuGlyLeuAlaAenLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
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Qy      181  IleProGlyLeuLysArgLysAlaAsp 189
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RESULT 75
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DEFINITION complete cds.
ACCESSION AF132046
VERSION    AF132046.1 GI:4838514
KEYWORDS   Rattus norvegicus (Norway rat)
SOURCE     Rattus norvegicus
ORGANISM   Rattus norvegicus
REFERENCE  1 (bases 1 to 2256)
AUTHORS    Ito,T. and Schwartz,S.M.
TITLE      Cloning of a member of the reticulon gene family in rat: One of two
            minor splice variants
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 2256)
AUTHORS    Ito,T. and Schwartz,S.M.
TITLE      Direct Submission
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Pred. No.: 4,828-83 Length: 2256  
Score: 901.00 Matches: 186  
Percent Similarity: 98.94% Conservative: 0  
Best Local Similarity: 98.94% Mismatches: 0  
Query Match: 97.41% Indels: 2  
DB: 10 Gaps: 1  
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Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaIle 181  
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DEFINITION Sequence 3170 from Patent EP1396543.  
ACCESSION CQ783030  
VERSION CQ783030.1 GI:45502969  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,  
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and  
Koga,H.  
TITLE Primers for synthesizing full length cDNA clones and their use  
JOURNAL Patent: EP 1396543-A 3170 10-MAR-2004;  
RESEARCH Association for Biotechnology (JP)  
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Db 908 TTGGCCCTGCTCTCTGTCAGCATTCAGCTTTAGGATATATAAGGGCGTGCATCCAGC 967  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 968 CAGAAATCAGATGAAGGCCACCCATTCAGGCATATTCGGAATCTGAAGTTGCTATATCT 1027  
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
Db 1028 GAGGAGTGGTTTCAGAGTACAGTAATCTGCTCTTGGTTCATGTGACCTGCACGATAAG 1087  
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValIle 121  
Db 1088 GAATCAGGCGCTCTTCTTAGTTGATGATTTAGTTGATTCCTGGAAGTTTGCAGTGTG 1147

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QY 122 MetTrrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleuLeuAla 141
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QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
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|
Db 1208 CTCATTTCACTCTTCAGTGTCTCTGTTATTATGAACGGCATCAGGCACAGATAGATCAT 1267
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QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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Db 1268 TATCTAGGACTTGCAATAGATGTTTAAAGATGCTATGCTTAAATCCAGCAAAATC 1327
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QY 182 ProGlyLeuLysArgLysAlaAsp 189
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Db 1328 CCTGGATTGAAGCGCAAGCTGAA 1351
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RESULT 77
BD127437
LOCUS BD127437 1694 bp DNA linear PAT 18-SEP-2002
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD127437
VERSION BD127437.1 GI:23222382
KEYWORDS JP 2002017375-A/2868.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Ota,T., Nishikawa,T., Isegai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
AUTHORS Ota,T., Nishikawa,T., Isegai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002017375-A 2868 22-JAN-2002;
COMMENT HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/2868
PD 22-JAN-2002
PF 07-JUL-2000 JP 20020253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISEGAI, KOJI HAYASHI, SHIZUKO
ISHII,
PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUO OTSUKI, HISASHI KOGA
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10,
PC C12P21/02, C12P1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
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ORIGIN
Alignment Scores:
Pred. No.: 4,23e-83 Length: 1694
Score: 900.00 Matches: 182
Percent Similarity: 98.40% Conservative: 3
Best Local Similarity: 96.81% Mismatches: 3
Query Match: 97.30% Indels: 0
DB: 6 Gaps: 0
US-09-830-972-2_COPY_975_1163 (1-189) x BD127437 (1-1694)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLeuThrGlyValValPheGlyAlaSer 21
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|
|
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerIleValThrAlaTyrIleAla 41
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|
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Db 848 CTATTCCTGCTGCTTTTCATTGACAGTATTGACATTGTGAGCGTAACAGCCTACATGGC 907
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QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
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Db 908 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATATCAAGGGGTGTGATCCAGCTATC 967
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QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
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Db 968 CAGAAATCAGATGAAGGCCACCCATTAGGGCATATCTGGAATCTGAAATCTGAAATCTATATCT 1027
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QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
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Db 1028 GAGGAGTTGGTTTCAAGATACAGTAATTTCTGCTCTGTGTCATGTGAACATGCACGATAAG 1087
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QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
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Db 1088 GAACTCAGCGCGCTCTTCTTAGTTCATGATTTAGTTGATTTCTCTGAAGTTTCAGTGTG 1147
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QY 122 MetTrrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleuLeuAla 141
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Db 1148 ATGTGGGTATTTACCTATGTTGGTCCCTGTTTAAATGGTCTGACACTACTGATTTGGCT 1207
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QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
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Db 1208 CTCATTTCACTCTTCAGTGTCTCTGTTATTATGAACGGCATCAGGCACAGATAGATCAT 1267
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QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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Db 1268 TATCTAGGACTTGCAATAGATGTTTAAAGATGCTATGCTTAAATCCAGCAAAATC 1327
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QY 182 ProGlyLeuLysArgLysAlaAsp 189
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Db 1328 CCTGGATTGAAGCGCAAGCTGAA 1351
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RESULT 78
AK075039 1694 bp mRNA linear PRI 03-SEP-2002
LOCUS AK075039 Homo sapiens cDNA FLJ90558 fis, clone OVARC1001030.
DEFINITION AK075039
ACCESSION AK075039
VERSION AK075039.1 GI:22760874
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Isegai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T.,
Sugiyama,T., Suzuki,Y., Sato,H., Nagai,K., Sugano,S., Ishii,S.,
Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y.,
Kojima,S., Nagahara,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y.,
Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and
Ninomiya,K.
AUTHORS Isegai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T.,
Sugiyama,T., Suzuki,Y., Sato,H., Nagai,K., Sugano,S., Ishii,S.,
Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y.,
Kojima,S., Nagahara,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y.,
Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and
Ninomiya,K.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1694)
AUTHORS Isegai,T. and Otsuki,T.
DIRECT SUBMISSION Direct Submission
JOURNAL Submitted (25-MAR-2002) Takao Isegai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction:
Institute of Medical Science, University of Tokyo, Laboratory of
Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass
sequencing and clone selection: Helix Research Institute (supported
by Japan Key Technology Center etc.).
FEATURES
source Location/Qualifiers
1. .1694
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

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/clone="OVARC1001030"  
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 misc\_difference 531  
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## ORIGIN

Alignment Scores:  
 Pred. No.: 4,238-83 Length: 1694  
 Score: 900.00 Matches: 182  
 Percent Similarity: 98.40% Conservative: 3  
 Best Local Similarity: 96.81% Mismatches: 3  
 Query Match: 97.30% Indels: 0  
 DB: 9 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AK075039 (1-1694)

QY 2 ValValAspLeuLeuTyrTyrArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 DB 788 GTTGTGACCTCTCTACTGGAGACATTAGAGACTGGAGTGGTGGTGTCTCAGC 847  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 DB 848 CTATTCTCTGCTTTCATTGACATTATTCAGCAATTTGTGAGCGTAACAGCCTACATTGCC 907  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 61  
 DB 908 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGGTGTGATCCAAAGCTATC 967  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 968 CAGAAATCAGATGAGGCCACCATTCAGGCAATCTGGAATCTGAAGTTGCTATATCT 1027  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 DB 1028 GAGGAGTTGGTTTCAAGATACAGTAATCTCTGCTTGTGTCATGTGAACCTGCACGATAAG 1087  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 DB 1088 GAACCTGAGCGCTCTCTTCTAGTTGATGATTTAGTTGATTTCTGAAGTTTGCAGTGTG 1147  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
 DB 1148 ATGTGGGTATTTACCTATGTTGGTGGCTGTTTAAATGTTCTGACACTACTGATTTGGCT 1207  
 QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 DB 1208 CTCAATTCACCTCTCAGTGTCTCTGTTTATTAAGCGCATCAGGCACAGATGATCAT 1267  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 DB 1268 TATCTAGGACTTGCAAATTAAGATGTTAAAGATGCTATGGCTAAATCAAGCAAAATC 1327  
 QY 182 ProGlyLeuLysArgLysAlaAsp 189  
 DB 1328 CCTGATTTGAAGCGCAAGCTGAA 1351

## RESULT 79

BD083733

## LOCUS

BD083733 1980 bp DNA linear PAT 27-AUG-2002  
 DEFINITION  
 Nucleic acid sequence characterized in that expression is  
 potentiated in human neuroblastoma with good prognosis, in  
 comparison between human neuroblastoma with good prognosis and human  
 neuroblastoma with bad prognosis.

## ACCESSION

BD083733

## VERSION

BD083733.1 GI:22629343

## KEYWORDS

JP 2001321175-A/22.

## SOURCE

Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 1980)  
 Nakagawara,A.  
 Nucleic acid sequence characterized in that expression is  
 potentiated in human neuroblastoma with good prognosis, in  
 comparison between human neuroblastoma with good prognosis and human  
 neuroblastoma with bad prognosis  
 Patient: JP 2001321175-A 22 20-NOV-2001;  
 CHIBA PREF,HISAMITSU PHARMACEUTICAL CO INC  
 OS Homo sapiens (human)  
 PN JP 2001321175-A/22  
 PD 20-NOV-2001  
 PF 12-MAY-2000 JP 2000140387  
 PI AKIRA NAKAGAWARA  
 PC C12N15/09,C12Q1/02,C12Q1/68,G01N33/50,C12N15/00 CC Nucleic  
 acid sequence characterized in that expression is CC  
 potentiated in  
 CC human neuroblastoma with good prognosis, in comparison between  
 CC human  
 CC neuroblastoma with good prognosis and human  
 CC neuroblastoma with  
 CC prognosis bad  
 CC key  
 FH key  
 FT source  
 FT source  
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 /mol\_type="genomic DNA"  
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## FEATURES

Source  
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## ORIGIN

Alignment Scores:  
 Pred. No.: 8,318-83 Length: 1980  
 Score: 898.00 Matches: 182  
 Percent Similarity: 98.41% Conservative: 4  
 Best Local Similarity: 96.30% Mismatches: 3  
 Query Match: 97.08% Indels: 0  
 DB: 6 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BD083733 (1-1980)

QY 1 SerValValAspLeuLeuTyrTyrArgAspIleLysThrGlyValValPheGlyAla 20  
 DB 1006 TCAGTTGTGACCTCTCTACTGGAGACATTAGAGACTGGAGTGGTGGTGGTGC 1065  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 1066 AGCCTATTCCAGCTGCTTTCATTGACATATTGAGCAATTTGAGCGTAACAGCCTACATT 1125  
 QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 1126 GCCTGGGCCCTGCTCTCTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCT 1185  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 1186 ATCCAGAAATCAGATGAGGCCACCATTCAGGCAATCTGGAATCTGAGTGTCTATA 1245  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 DB 1246 TCTGAGGAGTTGGTTTCAAGATGATGATTAATCTGCTCTGCTGATGTAACCTGCACGATA 1305  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 1306 AAGAACTCAGCGCCCTCTCTTAGTTGATTTAGTTGATTTCTCTGGAGTTTCAGGTG 1365  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 DB 1366 TTGATGGGTATTTTACCTATGTTGGTGGCTGTTTAAATGTTCTGACACTACTGATTTTG 1425  
 QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 DB 1426 GCTCTCTATTCTCTCAGTGTCTCTGTTTATTAAGACGCGCATCAGGCACAGATAGAT 1485

QY 161 HisTyrLeuGlyLeuAlaIleHisSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 1486 CATTATCTAGGACTTGCATAAATAGAAATGTTAAAGATGCTATGGCTAAATAATCCAAGCAAAA 1545

QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
 Db 1546 ATCCCTGGATTGAAGCGCAAGCTGAA 1572

RESULT 80  
 BD097380 1980 bp DNA linear PAT 27-AUG-2002  
 LOCUS  
 DEFINITION Nucleic acid sequences characterized by their enhanced expression in good prognostic human neuroblastoma upon comparison between good prognostic human neuroblastoma and poor prognostic human neuroblastoma.

ACCESSION BD097380  
 VERSION BD097380.1 GI:22642954  
 KEYWORDS WO 0166733-A/22.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1980)  
 AUTHORS Nakagawa, A.  
 TITLE Nucleic acid sequences characterized by their enhanced expression in good prognostic human neuroblastoma upon comparison between good prognostic human neuroblastoma and poor prognostic human neuroblastoma.  
 JOURNAL Patent: WO 0166733-A 22 13-SEP-2001;  
 CHIBA PREF. HISAMITSU PHARMACEUTICAL CO INC, AKIRA NAKAGAWARA

COMMENT OS Homo sapiens (human)  
 FN WO 0166733-A/22  
 PD 13-SEP-2001  
 PF 02-MAR-2001 WO 2001JP001631  
 PR 07-MAR-2000 JP OOP 159195,12-MAY-2000 JP OOP 140387 PI  
 AKIRA NAKAGAWARA  
 PC C12N15/12, C12Q1/68  
 CC Nucleic acid sequences characterized by their enhanced expression in good prognostic human neuroblastoma upon comparison between good prognostic human neuroblastoma and poor prognostic human neuroblastoma  
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 CC human neuroblastoma and poor prognostic human neuroblastoma PH

Key source Location/Qualifiers  
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 FT /organism="Homo sapiens (human)"  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 8,31e-83 Length: 1980  
 Score: 898.00 Matches: 182  
 Percent Similarity: 98.41% Conservative: 4  
 Best Local Similarity: 96.30% Mismatches: 3  
 Query Match: 97.08% Indels: 0  
 DB: 6 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BD097380 (1-1980)

QY 1 SerValValAspLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
 Db 1006 TCAGTTGTTGACCTCTCTACTGAGAGACATTAAAGAGCTGAGTGGTGGTGGTCC 1065

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 1066 AGCCTATTCAGCTGCTTTTCATGACAGATTACAGATTGTGAGCGTAACAGCTACATT 1125

QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 1126 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAGCT 1185

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
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QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 Db 1246 TCTGAGGAGTTGGTTTCAGAAGTACAGTAATTCCTGCTCTTGGTCATGTGAACTGCACGATA 1305

QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 1306 AAGGAACCTCAGCGGCTCTTCTAGTGTGATGATTTAGTTCTCTGAGTTGCAAGTGCAGTG 1365

QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuLeu 140  
 Db 1365 TTGATGTGGTATTTTACCTATGTTGGTGCCTTTGTTTAATGGTCTGACACTACTGATTTTG 1425

QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 1426 GCTCTCAATTCCTCTTCTAGTGTCTGTTTATTAAGCGCATCAGGCACAGATAGAT 1485

QY 161 HistyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 1486 CATTATCTAGGACTTGCATAAATAGAAATGTTAAAGATGCTATGGCTAAATAATCCAAGCAAAA 1545

QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
 Db 1546 ATCCCTGGATTGAAGCGCAAGCTGAA 1572

RESULT 81  
 BD139293 994 bp DNA linear PAT 18-SEP-2002  
 LOCUS  
 DEFINITION Extended cDNA of secretory protein.  
 ACCESSION BD139293  
 VERSION BD139293.1 GI:23234238  
 KEYWORDS JP 2002508182-A/45.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 994)  
 AUTHORS Bouguerel, L., Duclert, A. and Edwards, J.B.D.M.  
 TITLE Extended cDNA of secretory protein  
 JOURNAL Patent: JP 2002508182-A 45 19-MAR-2002;  
 GENSET

COMMENT OS Homo sapiens (human)  
 PN JP 2002508182-A/45  
 PD 19-MAR-2002  
 PF 17-DEC-1998 JP 2000539136  
 PR 17-DEC-1997 US 60/069957,09-FEB-1998 US 60/074121 PR  
 13-APR-1998 US 60/081563,10-AUG-1998 US 60/096116 PI LYDIE  
 BOUGUEREL, AYMERIC DUCLERT, JEAN BAPTISTE DUMAS MILNE PI EDWARDS  
 PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC  
 C12N1/21,  
 PC C12N5/10, C12P21/02, C12Q1/68, C12N15/00, C12N5/00, C12N15/00 CC  
 Von Heijne matrix  
 CC score 8.6  
 CC seq ASLFLLLSLTVFS/IV Location/Qualifiers  
 FT key 35..631  
 FT CDS  
 FT sig\_peptide 35..160  
 FT polyA\_signal 901..906  
 FT polyA\_site 979..994.  
 FT Location/Qualifiers  
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ORIGIN  
 Alignment Scores:  
 Pred. No.: 7e-83 Length: 994  
 Score: 895.00 Matches: 182



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Percent Similarity: 98.40%      Conservative: 3
Best Local Similarity: 96.81%    Mismatches: 3
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DB: 6                           Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x BD139293 (1-994)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
DB 68 GTTGTGACCTCTCTGCTACTGGAGACATTAAGAGACTGGAGTGGTGTGGTCCAGC 127
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 128 CTATTCTGCTGCTTTCATTGACAGTATTACAGCAATGTGAGCGTAAACAGCCTACATTGCC 187
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 188 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGATATACAGGGTGTGATCCAGCTATC 247
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 248 CAGAAATCAGATGAAGCCCAACCAATTCAGGCGATATCTGGAATCTGAAATCTGCTATATCT 307
QY 82 GluGluLeuValGlnLysTyrSerIleValSerAlaLeuGlyHisValAsnSerThrIleLys 101
DB 308 GAGGAGTGTGGTTTCAGAAATGACAGTAAATCTGCTCTTGGTTCATGTGAACTGCAGCATAAAG 367
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 368 GAACTCAGCGCGCTCTCTTGTAGTATGATGATTTAGTGTATCTCTGAAATTTGACGTGTG 427
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
DB 428 ATGTGGTATTACCTATGTTGGTGGCTGTTTAAATGTTGCTGACACTACTGATTTGGCT 487
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
DB 488 CTCAATTCACCTCTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCGACAGATAGATCAT 547
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
DB 548 TATCTAGTACTTGCAGAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAATC 607
QY 182 ProGlyLeuLysArgLysAlaAsp 189
DB 608 CTGGAATGAAGCGCAAGCTGAA 631

RESULT 82
AB049853
LOCUS Macaca fascicularis brain cDNA, clone: QnpA-18952.
DEFINITION Macaca fascicularis brain cDNA, linear PRI 14-OCT-2000
ACCESSION AB049853
VERSION AB049853.1 GI:10801643
KEYWORDS fis (full insert sequence).
SOURCE Macaca fascicularis (crab-eating macaque)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
Cercopitheciinae; Macaca.
REFERENCE 1 (sites)
AUTHORS Osada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirai,M.,
Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
TITLE Isolation of full-length cDNA clones from macaque brain cDNA
libraries
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2162)
AUTHORS Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S.
TITLE Direct Submission
JOURNAL Submitted (11-OCT-2000) Katsuyuki Hashimoto, National Institute of
Infectious Diseases, Division of Genetic Resources; 23-1, Toyama
1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
(E-mail: khashi@nih.go.jp, URL: http://www.nih.go.jp/yoken/genebank/,
Tel: 81-3-5285-1111 (ex.2120), Fax: 81-3-5285-1181)

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COMMENT Lab host: TOP10
Vector: pME18S-FL3 (Acc.No. AB009864)
R. Site1: DraIII (CACTGATG)
R. Site2: DraIII (CACCATGTG)
Description: 1st strand cDNA was primed with an oligo (dT) primer
using specific 5' and 3' primers and amplified by PCR. The PCR
product was digested with SfiI and size selection was performed to
exclude fragments <1.5kb. The SfiI-digested PCR product was cloned
into distinct DraIII sites of pME18S-FL3. XhoI sites just outside
the DraIII sites can be used to isolate the cDNA insert. Libraries
were constructed by Sugano et al. (University of Tokyo, Institute of
Medical Science). Custom primer used for sequencing
( 5' end primer [CTTCTGCTCTAAAGTGGCG];
3' end primer [CGACCTGCAGCTCGAGCACA] ).
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KDMAKIQAKIPGLKRAE"
CDS
ORIGIN
Alignment Scores:
Pred. No.: 1,9e-82 Length: 2162
Score: 895.00 Matches: 180
Percent Similarity: 98.94% Conservative: 6
Best Local Similarity: 95.74% Mismatches: 2
Query Match: 96.76% Indels: 0
DB: 9 Gaps: 0
US-09-830-972-2_COPY_975_1163 (1-189) x AB049853 (1-2162)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
DB 596 GTTGTGACCTCTCTCTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 655
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 656 CTATTCTGCTGCTTTCATTGACAGTATTCAGCATTTGAGTGTAAACAGCCTACATTGCC 715
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 716 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 775
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 776 CAGAAATCAGATGAAGCGCACCCATTCAGGCGATATCTGGAATCTGGAATGTGCGATATCT 835
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
DB 836 GAGGAGTGTGGTTCAGAAATGACAGTAAATCTCTCTTGTGTCATGTGAACTGCAGCATAAAG 895
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 896 GAACTCAGCGCGCTCTCTTGTAGTATGATTTAGTATTCTCTGAGGTTGCGAGTGTG 955
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
DB 956 ATGTGGGTATTACCTATGTTGGTGGCTTGTAAATGCTCTGACGCTACTGATTTGGCT 1015

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QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 1016 CTCATTTCACCTCTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1075
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 1076 TATCTAGGACTTGCAATTAAGAATGTTAAAGATGCTATGGCTAAATCCAGCGAANAATC 1135
QY 182 ProGlyLeuLysArgLysAlaAsp 189
Db 1136 CCTGGATTGAAGCGCAAGCTGAA 1159

RESULT 83
LOCUS AR379837 2610 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 382 from patent US 6607879.
ACCESSION AR379837
VERSION AR379837.1 GI:40087471
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2610)
AUTHORS Cocks, B.G., Stuart, S.G. and Seilhamer, J.J.
TITLE Compositions for the detection of blood cell and immunological response gene expression
JOURNAL Patent: US 6607879-A 382 19-AUG-2003;
FEATURES
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Best Local Similarity: 96.83% Mismatches: 2
Query Match: 96.32% Indels: 1
DB: Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x AR379837 (1-2610)

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Db 1311 GTTGTGTTGACCTCTGTTACTGGAGAGACATTAAAGAGACATGGAGTGGTGTGGTCCAGC 1370
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr-IleAl 41
Db 1371 CTATTCTGCTGCTTTTCATTGACAGTATTTCAGCATTTGAGCGTAAACAGCCTCAAAATGTC 1430
QY 41 aLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaI 61
Db 1431 CTTGGCCCTGCTCTCTGTGACCATCAGCTTAGGATATACAGGGTGTGATCAACCTAT 1490
QY 61 eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 81
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QY 81 rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLy 101
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QY 101 sGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValle 121
Db 1611 GGAACCTCAGCGGCTCTCTTAGTGTGATTTAGTTGATTCCTCAGAGTTTGCAGTGT 1670
QY 121 uMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAl 141
Db 1671 GATGTGGGTATTTACCTATGTGGTCCCTTTGTTAAATGGTCTGACACTACTGATTTTGGC 1730
QY 141 aLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHi 161

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Db 1791 TTATCTAGGACTTGCAATTAAGAATGTTAAAGATGCTATGGCTAAATCCAGCAAAAT 1850
QY 181 eProGlyLeuLysArgLysAlaAsp 189
Db 1851 CCTGGTTGAAGCGCAAGCTGAA 1875

RESULT 84
LOCUS BX934715 1591 bp mRNA linear VRT 02-FEB-2004
DEFINITION Gallus gallus finished cdna, clone CHEST117m23.
ACCESSION BX934715
VERSION BX934715.1 GI:41635243
KEYWORDS
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
REFERENCE 1 (bases 1 to 1591)
AUTHORS Boardman, P.E., Bonfield, J.K., Brown, W.R.A., Carder, C., Chalk, S.E., Croining, M.D.R., Davies, R.M., Francis, M.D., Grafham, D.V., Hubbard, S.J., Humphray, S.J., Hunt, P.J., Maddison, M., McLaren, S.R., Niblett, D., Overton, I.M., Rogers, J., Scott, C.E., Taylor, R.G., Tickle, C. and Wilson, S.A.
TITLE Direct Submission
JOURNAL Submitted (02-FEB-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: chickest@bms.unist.ac.uk
COMMENT BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cdna sequencing project.
    This sequence is from the
    BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cdna collection,
    from a library constructed by Elizabeth Bosch. cDNA was prepared
    from RNA extracted from brain,
    and poly A-trimmed. EcoRI-NotI cut cDNA was then ligated into the
    vector. Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI
    Host: Escherichia coli DH10B.
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    /dev_stage="16 days"

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Pred. No.: 5-72e-81 Length: 1591
Score: 879.00 Matches: 174
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Best Local Similarity: 92.08% Mismatches: 6
Query Match: 95.03% Indels: 0
DB: Gaps: 5

US-09-830-972-2_COPY_975_1163 (1-189) x BX934715 (1-1591)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
Db 185 TCAGTTGTTGACCTCTTACTGGCGAGACATTAAAGACAGAGGAGTGGTGTGGTGGC 244
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 245 AGCTTGTTCCTGCTCTCATTAACAGTTCAGCATCTGAGCGGTGACGCTTACATT 304
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 305 GCCTTGGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAGGGAGTATTCCAGGCA 364

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QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
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QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrile 100
Db 425 TCTGAAGAGCTGATTACAGAAATACAGCAGTGTGTGCTTGGTTCACATCAACGGCACATC 484
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 485 AAGGAGCTGAGAGCGCTCTCTCTGTTGATGATCTGTTGATCTCTGAAGTTTCCAGTG 544
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db 545 TTGATGTGGGTGTTCACTTACGTGTGGTGGCTGTTTATGTTGCTGACATTACTGATATG 604
QY 141 AlaLeuLysSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 605 GCTTTGATTTCCGCTGTCAGTGTCTCTGTTATTTATGAGAGACATCAGGCCCGCATCGAC 664
QY 161 HistyLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
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QY 181 IleProGlyLeuLysArgLysAlaAsp 189
Db 725 ATCCCTGGGCTGAAGCGCAAACTGAG 751

RESULT 85
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LOCUS Gallus gallus neurite outgrowth inhibitor NOGO-A (NOGO) mRNA,
partial cds.
ACCESSION AY494005
VERSION AY494005.1 GI:42528324
KEYWORDS Gallus gallus (chicken)
SOURCE Gallus gallus
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
Catharp,S.A., Pira,C.U., McNeill,D.S., Liwnicz,B.H. and Oberg,K.C.
1 (bases 1 to 2835)
Expression and Regulation of NOGO-A During Development of the Avian
Central Nervous System
Unpublished
JOURNAL 2 (bases 1 to 2835)
REFERENCE Catharp,S.A., McNeill,D.S., Pira,C.U. and Oberg,K.C.
AUTHORS Direct Submission
TITLE Submitted (02-DEC-2003) Anatomy, Loma Linda University, 24785
JOURNAL Stewart St. Evans Hall B09, Loma Linda, CA 92350, USA
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IKETKVSQSLTDYSTPTTTHLSQDVSEHKELAKLSPQFGKDLSPQVMPD
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/Note="NOGO-A specific probe"
1979..2835
/gene="NOGO"

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3'UTR
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Alignment Scores:
Pred. No.: 1,2e-80 Length: 2835
Score: 879.00 Matches: 174
Percent Similarity: 96.83% Conservatative: 9
Best Local Similarity: 92.06% Mismatches: 6
Query Match: 95.03% Indels: 0
DB: 5 Gaps: 0
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QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
Db 1409 TCAGTTGTTGACCTCTTACTGCGCAGACATTAAGAAGACAGGAGTGGTGTTCGTGCC 1468
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 1469 AGCTTGTTCCTGCTGCTCTCAATTAACAGTTCAGCATCGTGAGCGGTGACAGCTTACATT 1528
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 1529 GCCTTGGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAGGGAGTATCCAGGCA 1588
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 1589 ATCCAAAGTCCGATGAAGGCCATCCATTTAGGGCTTACTTGGAGTCTGATGACTGTG 1648
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrile 100
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QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
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QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db 1769 TTGATGTGGGTGTTCACTTACGTGTGGTGGCTTGTATATGCTCTGACATTACTGATCTG 1828
QY 141 AlaLeuLysSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 1829 GCTTTGATTTCCGCTGTTCAAGTGTTCCTGTTATTTATGAGAGACATCAGGCCCGCATCGAC 1888
QY 161 HistyLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 1889 CATTATTGGGACTAGTGAACAAGAACGTCAAAGATGCGATGCGCAAGATCCAAAGCAAAG 1948
QY 181 IleProGlyLeuLysArgLysAlaAsp 189
Db 1949 ATCCCTGGGCTGAAGCGCAAACTGAG 1975

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DEFINITION BX933922
ACCESSION BX933922
VERSION BX933922.1 GI:41634450
KEYWORDS Gallus gallus (chicken)
SOURCE Gallus gallus
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

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Phasianinae; Gallus.  
1 (bases 1 to 1363)  
REFERENCE Boardman,P.E., Bonfield,J.K., Brown,W.R.A., Carder,C., Chalk,S.E.,  
AUTHORS Croning,M.D.R., Davies,R.M., Francis,M.D., Graham,D.V.,  
Hubbard,S.J., Humphray,S.J., Hunt,P.J., Maddison,M., McLaren,S.R.,  
Niblett,D., Overton,I.M., Rogers,J., Scott,C.E., Taylor,R.G.,  
Tickle,C. and Wilson,S.A.  
Direct Submission  
Submitted (02-FEB-2004) Sanger Institute, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: chickstombs.umist.ac.uk  
COMMENT BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cdna  
sequencing project.  
This sequence is from the  
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cdna collection,  
from a library constructed by Elizabeth Bosch. cdna was prepared  
from RNA extracted from cerebrum, and poly A-trimmed. EcoRI-NotI  
cut cdna was then ligated into the vector. Vector: pBluescript II  
KS(+); Site 1: EcoRI; Site 2: NotI Host: Escherichia coli DH10B.  
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Percent Similarity: 96.81% Conservative: 9  
Best Local Similarity: 92.02% Mismatches: 6  
Query Match: 94.59% Indels: 0  
DB: 5 Gaps: 0  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x BX933922 (1-1363)  
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 177 GTTGTGACCTCTTACTGGCGAGACATTAGAGACAGGAGTGTGTGGTGCACG 236  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 237 TTGTTCTCGTCTCTCAATTAACAGTGTTCAGCATCGTGAGCGTGACAGCTTACATTCGC 296  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAlaIle 61  
Db 297 TTGGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAGGAGGATTCACAGGCAATC 356  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 357 CAAAGTCCGATGAAGCCCATCATTTAGGCTTACTTGGAGTCTCATGTAGTGTGTCT 416  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
Db 417 GAAGAGCTGATTGAGAAATACAGCAGTGTGTGCTTGGTCACATCAACGGCAGTCAAG 476  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 477 GAGCTGAGAGCGCTCTTCCTCGTGAAGTCTGGTGAATCTCTGAAGTTTCAGAGTTGTG 536  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
Db 537 ATGTGGGTGTTCATTACGTGTGTGCTGCTTTAATGGTCTGACATTTACTGATCTGGCT 596  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
Db 597 TTGATTTCGCTGTGTAGTGTCTCTGTTATTATTATGAGACATCAGGCCCATTCGACCAT 656  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

Db 657 TATTGGGACTAGTGAACAAGACGCTCAAGATGCGATGGCAAGATCCAGCAAGATC 716  
QY 182 ProGlyLeuLeuLysArgLysAlaAsp 189  
Db 717 CTGTGGGTGAAGCGCAAAACTGAG 740  
RESULT 87  
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DEFINITION Gallus gallus finished cdna, clone CHEST12704.  
ACCESSION CR353502  
VERSION CR353502.1 GI:45424789  
KEYWORDS Gallus gallus (chicken)  
SOURCE Gallus gallus  
ORGANISM Gallus gallus  
REFERENCE 1 (bases 1 to 1578)  
AUTHORS Boardman,P.E., Bonfield,J.K., Brown,W.R.A., Carder,C., Chalk,S.E.,  
Croning,M.D.R., Davies,R.M., Francis,M.D., Graham,D.V.,  
Hubbard,S.J., Humphray,S.J., Hunt,P.J., Maddison,M., McLaren,S.R.,  
Niblett,D., Overton,I.M., Rogers,J., Scott,C.E., Taylor,R.G.,  
Tickle,C. and Wilson,S.A.  
Direct Submission  
Submitted (09-MAR-2004) Sanger Institute, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: chickstombs.umist.ac.uk  
COMMENT BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cdna  
sequencing project.  
This sequence is from the  
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cdna collection,  
from a library constructed by Elizabeth Bosch. cdna was prepared  
from RNA extracted from cerebrum, and poly A-trimmed. EcoRI-NotI  
cut cdna was then ligated into the vector. Vector: pBluescript II  
KS(+); Site 1: EcoRI; Site 2: NotI Host: Escherichia coli DH10B.  
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Alignment Scores:  
Pred. No.: 1,46e-80 Length: 1578  
Score: 875.00 Matches: 173  
Percent Similarity: 96.81% Conservative: 9  
Best Local Similarity: 92.02% Mismatches: 6  
Query Match: 94.59% Indels: 0  
DB: 5 Gaps: 0  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x CR353502 (1-1578)  
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
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QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 354 CAAAGTCCGATGAAGCCCATCATTTAGGCTTACTTGGAGTCTCATGTAGTGTGTCT 413  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101



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CC Topology: Linear; Location/Qualifiers.
FH Key Location/Qualifiers
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Score: 871.50 Matches: 179
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Best Local Similarity: 94.71% Mismatches: 2
Query Match: 94.22% Indels: 5
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VERSION AX099401.1 GI:13538524
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AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Jacobs,K., McCoy,J.M., Lavallie,E.R., Collins-Racie,L.A., Evans,C.,
Merberg,D., Treacy,M., Bowman,M.R., Spaulding,V. and Agostino,M.J.

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DEFINITION Xenopus laevis RTN4.1-A3 (RTN4) mRNA, complete cds; alternatively
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VERSION AY316195.1 GI:34809221
KEYWORDS Xenopus laevis (African clawed frog)
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ORGANISM Xenopus laevis
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AUTHORS Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
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REFERENCE
AUTHORS      1 (bases 1 to 3967)
Klinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hannbeck von
Hanwehr,S., Petrasch,B., Oertle,T., Schwab,M.E. and Stuermer,C.A.
TITLE        Identification of two NOGO/RTN4 genes and analysis of Nogo-A
JOURNAL      expression in Xenopus laevis
PUBMED       Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
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Stuermer,C.A.O.
TITLE        Direct Submission
JOURNAL      Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
Universitaetsstrasse 10, Konstanz 78457, Germany
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Xenopus laevis (bases 1 to 4024)
Klinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hannbeck von
Hanwehr,S., Petrasch,B., Oertle,T., Schwab,M.E. and Stuermer,C.A.
REFERENCE   Identification of two NOGO/RTN4 genes and analysis of Nogo-A
AUTHORS     expression in Xenopus laevis
Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
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2 (bases 1 to 4024)
Klinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hannbeck von
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TITLE       Direct Submission
JOURNAL     Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
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Klinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hannbeck von
Hanwehr, S., Petrausch, B., Oertle, T., Schwab, M.E. and Stuermer, C.A.
Identification of two NOGO/RTN4 genes and analysis of Nogo-A
expression in Xenopus laevis
Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
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JOURNAL
PUBMED
2 (bases 1 to 4060)
Klinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hannbeck von
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Stuermer, C.A.O.
Direct Submission
Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
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Best Local Similarity: 78.84% Mismatches: 19
Query Match: 82.59% Indels: 0
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TITLE       Identification of two NOGO/RTN4 genes and analysis of Nogo-A
            expression in Xenopus laevis
JOURNAL     Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
PUBMED     15019938
REFERENCE   2 (bases 1 to 1467)
AUTHORS     Klinger M., Diekmann H., Heinz D., Hirsch C., Hambeck von
            Hanwehr S., Petrusch B., Oertle T., Schwab M.E. and
            Stuermer, C.A.O.
TITLE       Direct Submission
JOURNAL     Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
            Universitaetsstrasse 10, Konstanz 78457, Germany
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            1 (bases 1 to 1758)
            Klinger M., Diekmann H., Heinz D., Hirsch C., Hambeck von
            Hanwehr S., Petrusch B., Oertle T., Schwab M.E. and Stuermer, C.A.
            Identification of two NOGO/RTN4 genes and analysis of Nogo-A
            expression in Xenopus laevis
            Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
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            Klinger M., Diekmann H., Heinz D., Hirsch C., Hambeck von
            Hanwehr S., Petrusch B., Oertle T., Schwab M.E. and
            Stuermer, C.A.O.
            Direct Submission
            Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
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Xenopodinae; Xenopus; Xenopus.
REFERENCE
1 (bases 1 to 1512)
Klein, S.L., Strausberg, R.L., Wagner, L., Pontius, J., Clifton, S.W.
and Richardson, P.
Genetic and genomic tools for Xenopus research: The NIH Xenopus
Initiative
Dev. Dyn. 225 (4), 384-391 (2002)
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2 (bases 1 to 1512)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,
Scherer, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
3 (bases 1 to 1512)
Klein, S. and Strausberg, R.
Direct Submission
Submitted (10-OCT-2003) National Institutes of Health, Xenopus Gene
Collection (XGC), National Institute of Child Health and Human
Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD
20892-7510, USA
NIH-MGC Project
Contact: XGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Igor Dawid
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@hgrl.nih.gov
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency analysis, Similarity but not identity to protein.

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Klinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hambeck von
Hanwehr,S., Petrusch,B., Oertle,T., Schwab,M.E. and Stuermer,C.A.
Identification of two NOGO/RTN4 genes and analysis of Nogo-A
expression in Xenopus laevis
Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
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Klinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hambeck von
Hanwehr,S., Petrusch,B., Oertle,T., Schwab,M.E. and
Stuermer,C.A.O.
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Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
Universitaetsstrasse 10, Konstanz 78457, Germany
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TITLE	Identification of two NOGO/RTN4 genes and analysis of Nogo-A expression in Xenopus laevis		
JOURNAL	Mol. Cell. Neurosci. 25 (2), 205-216 (2004)		
PUBMED	15019938		
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AUTHORS	Klinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hannbeck von Hanwehr, S., Petrasch, B., Oertle, T., Schwab, M.E. and Stuermer, C.A.O.		
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JOURNAL	Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz, Universitaetstrasse 10, Konstanz 78457, Germany		
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RESULT 99
AY316188      3886 bp      mRNA      linear      VRT 25-MAY-2004
LOCUS
DEFINITION
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spliced.
ACCESSION
AY316188
VERSION
AY316188.1 GI:34809209
KEYWORDS
Xenopus laevis (African clawed frog)
ORGANISM
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus; Xenopus.
REFERENCE
1 (bases 1 to 3886)
Klinger M., Diekmann, H., Heinz, D., Hirsch, C., Hambeck von
Hanwehr, S., Petrusch, B., Oertle, T., Schwab, M.E. and Stuermer, C.A.
Identification of two NOGO/RTN4 genes and analysis of Nogo-A
expression in Xenopus laevis
Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
15019938
PUBMED
JOURNAL
Xenopus laevis (African clawed frog)
REFERENCE
2 (bases 1 to 3886)
Klinger M., Diekmann, H., Heinz, D., Hirsch, C., Hambeck von
Hanwehr, S., Petrusch, B., Oertle, T., Schwab, M.E. and
Stuermer, C.A.O.
Direct Submission
Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
Universitaetsstrasse 10, Konstanz 78457, Germany
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Alignment Scores:

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Pred. No.: 7,38e-67 Length: 3886
Score: 747.00 Matches: 147
Percent Similarity: 89.95% Conservative: 23
Best Local Similarity: 77.78% Mismatches: 19
Query Match: 80.76% Indels: 0
DB: 5 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x AY316188 (1-3886)

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RESULT 100
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LOCUS
DEFINITION
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spliced.
ACCESSION
AY316190
VERSION
AY316190.1 GI:34811716
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Xenopus laevis (African clawed frog)
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Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 3943)
Klinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hambeck von
Hanwehr, S., Petrusch, B., Oertle, T., Schwab, M.E. and Stuermer, C.A.
Identification of two NOGO/RTN4 genes and analysis of Nogo-A
expression in Xenopus laevis
Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
15019938
PUBMED
JOURNAL
Xenopus laevis (African clawed frog)
REFERENCE
2 (bases 1 to 3943)
Klinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hambeck von
Hanwehr, S., Petrusch, B., Oertle, T., Schwab, M.E. and
Stuermer, C.A.O.

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TITLE Direct Submission
JOURNAL Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
FEATUERS Universitaetsstrasse 10, Konstanz 78457, Germany
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Score: 747.00 Matches: 147  
Percent Similarity: 89.95% Conservative: 23  
Best Local Similarity: 77.78% Mismatches: 19  
Query Match: 80.76% Indels: 0  
DB: 5 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AY316190 (1-3943)

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Search completed: June 19, 2005, 08:51:41  
Job time : 2800 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005. Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 19, 2005, 04:27:16 ; Search time 354 Seconds  
(without alignments)  
3160.540 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163

Perfect score: 925

Sequence: 1 SWDLYWRDIKKTGWVFGA.....VKDAMAKIQAKIPGLKRRKAD 189

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Fgapop 6.0 , Fgapext 7.0  
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Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	922	99.7	2782	10 ADB85284	Adb85284 Rat fooco
5	921	99.6	1568	3 AAD01175	Aad01175 Rat neuro

6	913	98.7	734	12	ADF42781	Adf42781 Mouse CYP
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8	908	98.2	3579	4	AAF90324	Aaf90324 Human NOG
9	908	98.2	3579	6	ABK90134	Abk90134 DNA encod
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13	908	98.2	3833	3	AAO11174	Aao11174 Bovine ne
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PD 24-JUN-2004.  
XX  
PP 09-DEC-2003; 2003MO-EP013960.  
XX  
PR 10-DEC-2002; 2002GB-00028832.



CC growth, regeneration or maintenance are deficient or desired. The animal  
 CC models can be used in diagnostic and screening methods for predisposition  
 CC to disorders and to screen for or test molecules which can treat or  
 CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are  
 CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the  
 CC specification. However the specification does not include sequences for  
 CC these SEQ ID numbers

XX SQ Sequence 4684 BP; 1358 A; 1048 C; 1112 G; 1166 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.7e-100 Length: 4684  
 Score: 925.00 Matches: 189  
 Percent Similarity: 100.00% Conservativity: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAD01173 (1-4684)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
 DB 3175 TCAGTGTGTGACTCTCTACTGGAGACATTAAGAGACTGGAGTGGTGTGGTGGCC 3234  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 3235 AGCTTATTCTGCTGCTGCTGACAGTGTTCAGCATTTGTCAGTGAAGCGCTACATT 3294  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 3295 GCCTTGGCGCTCTCTCGTGACTATCAGCTTTAGGATATATAAGGGCGGTGATCCAGGCT 3354  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 3355 ATCCAGAAATCAGATGAGCCACCCTTCAGGCAATTTAGAAATCTGAAGTTCCTATA 3414  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 DB 3415 TCAGAGGAATGGTTTCAGAAATACAGTAATCTCTGCTTGGTTCATGTGAACAGCAATA 3474  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 3475 AAGAAGCTGAGCGCGCTTCTTAGTGTGATGATTTAGTTGATTCCTCCGAAGTTTCAGTG 3534  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 DB 3535 TTGATGTGGGTGTTTACTTAAGTGGTGGCTTGCTCAATGGTCTGACACTACTGATTTTA 3594  
 QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 DB 3595 GCTCTGATCTCACTCTTCAGTATTCTCTGTTATTTATGAACGGCATCAGGTGCAGATAGAT 3654  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 3655 CATTATCTAGGACTTGCACAAAGAGTGTTAGGATGCCATCGCCCAAAATCAAGCAAAA 3714  
 QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
 DB 3715 ATCCCTGGATTGAGCGCAAGACAGAT 3741

## RESULT 3

ABN86600

ID ABN86600 standard; DNA; 4684 BP.

XX AC ABN86600;

XX DT 05-NOV-2002 (first entry)

XX DE Rat neurotransmitter receptor protein Nogo encoding DNA.

XX KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;

XX KW central nervous system; peripheral nervous system; tranquilizer; Nogo;

XX KW vulnary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;

KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;  
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;  
 KW neurotransmitter receptor; rat; gene; ds.

XX OS Rattus norvegicus.

XX FH Key Location/Qualifiers  
 FT CDS 253..3744  
 FT /\*tag= a  
 FT /product= "Nogo-A"

XX US2002072493-A1.

XX 13-JUN-2002.

XX 28-JUN-2001; 2001US-00893348.

XX 19-MAY-1998; 98IL-00124500.

XX 21-JUL-1998; 98WO-US014715.

XX 22-DEC-1998; 98US-00218277.

XX 19-MAY-1999; 99US-00314161.

XX (YEDA ) YEDA RES & DEV CO LTD.

XX Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;  
 PI Moalem G;

DR WPI; 2002-607255/65.

DR P-PSDB; ABB81074, ABB81076, ABB81077.

XX Promoting nerve regeneration and preventing neuronal degeneration in the  
 PT central/peripheral nervous system from injury/disease, comprises  
 PT administering nervous system-specific activated T cells/antigen, or  
 PT analogs/peptides.

XX Disclosure; Page 40-44; 93pp; English.

XX The invention relates to promoting nerve regeneration or conferring  
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the  
 CC central/peripheral nervous system (NS). The method involves administering  
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its  
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or  
 CC combinations. The method is useful for promoting nerve regeneration and  
 CC preventing neuronal degeneration in central/peripheral nervous system  
 CC from injury/disease, where the injury is spinal cord injury, blunt  
 CC trauma, penetrating trauma, hemorrhagic stroke, ischemic stroke or  
 CC damages caused by surgery such as tumor excision. The disease is not an  
 CC autoimmune disease or neoplasm. The disease results in a degenerative  
 CC process occurring in either gray or white matter or both. The disease is  
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,  
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and  
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such  
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral  
 CC neuropathies associated with various diseases, including but not limited  
 CC to uremia, porphyria, hypoglycemia, Sjogren Larsson syndrome, acute  
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary  
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption  
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-  
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins  
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia  
 CC telangiectasia, Friedreich's ataxia, amyloid polyneuropathies,  
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's  
 CC disease, or lipoproteinemia. The present sequence represents a DNA  
 CC encoding the rat neurotransmitter receptor protein Nogo (Nogo-A, Nogo-B  
 CC and Nogo-C), an example of NS-specific antigen

XX SQ Sequence 4684 BP; 1358 A; 1047 C; 1112 G; 1167 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.7e-100 Length: 4684  
 Score: 925.00 Matches: 189  
 Percent Similarity: 100.00% Conservativity: 0

Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ABB86600 (1-4684)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 DB 3175 TCAGTTGTTGACCTCTCTACTGGAGAGACATTAAAGAGACTGGAGTGGTGGTGGC 3234

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 3235 AGCTTATTCTGCTGCTGCTGAGAGTTCAGCAATGTCAGTGTACGGCCTACATT 3294

QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIlyGlyValIleGlnAla 60  
 DB 3295 GCCTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGCGGTGATCCAGGCT 3354

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleuGluSerGluValAlaIle 80  
 DB 3355 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATTTAGAAATCTGAAGTTGCTATA 3414

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 DB 3415 TCAGAGGAATGGTTCAGAAATACAGTAATCTGCTCTTGGTCAATGTCGACACCAATA 3474

QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 3475 AAGAACTGAGCGCGCTTTCTTAGTTGATGATTGATTTGATTCCTGAAGTTGCGAGTG 3534

QY 121 LeuMetTrpValPheThrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 DB 3535 TTGATGTTGGTGTCTTACTTATGTTGGTGGCTGTTTCAATGGTCTGACACTACTGATTTTA 3594

QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 DB 3595 GCTCTGATCTCACTCTTCAGTATCTCTGTTATTATGAACGGCATCAGTGCAGATAGAT 3654

QY 161 HisTyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 3655 CATTATCTAGGACTTGCAAAACAGAGTGTAAAGATGTCATGCGCAAAATCCAAAGCAAAA 3714

QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
 DB 3715 ATCCCTGGATTGAAGCGCAAGCAGAT 3741

RESULT 4  
 ADB85284  
 ID ADB85284 standard; DNA; 2782 BP.  
 XX  
 AC ADB85284;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 XX Rat foocen-m2 reticulon gene SEQ ID NO:165.  
 DE  
 XX rat; streptozocin; kinase; phosphatase; ion channel protein; receptor;  
 KW transporter; G-protein coupled receptor; GPCR; DNA-binding proteins;  
 KW protease; enzyme; analgesic; gene therapy; pain; diabetes; ds; gene.  
 XX  
 OS Rattus norvegicus.  
 XX  
 XX EP1284297-A2.  
 PN  
 XX  
 PD 19-FEB-2003.  
 XX  
 XX 26-JUL-2002; 2002BP-00255228.  
 PF  
 XX 27-JUL-2001; 2001GB-00018354.  
 PR  
 XX 07-FEB-2002; 2002GB-00002880.  
 XX  
 PA (WARN ) WARNER LAMBERT CO.  
 XX

PI Brooksbank RA, Dixon AK, Lee K, Pinnock RD;  
 XX WPI; 2003-364994/35.  
 DR P-PSDB; ADB85283.  
 XX  
 PT Use of gene sequence that is down-regulated in response to streptozocin-  
 PT induced diabetes, vector, host cell, animal, polypeptide and antibody, in  
 XX screening of compounds for treating or diagnosing pain.  
 PS Claim 1; Page 240-241; 256pp; English.  
 XX  
 CC The invention relates to a novel isolated gene sequence that is down-  
 CC regulated in the spinal cord in response to streptozocin-induced  
 CC diabetes, or comprising, hybridising or having at least 80% sequence  
 CC identity to a sequence whose expression products are kinases,  
 CC phosphatases, ion channel proteins, receptors, transporters, G-protein  
 CC coupled receptor proteins, DNA-binding proteins, proteases or enzymes,  
 CC given in the specification. A gene of the invention has analgesic  
 CC activity, and may have a use in gene therapy. The gene sequences, vector,  
 CC host cell, animal, polypeptide and antibody are useful for screening of  
 CC compounds for diagnosing or treating pain. The kits are useful for  
 CC simultaneous, separate or sequential detecting and/or quantifying down-  
 CC regulation of a gene sequence in the spinal cord of a mammal in response  
 CC to streptozocin-induced diabetes. The compound or pharmaceutical  
 CC composition is useful as a medicament for treating or diagnosing pain.  
 CC The present sequence represents a gene of the invention.  
 XX  
 SQ Sequence 2782 BP; 635 A; 728 C; 765 G; 654 T; 0 U; 0 Other;  
 XX

Alignment Scores:  
 Pred. No.: 1,89e-100 Length: 2782  
 Score: 922.00 Matches: 188  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 99.47% Mismatches: 0  
 Query Match: 99.68% Indels: 0  
 DB: 10 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADB85284 (1-2782)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 DB 1271 GCAGTTGTTGACCTCTCTACTGGAGAGACATTAAAGAGACTGGAGTGGTGGTGGC 1330

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 1331 AGCTTATTCTGCTGCTGCTGAGAGTTCAGCAATGTCAGTGTACGGCCTACATT 1390

QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 1391 GCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGCGCTGATCCAGGCT 1450

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 1451 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATTTAGAAATCTGAAGTTGCTATA 1510

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 DB 1511 TCAGAGGAATGGTTCAGAAATACAGTAATCTGCTCTTGGTCAATGTCAGTGTGAACAGCAATA 1570

QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 1571 AAGAACTGAGCGCGCTTTCTTAGTTGATGATTGATTCCTGAGTTCCTGAGTTCGAGTG 1630

QY 121 LeuMetTrpValPheThrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 DB 1631 TTGATGTTGGTGTCTTACTTATGTTGGTGGCTTGTTCATGCTGCTGACACTACTGATTTTA 1690

QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 DB 1691 GCTCTGATCTCACTCTTCAGTATCTCTGTTATTATGAACGGCATCAGTGCAGATAGAT 1750

QY 161 HisTyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180

```
Db 1751 CATTATCTAGGACTTCAACAAAGAGTGTAAAGGATGCCATGCCCAAAATCAAGCAAAA 1810
Qy 181 IleProGlyLeuLysArgLysAlaAsp 189
Db 1811 ATCCCTGGATTGAAGCCCAAGCAGAT 1837

RESULT 5
AAD01175
XX AAD01175 standard; cDNA; 1568 BP.
AC AAD01175;
XX
XX 02-NOV-2000 (first entry)
XX
XX Rat neurite growth inhibitor Nogo C cDNA.
XX
XX Rat; neurite growth inhibitor; Nogo C; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening; ss.
XX
XX Rattus sp.
XX
XX Key Location/Qualifiers
XX CDS 1..1566
XX /*tag= a
XX /product= "Nogo C protein (residues 40-238) flanked by 1-
XX 39 residues at the N-terminal and 239-522 residues at the
XX C-terminal"
XX /transl_except= (pos:7..9, aa:Xaa)
XX /transl_except= (pos:85..87, aa:Xaa)
XX /transl_except= (pos:787..789, aa:Xaa)
XX /transl_except= (pos:826..828, aa:Xaa)
XX /transl_except= (pos:841..843, aa:Xaa)
XX /transl_except= (pos:883..885, aa:Xaa)
XX /transl_except= (pos:889..891, aa:Xaa)
XX /transl_except= (pos:940..942, aa:Xaa)
XX /transl_except= (pos:952..954, aa:Xaa)
XX /transl_except= (pos:1003..1005, aa:Xaa)
XX /transl_except= (pos:1111..1113, aa:Xaa)
XX /transl_except= (pos:1120..1122, aa:Xaa)
XX /transl_except= (pos:1138..1140, aa:Xaa)
XX /transl_except= (pos:1216..1218, aa:Xaa)
XX /transl_except= (pos:1222..1224, aa:Xaa)
XX /transl_except= (pos:1228..1230, aa:Xaa)
XX /transl_except= (pos:1264..1266, aa:Xaa)
XX /transl_except= (pos:1297..1299, aa:Xaa)
XX /transl_except= (pos:1318..1320, aa:Xaa)
XX /transl_except= (pos:1357..1359, aa:Xaa)
XX /transl_except= (pos:1393..1395, aa:Xaa)
XX /transl_except= (pos:1444..1446, aa:Xaa)
XX /transl_except= (pos:1537..1539, aa:Xaa)
XX /note= "Xaa corresponds to in-frame stop codon; the CDS
XX does not end in a stop codon"
XX /partial
XX 118..120
XX misc_feature
XX /*tag= b
XX /note= "Start codon of Nogo C coding region"
XX 715..717
XX misc_feature
XX /*tag= c
XX /note= "Stop codon of Nogo C coding region"
XX
XX WO200031235-A2.
XX
XX 02-JUN-2000.
XX
XX 05-NOV-1999; 99WO-US026160.
XX
XX 06-NOV-1999; 98US-0107446P.
XX
```

```
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
XX Schwab ME, Chen MS;
XX
XX WPI; 2000-400052/34.
XX P-PSDB; AAY71312.
XX
XX Nogo proteins and nucleic acids useful for treating neoplastic disorders
XX of the central nervous system and inducing regeneration of neurons.
XX
XX Claim 23; Fig 14; 122pp; English.
XX
XX The present sequence is a cDNA encoding rat Nogo C protein which is a
XX potent neural cell growth inhibitor and is free of all central nervous
XX system (CNS) myelin material with which it is natively associated. Nogo
XX proteins and fragments displaying neurite growth inhibitory activity are
XX used in the treatment of neoplastic disease of the CNS e.g. glioma,
XX glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma,
XX haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma,
XX neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.
XX Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo
XX activity can be used to treat or prevent hyperproliferative or benign
XX dysproliferative disorders e.g. psoriasis and tissue hypertrophy.
XX Ribozymes or antisense Nogo nucleic acids can be used to inhibit
XX production of Nogo protein to induce regeneration of neurons or to
XX promote structural plasticity of the CNS in disorders where neurite
XX growth, regeneration or maintenance are deficient or desired. The animal
XX models can be used in diagnostic and screening methods for predisposition
XX to disorders and to screen for or test molecules which can treat or
XX prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are
XX referred in claim 32 and SEQ ID NO: 29 in disclosure of the
XX CC specification. However the specification does not include sequences for
XX these SEQ ID numbers
XX
XX SQ Sequence 1568 BP; 435 A; 274 C; 375 G; 484 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 1..11e-100 Length: 1568
XX Score: 921.00 Matches: 188
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 99.57% Indels: 0
XX DB: 3 Gaps: 0
XX
XX US-09-830-972-2_COPY_975_1163 (1-189) x AAD01175 (1-1568)
XX
XX Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
XX 151 GTTGTTCACCTCTCTACTCGAGAGACATTAAGAAGACTGGAGTGTGTTGGTCCAGC 210
XX
XX Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
XX 211 TTATTCCTCGCTGCTCTCTGACAGTGTTCAGCATTTGTCAAGTGTAAACGGCTTACATTGCC 270
XX
XX Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
XX 271 TTGGCCCTGCTCTCGTGACACTATCAGCTTTAGGATATATAAGGGCGTGATTCAGGCTATC 330
XX
XX Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
XX 331 CAGAAATCAGATGAAGGCCACCCATTCAGGCGCATTTAGAAATCTGAAGTTGCTATATCA 390
XX
XX Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
XX 391 GAGGAATTGGTTTCAGAAATACAGTAATTTCTCTCTTGCTCATGTGTGAACAGCACATATAA 450
XX
XX Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
XX 451 GAACGTAGGCGGCTTTCTTCTTAGTGATTTAGTTGATTCCTCGAAGTTTGCAGTGTG 510
XX
XX 122 MetTrpValPheThrTyrValGlyValAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
```



QY 182 ProGlyLeuLysArgLysAlaAsp 189  
 |||||  
 Db 640 CCTGGATTGAAGCGCAAGACGAA 663

## RESULT 7

AAZ56886

ID AAZ56886 standard; DNA; 3579 BP.

XX

AC AAZ56886;

XX

DT 25-APR-2000 (first entry)

XX

DE Human MAGI polypeptide encoding DNA.

XX

KW MAGI protein; neuroendocrine-specific protein; neuropathy; human;  
 KW spinal injury; neuronal degeneration; neuromuscular disorder; cancer;  
 KW psychiatric disorder; developmental disorder; inflammatory disorder;  
 KW stroke; cytostatic; cerebroprotective; neuroprotective; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..3579

FT /\*tag= a

FT /product= "MAGI polypeptide"

XX

XX WO200005364-A1.

XX

XX PD 03-FEB-2000.

XX

XX PF 21-JUL-1999; - 99WO-GB002360.

XX

XX PR 22-JUL-1998; 98GB-00016024.

XX

XX PR 19-JUL-1999; 99GB-00016898.

XX

XX PA (SMIK ) SMITHKLINE BEECHAM PLC.

XX

XX PI Michalovich D, Prinjha RK;

XX

XX DR WPI; 2000-182693/16.

XX

XX DR P-PSDB; AAY56967.

XX

PT Novel polypeptides related to neuroendocrine-specific proteins and

PT polynucleotides useful for diagnosis of various diseases and for

PT treatment of cancer and neurological disorders.

XX

XX PS Claim 5; Page 19-20; 35pp; English.

XX

CC The invention relates to human MAGI protein, which is similar to  
 CC neuroendocrine-specific protein. The MAGI protein can be expressed by  
 CC standard recombinant methodology. The MAGI polypeptides, polynucleotides  
 CC and antibodies are useful for treating diseases, including neuropathies,  
 CC spinal injury, neuronal degeneration, neuromuscular disorders,  
 CC psychiatric disorders and developmental disorders, cancer, stroke and  
 CC inflammatory disorders. The polynucleotide is also useful for chromosome  
 CC localization and for tissue expression studies. The present sequence  
 CC represents a DNA encoding the human MAGI protein

XX

SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	1..31e-98	Length:	3579
Scores:	208.00	Matches:	184
Percent Similarity:	98.94%	Conservative:	3
Best Local Similarity:	97.35%	Mismatches:	2
Query Match:	98.16%	Indels:	0
DB:	3	Gaps:	0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAZ56886 (1-3579)

QY 1 SerValValAspLeuLeuTyrTrpArgAspLeuLysThrGlyValValPheGlyVala 20  
 |||||

Db 3010 TCAGTTGTGACCTCCTCTACTGGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGGC 3069

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40

Db 3070 AGCTATTTCCTGCTGCTTTCAATGACAGTATTGACGATTTGAGCGTAAACAGCCTACATT 3129

QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60

Db 3130 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGGTGTGATCCAAGCT 3189

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80

Db 3190 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGCGCATATCTGGATCTGAAGTTGCTATA 3249

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100

Db 3250 TCTGAGGAGTTGGTTTCAAGATACAGTAATTTCTGCTCTTGTGTCATGTGAACGACGATA 3309

QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120

Db 3310 AAGGAACCTCAGCGCCCTCTTCTTAGTTGATGATTAGTTGATTTCTCTGAAGTTTGACGTG 3369

QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140

Db 3370 TTGATGTGGGTATTTACCTATGTTGGTGCCTTGTGTTAATGCTCTGACACTACTGATTTTG 3429

QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160

Db 3430 GCTCTCATTTTCACGTCCTTCAGTGTTCTCTGTTATTTATGAACGCGCATCAGCGCAGATAGAT 3489

QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180

Db 3490 CATTATCTAGGACTTGCAATAAGAAATGTTAAAGATGCTATGGCTAAATCCAGCAAAA 3549

QY 181 IleProGlyLeuLysArgLysAlaAsp 189

Db 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

XX

XX RESULT 8

XX AAF90324

XX ID AAF90324 standard; cDNA; 3579 BP.

XX

XX AC AAF90324;

XX

XX DT 23-JUL-2001 (first entry)

XX

XX DE Human NOGO-A cDNA.

XX

XX KW NOGO-A; human; chromosome 2p21; neuropathy; spinal injury; brain injury;

XX KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;

XX KW neuromuscular disorder; psychiatric disorder; developmental disorder;

XX KW neuroprotective; neurotropic; neuroleptic; antiparkinsonian;

XX KW cerebroprotective; neuroleptic; diagnosis; therapy; ss.

XX

XX OS Homo sapiens.

XX

XX PN WO200136631-A1.

XX

XX PD 25-MAY-2001.

XX

XX PF 14-NOV-2000; 2000WO-GB004345.

XX

XX PR 15-NOV-1999; 99GB-00026995.

XX

XX PR 24-JAN-2000; 2000GB-00001550.

XX

XX PA (SMIK ) SMITHKLINE BEECHAM PLC.

XX

XX PI Michalovich D, Prinjha R;

XX

XX DR WPI; 2001-343822/36.

XX

XX DR P-PSDB; AAB82349.

XX

XX PT New polypeptide designated NOGO-C is a splice variant of the human NOGO

PT gene and may be useful in the treatment of neural disorders including

PS Alzheimer's and Parkinson's diseases.

XX Disclosure; Page 25-26; 25pp; English.

XX The present sequence is that of cDNA encoding human Nogo-A (see  
CC AAB82349). Nogo-A is a previously known splice variant of the human Nogo  
CC gene on chromosome 2p21. Nogo-A cDNA was obtained by PCR amplification of  
CC human spinal cord cDNA. The invention relates to a novel splice variant,  
CC Nogo-C (see AAF90323). It provides Nogo-C polypeptides and  
CC polynucleotides, and methods for producing such polypeptides by  
CC recombinant techniques. Also disclosed are methods for utilizing Nogo-C  
CC polypeptides and polynucleotides in the treatment of diseases including  
CC neuropathies, spinal injury, brain injury, stroke, neuronal degeneration,  
CC for example Alzheimer's disease and Parkinson's disease, neuromuscular  
CC disorders, psychiatric diseases and developmental disorders. Also  
CC provided are methods for identifying agonists and agonists for use in  
CC treating conditions associated with Nogo-C imbalance, and diagnostic  
CC assays for detecting diseases associated with inappropriate Nogo-C  
CC activity or levels

XX Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 1.31e-98 Length: 3579  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAF90324 (1-3579)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLeuThrGlyValValPheGlyAla 20  
Db 3010 TCAGTTGTTGACCTCTGCTAGTGGAGAGACATTAAAGAGACTGGAGTGGTGGTGGCC 3069  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 3070 AGCCTATTCTGCTGCTTTTCATTGACAGATTATTCAGCATTTGTGAGCGTAACAGCCTACAT 3129  
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 3130 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCT 3189  
QY 61 IleGlnLysSerAspGluGlyHisPropheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 3190 ATCCAGAAATCAGATCAGAGCCACCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3249  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
Db 3250 TCTGAGGAGTTGGTTCAGAGTACAGATAATCTCTGCTCTTGGTCATGTGAACCTGCACGATA 3309  
QY 101 LysGluLeuArgGluPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3310 AAGAACTCAGGCGCTCTCTTAGTTAGTATGATTAGTTAGTTCTCTGAAGTTTGAGTG 3369  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
Db 3370 TTGATGTTGGTATTACCTATGTTGTTGGCTTGTAAATGTTCTGACACTACTGATTTTG 3429  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db 3430 GCTCTCATTTCACTTCTAGTGTCTCTGTTATTTATTAACGGCATCAGGCGCATAGAT 3489  
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3490 CATTATCTAGGACTTGCATTAATAGAAATGTTAAGATGCTATGGCTAAATCCAGCAAAA 3549  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
Db 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

#### RESULT 9

ABK90134

ID ABK90134 standard; DNA; 3579 BP.

XX

AC ABK90134;

XX

DT 21-OCT-2002 (first entry)

XX

DE DNA encoding human NogoA protein.

XX

KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;  
KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;  
KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;  
KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;  
KW tissue hypertrophy; central nervous system; axon regeneration; NogoA;  
KW Nogo-associated disease; metastasis; gene; ds.

OS Homo sapiens.

XX

Key Location/Qualifiers  
CDS 1..3579

FT /\*tag= a

FT /product= "Human NogoA protein"

XX

WO200257483-A2.

XX

PD 25-JUL-2002.

XX

PF 18-JAN-2002; 2002WO-GB000228.

XX

PR 18-JAN-2001; 2001GB-00001312.

XX

(GLAX ) GLAXO GROUP LTD.

PA

(SMIK ) SMITHKLINE BEECHAM PLC.

XX

PI Blackstock WP, Hale RS, Prinjha R, Rowley A;

XX

DR WPI; 2002-599722/64.

XX

P-PSDB; ABG30938.

XX

PT Identifying modulators of Nogo or BACE activity for treating acute

PT neuronal injuries, neoplastic or dysproliferative disorders, comprises

PT providing and monitoring interaction between Nogo and BACE polypeptides.

XX

PS Disclosure; Page 53-58; 68pp; English.

XX

CC The present invention relates to a new method of identifying modulators  
CC of Nogo function or BACE activity. The method involves providing Nogo and  
CC BACE polypeptides capable of binding with each other, monitoring the  
CC interaction between these polypeptides, and determining if the test agent  
CC is a modulator of Nogo or BACE activity. The method is useful in treating  
CC acute neuronal injuries, such as spinal or head injury, stroke,  
CC peripheral nerve damage, and in neoplastic (e.g. glioblastomas,  
CC neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.  
CC cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue  
CC hypertrophy) of the central nervous system. The BACE polypeptide is  
CC useful in screening methods to identify agents that may act as modulators  
CC of BACE activity and in particular agents that may be useful in treating  
CC Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,  
CC and the polynucleotide encoding the BACE polypeptide are useful in  
CC manufacturing a medicament for the treatment or prevention of disorders  
CC responsive to the modulation of Nogo activity, in alleviating the  
CC symptoms or improving the condition of a patient suffering from this  
CC disorder, in axon regeneration, or in preventing metastasis or spreading  
CC of a cancer. The polynucleotide may also be an essential component in  
CC assays, a probe, in recombinant protein synthesis, and in gene therapy  
CC techniques. The present nucleic acid sequence encodes the human NogoA  
CC protein of the invention

SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.31e-98 Length: 3579





|||||  
3070 AGCCTATTCTGCTGCTTTTCATTCAGCATTTTCAGCATTTGTGAGCGTAAACAGCCTACATT 3129  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60  
Db 3130 GCCTTGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAGCT 3189  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleuGluSerGluValAlaIle 80  
Db 3190 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGAATCTGAAGTTGCTATA 3249  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
Db 3250 TCTGAGAGTTGTTTCTGAGAGTACAGTAATCTGCTCTTGGTCATGTGAACCTGCAGATA 3309  
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3310 AAGGAATCAGGCGCTCTCTTCTGATGATTAGTTGATTTCTGAAAGTTGCGAGTG 3369  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
Db 3370 TTGATGTGGGTATTTACCTATGTGTGCTGCTTTTAATGGTCTGACACTACTGATTTTG 3429  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db 3430 GCTCTCATTTCACTCTTCAGTGTCTCTGTTTATTAAGCGCATTCAGCGCGAGATAGAT 3489  
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3490 CATTATCTAGGACTTGCAATAGAATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAA 3549  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
Db 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

RESULT 11  
AD007886  
ID AD007886 standard; cDNA; 3579 BP.  
AC AD007886;  
XX  
DT 01-JUL-2004 (first entry)  
DE Human polynucleotide #65.  
XX  
KW Human; gene; ss; fat cell number; fat cell size; obesity; diabetes;  
KW anorectic; antidiabetic.  
XX  
OS Homo sapiens.  
XX  
FN US2004071700-A1.  
XX  
PD 15-APR-2004.  
XX  
PF 09-OCT-2002; 2002US-00267502.  
XX  
PR 09-OCT-2002; 2002US-00267502.  
XX  
PA (LIFE-) LIFE SCI DEV CORP.  
XX  
PI Kim J, Galant R;  
XX  
DR WPI; 2004-328526/30.  
DR P-PSDB; ADO08103.  
XX  
PT Identifying compounds that influence fat cell number or size for treating  
PT or preventing obesity or diabetes by exposing the cell to the agent and  
PT identifying fat cell number or size relative to cells not exposed to the  
PT agent.  
XX  
PS Claim 1; SEQ ID NO 212; 275pp; English.  
XX  
CC The invention relates to a method of identifying compounds that influence

CC fat cell number or size comprising providing a cell that expresses a gene  
CC and an agent, exposing the cell to the agent and identifying fat cell  
CC number or size relative to cells not exposed to the agent. The method  
CC also comprises providing an expression vector and an agent, exposing the  
CC vector to the agent, detecting a change in expression of the gene  
CC relative to expression of the gene in an expression vector not exposed to  
CC the agent, treating a subject with the agent and identifying fat cell  
CC number or size in the subject. The agent comprises an antisense  
CC oligonucleotide. The subject comprises a mammal, preferably a human. The  
CC method also comprises providing a polypeptide and an agent, exposing the  
CC polypeptide to the agent, detecting binding of the agent to the  
CC polypeptide or a change in an activity of the polypeptide, treating a  
CC subject with the agent and identifying fat cell number or size in the  
CC subject. The agent comprises an antibody. A method of regulating fat cell  
CC number or size comprises providing a subject containing fat cells and an  
CC agent that changes the expression of a gene, and treating the subject  
CC with the agent under conditions so that fat cell size or number in the  
CC subject is altered. The method is useful for identifying compounds that  
CC influence fat cell number or size, for preparing a composition for  
CC treating or preventing obesity or diabetes. This sequence represents  
CC human cDNA used in the scope of the invention.  
XX  
SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 1,318-98 Length: 3579  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 12 Gaps: 0  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x AD007886 (1-3579)  
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 3010 TCAGTTGTTGACCTCTCTGTACTGGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGC 3069  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 3070 AGCCTATTCTGCTGCTTTTCATTTGACAGTATTTCAGCATTTGTGAGCGTAAACGCTACATT 3129  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 3130 GCCTTGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAGCT 3189  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 3190 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGAATCTGAAGTTGCTATA 3249  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
Db 3250 TCTGAGAGTTGTTTCTGAGAGTACAGTAATCTGCTCTTGGTCATGTGAACCTGCAGATA 3309  
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3310 AAGGAATCAGGCGCTCTCTTCTGATGATTAGTTGATTTCTGAAAGTTGCGAGTG 3369  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
Db 3370 TTGATGTGGGTATTTACCTATGTGTGCTGCTTTTAATGGTCTGACACTACTGATTTTG 3429  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db 3430 GCTCTCATTTCACTCTTCAGTGTCTCTGTTTATTAAGCGCATTCAGCGCGAGATAGAT 3489  
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3490 CATTATCTAGGACTTGCAATAGAATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAA 3549  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
Db 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

```

RESULT 12
ADRL13965
ID ADRL13965 standard; cDNA; 3579 BP.
XX
AC ADRL13965;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human NOGO-A cDNA.
XX
KW ss; gene; human; myelin-associated glycoprotein; MAG; neural growth;
KW neural regeneration; apoptosis; amyotrophic lateral sclerosis;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
KW multiple sclerosis; Creutzfeldt-Jacob disease; Kuru;
KW multiple system atrophy; Lou Gehrig's disease;
KW progressive supranuclear palsy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..3579
FT /tag= a
FT /product= "NOGO-A"
XX
XX US2004121341-A1.
XX
XX 24-JUN-2004.
XX
XX 20-DEC-2002; 2002US-00327213.
XX
XX 20-DEC-2002; 2002US-00327213.
XX
XX (FILB/) FILBIN M T.
XX (DOME/) DOMENICONI M.
XX (CAOZ/) CAO Z.
XX
XX Filbin MT, Domeniconi M, Cao Z;
XX
XX WPI: 2004-479666/45.
XX P-PSDB; ADRL13966.
XX
XX New myelin-associated glycoprotein (MAG) derivative comprises a mutation
XX in or flanking MAG Ig-like domain 5 (Igds), excluding the MAG derivative
XX MAG (dl-3)-Fc, useful promoting neural growth and regeneration.
XX
XX Disclosure; SEQ ID NO 8; 81pp; English.
XX
XX The invention relates to a myelin-associated glycoprotein (MAG)
XX derivative comprising a mutation in or flanking MAG Ig-like domain 5
XX (Igds), excluding the MAG derivative MAG (dl-3)-Fc, where the mutation
XX reduces or eliminates the ability of the derivative to regulate neurite
XX outgrowth as compared to endogenous or soluble MAG without eliminating
XX binding to neuronal surfaces. The inhibitors of MAG are useful for
XX promoting neural growth and regeneration. They are also useful for
XX treating neural degeneration associated with injuries, disorders, or
XX diseases. The disorder, disease, or condition is associated with
XX apoptosis or results from a demyelinating disease and includes
XX amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease,
XX Huntington's disease, multiple sclerosis, Creutzfeldt-Jacob disease,
XX Kuru, multiple system atrophy, amyotrophic lateral sclerosis (Lou
XX Gehrig's disease), or progressive supranuclear palsy. The present
XX sequence represents the human NOGO-A cDNA.
XX
SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,31e-98 Length: 3579
Score: 908.00 Matches: 184
Percent Similarity: 98.94% Conservatives: 3
Best Local Similarity: 97.35% Mismatches: 2
Query Match: 98.16% Indels: 0
DB: 12 Gaps: 0

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US-09-830-972-2_COPY_975_1163 (1-189) x ADRL13965 (1-3579)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyVal 20
DB 3010 TCAGTTGTTGACCTCTCTGTGACCATCAAGAGAGACATTAAGAAAGCTGGAGTGTGTTGGTCC 3069
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 3070 AGCCTATTCTCTGCTGCTTCATTGACAGTATTACAGCATTTGTGAGCGTAACAGCTACATT 3129
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIlyGlyValIleGlnAla 60
DB 3130 GCCTTGGCCCTCTCTCTGTGACCATCAAGTATATCAAGGGTGTGATCCAAGCT 3189
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 3190 ATCCAGAAATCAGATGAAGGCCACCCCATTCAGGGCATATCTCGAAATCTCGAAGTTGCTATA 3249
QY 81 SerGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAenSerThrIle 100
DB 3250 TCTGAGGAGTTGGTTCAGNAGTACAGTAAATCTCTCTTGGTCATGTGAACTGCACGATA 3309
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
DB 3310 AAGGAACTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTG 3369
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuLeu 140
DB 3370 TTGATGGGTATTTACCTATGTTGGTGCCTTTGTTTAATGGTCTGACACTACTGATTTTG 3429
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
DB 3430 GCTCTCATTTCTACTCTTCAGTGTTCCTGTTATTATGAACGCATCAGCGCGCATAGAT 3489
QY 161 HisTyrLeuGlyLeuAlaAenLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
DB 3490 CATTATCTAGGACTTGCATAAATAAGAAATGTTAAAGATGCTATGGCTAAATCCAAGCAAAA 3549
QY 181 IleProGlyLeuLysArgLysAlaAsp 189
DB 3550 ATCCCTGGATTGAAGCGCAAAAGCTGAA 3576
RESULT 13
AD001174
ID AAD01174 standard; cDNA; 3833 BP.
XX
AC AAD01174;
XX
DT 02-NOV-2000 (first entry)
XX
DE Bovine neurite growth inhibitor Nogo cDNA.
XX
KW Bovine; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menigioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening; ss.
XX
OS Bos sp.
XX
XX WO200031235-A2.
XX
XX 02-JUN-2000.
XX
XX 05-NOV-1999; 99WO-US026160.
XX
XX 06-NOV-1998; 98US-0107446P.
XX (SCHW/) SCHWAB M E.
XX (CHEN/) CHEN M S.

```

XX Schwab ME, Chen MS;  
 XX WPI; 2000-400052/34.  
 XX Nogo proteins and nucleic acids useful for treating neoplastic disorders  
 PT of the central nervous system and inducing regeneration of neurons.  
 XX Claim 26; Fig 12; 122pp; English.  
 XX The present sequence is a cDNA encoding bovine Nogo protein which is a  
 CC potent neural cell growth inhibitor and is free of all central nervous  
 CC system (CNS) myelin material with which it is natively associated. The  
 CC present sequence was obtained from bovine spinal cord white matter cDNA  
 CC library. Nogo proteins and fragments displaying neurite growth inhibitory  
 CC activity are used in the treatment of neoplastic disease of the CNS e.g.  
 CC glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma,  
 CC pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma,  
 CC meningioma, neuroblastoma or retinoblastoma and degenerative nerve  
 CC diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which  
 CC promote Nogo activity can be used to treat or prevent hyperproliferative  
 CC or benign dysproliferative disorders e.g. psoriasis and tissue  
 CC hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to  
 CC inhibit production of Nogo protein to induce regeneration of neurons or  
 CC to promote structural plasticity of the CNS in disorders where neurite  
 CC growth, regeneration or maintenance are deficient or desired. The animal  
 CC models can be used in diagnostic and screening methods for predisposition  
 CC to disorders and to screen for or test molecules which can treat or  
 CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are  
 CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the  
 CC specification. However the specification does not include sequences for  
 CC these SEQ ID numbers  
 XX Sequence 3833 BP; 1235 A; 717 C; 818 G; 1063 T; 0 U; 0 Other;  
 SQ

Alignment Scores:  
 Pred. No.: 1,44e-98 Length: 3833  
 Score: 908.00 Matches: 184  
 Percent Similarity: 98.94% Conservative: 3  
 Best Local Similarity: 97.35% Mismatches: 2  
 Query Match: 98.16% Indels: 0  
 DB: 3 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAD01174 (1-3833)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 XX  
 DB 2301 TCAGTTGTTGACCTCTCTACTGAGAGACATTAAAGAGACTGGAGTGGTGTGGTCC 2360  
 XX  
 QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 2361 AGCTTGTTCTGCTGCTGCTGCTGACAGTATTGAGCAATTTGAGTGTAAAGCGGCTACATT 2420  
 XX  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 2421 GCCTTGGCCCTGCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCT 2480  
 XX  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 2481 ATCCAGAAATCTGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGTATA 2540  
 XX  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 DB 2541 TCTGAGGAGTTGGTTCTGAGAAGTACAGCAATTTCTGCTCTTGGTCATGTTAACTGCACAATA 2600  
 XX  
 QY 101 LysGluLeuArgGluPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 2601 AAAGAACTCAGACGCTCTCTTAGTGTAGTATTTAGTTGATTTCTCTGAAGTTTGAGTG 2660  
 XX  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 DB 2661 TTGATGTGGGTATTTACCTATGTTGGTCTTGTTCATGCTGTGACACTACTAAATTTTG 2720  
 XX

QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArqHisGlnValGlnIleAsp 160  
 XX  
 DB 2721 GCTCTGATTTCACTCTTCTAGTGTCTTATTTATGAACGGCATCAGCGCAAAATAGAT 2780  
 XX  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 2781 CATTATCTGGGACTTGCATAATGAATGTTAAAGATGCTATGGCTAAATCCAGCAAAA 2840  
 XX  
 QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
 DB 2841 ATCCCTGGATTGAAGCGTAAAGCTGAA 2867  
 XX

RESULT 14  
 ID ADP45550 standard; cDNA; 3919 BP.  
 XX ADP45550;  
 XX AC ADP45550;  
 XX DT 09-SEP-2004 (first entry)  
 XX DE Human NogoA encoding cDNA SEQ ID NO:4.  
 XX KW binding molecule; human; NogoA; NiG; NiG-D20; NogoA\_623-640;  
 KW nerve repair; neuroprotective; gene therapy;  
 KW central nervous system injury; CNS injury; neurodegenerative disorder;  
 KW gene; ss.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT CDS 1..3579  
 FT FT /\*tag= a  
 FT FT /product= "NogoA"  
 XX PN WO2004052932-A2.  
 XX PD 24-JUN-2004.  
 XX PF 09-DEC-2003; 2003WO-EP013960.  
 XX PR 10-DEC-2002; 2002GB-00028832.  
 XX PA (NOVS ) NOVARTIS AG.  
 PA (NOVS ) NOVARTIS PHARMA GMBH.  
 PA (UY20-) UNIV ZUERICH.  
 XX PI Barske C, Mir AK, Oertle T, Schnell L, Schwab ME, Vitaliti A;  
 PI Zurini M;  
 XX WPI; 2004-468818/44.  
 DR F-PSDB; ADP45551.  
 XX New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-D20 or NogoA623-640, useful in preparing a composition for treating CNS injury or neurodegenerative disorders.  
 XX Example 1; SEQ ID NO 4; 121pp; English.  
 XX The present invention describes a binding molecule which binds to human NogoA polypeptide, human NiG, human NiG-D20 or human NogoA 623-640 with a dissociation constant of less than 1000nM. Also described: (1) a polynucleotide encoding the binding molecule; (2) an expression vector or system comprising the polynucleotide; (3) a host cell comprising the expression system; (4) a pharmaceutical composition comprising the binding molecule and a carrier or diluent; and (5) treating diseases associated with nerve repair. The binding molecule has neuroprotective activity, and can be used in gene therapy. The binding molecule is useful in preparing a composition for treating central nervous system (CNS) injury or neurodegenerative disorders. The present sequence encodes human NogoA, which is used in the exemplification of the present invention.  
 XX Sequence 3919 BP; 1168 A; 857 C; 890 G; 1004 T; 0 U; 0 Other;  
 SQ

```
Alignment Scores:
Pred. No.: 1,48e-98 Length: 3919
Score: 908.00 Matches: 184
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.35% Mismatches: 2
Query Match: 98.16% Indels: 0
DB: 12 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x ADP45550 (1-3919)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
DB 3010 TCAGTTGTTGACCTCTCTGTACTGGAGACATTAAGAGACTGGAGTGGTGTGGTCC 3069

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 3070 AGCCTATTCTCTGCTTCTTCATTGACAGTATTCAGCATTTGTGAGGTAACAGCCTACATT 3129

QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
DB 3130 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGTTGTGATCCAAGCT 3189

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 3190 ATCCAGAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3249

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
DB 3250 TCTGAGGAGTTGTTGAGAGTACAGTAATTTCTCTTGTGTCATGTGACTGACGATG 3309

QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
DB 3310 AAGGAACCTCAGCGGCTCTCTTAGTTGATGATTTAGTTGATCTCTGAAGTTTGCAGTG 3369

QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
DB 3370 TTGATGTGGGTATTTACCTATCTGTGCTGCTGTTGTTAAATGGTCTGACACTACTGATTTG 3429

QY 141 AlaLeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
DB 3430 GCTCTCATTTCTCTCTGAGTGTCTGTTATTATGAAGGCATCAGGCACAGATAGAT 3489

QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
DB 3490 CATTATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAA 3549

QY 181 IleProGlyLeuLysArgLysAlaAsp 189
DB 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

RESULT 15
AAS09453
ID AAS09453 standard; cDNA; 4053 BP.
XX AC AAS09453;
XX AC AAS09453;
DT 26-SEP-2001 (first entry)
DE Human cDNA encoding the Nogo protein.
XX Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein;
KW cranial trauma; cerebral trauma; spinal cord injury; stroke;
KW demyelinating disease; multiple sclerosis; monophasia demyelination;
KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis;
KW Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy;
KW Pelizaeus-Merzbacher disease; Spongy degeneration; Alexander's disease;
KW Canavan's disease; metachromatic leukodystrophy; viral infection;
KW Krabbe's disease; AB020693; ss.
XX Homo sapiens.
OS Key
XX Location/Qualifiers
FH 135. .3713
FT CDS
```

/\*tag= a  
/product= "Nogo protein"

WO200151520-A2.

19-JUL-2001.

12-JAN-2001; 2001WO-US001041.

12-JAN-2000; 2000US-0175707P.

26-MAY-2000; 2000US-0207366P.

29-SEP-2000; 2000US-0236378P.

(UYVA ) UNIV YALE.

Strittmatter SM;

WPI; 2001-442138/47.

P-PSDB; AAU09453.

Novel Nogo receptor protein useful for identifying modulator of Nogo protein or Nogo receptor protein, which is useful for treating central nervous system disorders.

Example 1; Page 95-100; 109pp; English.

The sequence (Genbank accession number AB0202693) encodes the human Nogo protein, a 250kDa myelin-associated axon growth inhibitor. The invention relates to the use of the nogo receptor, nogo protein, their nucleic acids, vectors expressing them and antibodies against them, to isolate agents which block nogo receptor mediated axonal growth. The agent is useful for treating a central nervous system disorder which is a result of cranial or cerebral trauma, spinal cord injury, stroke or a demyelinating disease selected from multiple sclerosis, monophasia demyelination, encephalomyelitis, multifocal leukoencephalopathy, panencephalitis, Marchiafava-Bignami disease, pontine myelinolysis, adrenoleukodystrophy, Pelizaeus-Merzbacher disease, Spongy degeneration, Alexander's disease, Canavan's disease, metachromatic leukodystrophy, viral infection and Krabbe's disease

Sequence 4053 BP; 1189 A; 922 C; 922 G; 1020 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1,56e-98 Length: 4053  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAS09453 (1-4053)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20

DB 3144 TCAGTTGTTGACCTCTCTGTACTGGAGACATTAAGAGACTGGAGTGGTGTGGTCC 3203

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40

DB 3204 AGCCTATTCTCTGCTTCTTCATTGACAGTATTCAGCATTTGTGAGGTAACAGCCTACATT 3263

QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60

DB 3264 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGTTGTGATCCAAGCT 3323

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80

DB 3324 ATCCAGAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3383

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100

DB 3384 TCTGAGGAGTTGGTTTCAGAAAGTACAGTAATTTCTGCTCTTGTGTCATGTGAACCTGCAGATA 3443

QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120

Db 3444 AAGAACTCAGGCGCTCTCTAGTTGATGATTTAGTTGATTTCTCGAAGTTGCAGTG 3503  
 QY 121 LeuMetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 Db 3504 TTGATGGGTATTTACCTATGTTGGTGGCTTGTAAAGTCTGACACTACTGATTTG 3563  
 QY 141 AlaLeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 3564 GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 3623  
 QY 161 HisTyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 3624 CATTAATCTAGGACTTCGAATTAAGATGTTAAAGATGCTATGGCTAAATCAAGCAAAA 3683  
 QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
 Db 3684 ATCCCTGGATTGAGCGCAAGCTGAA 3710  
 RESULT 16  
 ACC81048  
 ID ACC81048 standard; cDNA; 4053 BP.  
 XX ACC81048;  
 XX 22-JUL-2003 (first entry)  
 DE Human NogoA gene.  
 KW Human: Nogo receptor; Ngr; CTS domain; neuroprotective; gene therapy;  
 KW axonal growth; central nervous system; CNS; Nogo; spinal cord injury;  
 KW cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;  
 KW demyelinating disease; multiple sclerosis; monophasic demyelination;  
 KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; gene;  
 KW ss.  
 XX Homo sapiens.  
 XX Key  
 FH 135. .3713  
 FT CDS  
 FT /\*tag= a  
 FT /product= "Human NogoA"  
 XX WO2003031462-A2.  
 PN 17-APR-2003.  
 XX 04-OCT-2002; 2002WO-US032007.  
 XX 06-OCT-2001; 2001US-00972599.  
 XX (UYAA ) UNIV YALE.  
 PA Strittmatter SM;  
 XX WPI; 2003-393433/37.  
 DR P-PSDB; ABR59667.  
 XX New human Nogo receptor polypeptides and nucleic acids, useful for  
 PT decreasing inhibition of axonal growth by a central nervous system  
 PT neuron, or in treating central nervous system disease, disorder or  
 PT injury, e.g. spinal cord injury.  
 XX Disclosure; Page 126-131; 148pp; English.  
 PS The invention relates to a novel nucleic acid encoding a polypeptide  
 CC comprising amino acid residues 27-309 of a 473 amino acid sequence (P1,  
 CC human Nogo receptor (Ngr) NLRRT domain), or residues 27-309 of P1 with  
 CC 1-20 conservative amino acid substitutions, and less than a complete CTS  
 CC domain, provided that a partial CTS domain, if present, consists of no  
 CC more than the first 39 consecutive residues. The nucleic acid of the  
 CC invention has neuroprotective activity. The polynucleotide may have a use  
 CC in gene therapy. The nucleic acid is useful for decreasing inhibition of

CC axonal growth by a central nervous system (CNS) neuron. The Ngr  
 CC polypeptide or an agent inhibits the binding of Nogo to Ngr or Ngr-  
 CC dependent signal transduction in the central nervous system neuron may be  
 CC used in treating central nervous system disease, disorder or injury, e.g.  
 CC spinal cord injury. Expression of an Ngr protein may be associated with  
 CC inhibition of axonal regeneration following cranial, cerebral or spinal  
 CC trauma, stroke or a demyelinating disease, such as multiple sclerosis,  
 CC monophasic demyelination, encephalomyelitis, multifocal  
 CC leukoencephalopathy, panencephalitis, or Krabbe's disease. The present  
 CC sequence is used in the exemplification of the invention  
 XX  
 SQ Sequence 4053 BP; 1189 A; 922 C; 922 G; 1020 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.56e-98 Length: 4053  
 Score: 908.00 Matches: 184  
 Percent Similarity: 98.94% Conservative: 3  
 Best Local Similarity: 97.35% Mismatches: 2  
 Query Match: 98.16% Indels: 0  
 DB: Gaps: 0  
 US-09-830-972-2\_COPY\_975\_1163 (1-189) x ACC81048 (1-4053)  
 QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 Db 3144 TCAGTTGTTGACCTCTGCTGAGAGACATTAAGAGACTGGAGTGGTGGTGGTGGTGGC 3203  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 3204 AGCCTATTCTGCTGCTTTCATTGACAGTATTTCAGCATTTGTGAGCGTAACAGCCTACATT 3263  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 3264 GCCTTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGTGTCACAGCT 3323  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 3324 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGCATATCTGGAAATCTGAAATGCTGATA 3383  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 Db 3384 TCTGAGGAGTTGGTTTCAGAAAGTACAGTAATTCCTGCTCTTGTGTCATGTGAACGTCACGATA 3443  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 3444 AAGGAACTCAGCGCCCTCTCTTAGTGTATGATTTAGTTGATTTCTCTGAAGTTTCAGTG 3503  
 QY 121 LeuMetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 Db 3504 TTGATGGGTATTTACCTATGTTGGTGGCTTGTAAAGTCTGACACTACTGATTTG 3563  
 QY 141 AlaLeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 3564 GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 3623  
 QY 161 HisTyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 3624 CATTAATCTAGGACTTCGAATTAAGATGTTAAAGATGCTATGGCTAAATCAAGCAAAA 3683  
 QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
 Db 3684 ATCCCTGGATTGAGCGCAAGCTGAA 3710  
 RESULT 17  
 ADP13574  
 ID ADP13574 standard; DNA; 4053 BP.  
 XX ADP13574;  
 AC ADP13574;  
 XX 26-AUG-2004 (first entry)  
 DT Renal cell carcinoma differentially expressed gene #310.  
 XX

KW ds; diagnosis; non-blood disease; solid tumor; gene expression;  
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;  
KW head/neck cancer; differential expression.

OS Homo sapiens.  
XX WO2004048933-A2.  
XX 10-JUN-2004.  
XX 21-NOV-2003; 2003WO-US037481.  
XX 21-NOV-2002; 2002US-0427982P.  
PR 03-APR-2003; 2003US-0459782P.  
XX (AMHP ) WYETH.  
PA (TWIN/) TWINE N C.  
PA (BURC/) BURCZYNSKI M E.  
PA (TREP/) TREPICCHIO W L.  
PA (DORN/) DORNER A.  
PA (STOV/) STOVER J A.  
PA (SLON/) SLONI D K.

XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;  
PI Sloni DK;

XX WPI; 2004-460799/43.

XX Diagnosing non-blood disease such as solid tumor, involves comparing  
PT differential expression profile of specific genes in peripheral blood  
PT sample of subject with reference expression profile of specific genes.

XX Disclosure; SEQ ID NO 310; 350pp; English.

XX The invention relate to a method of diagnosing (M1) non-blood disease  
CC such as solid tumor by providing peripheral blood sample of human having  
CC non-blood disease, and comparing an expression profile of specific genes  
CC in the peripheral blood sample to reference expression profile of the  
CC genes, where each of the genes is differentially expressed in peripheral  
CC blood mononuclear cells (PBMCs) of patients having the disease as  
CC compared to PBMCs of normal humans. The method is useful for diagnosing  
CC non-blood disease such as solid tumor. The solid tumor is chosen from  
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The  
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood  
CC sample is a whole blood sample (claimed). (M1) is useful for identifying  
CC genes that are differentially expressed in peripheral blood samples  
CC isolated at different stages of progression, development or treatment of  
CC RCC and/or solid tumors. This sequence corresponds to a gene that  
CC is differentially expressed and detected by the method of the invention.  
CC (Note: this sequence is not given as part of the printed specification  
CC but was obtained from WIPO in electronic format at  
CC ftp.wipo./pub/published\_pct\_sequences).

XX SQ Sequence 4053 BP; 1189 A; 922 C; 922 G; 1020 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1,566-98 Length: 4053  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 12 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADP13574 (1-4053)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleTyrThrGlyValValPheGlyAla 20  
Db 3144 TCAGTTGTTGACCTCCTGCTACTGGAGACATTAAAGAGCTGGAGTGGTGTGGTCC 3203  
Qy 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 3204 AGCCTATTCTCTGCTCTTTCATTGACAGTATTTCAGCATTTGTGAGCGTAACGCTACATT 3263

Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 3264 GCCTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAGCT 3323  
Qy 61 IleGlnIysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 3324 ATCCAGAAATCAGATGAAGGCCACCCCATTCAGGGCATATCTGGAATCTGGAAGTTGCTATA 3383  
Qy 81 SerGluGluLeuValGlnIysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
Db 3384 TCTGAGGAGTTGGTTTCAGAGTACAGTAATTTCTGCTCTTGGTCATGTCAGCTGCAGATA 3443  
Qy 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3444 AAGGAACCTCAGCGCCTCTCTTAGTTGATGATTAGTTGATTTCTCTGAAGTTTCAGTG 3503  
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuLeu 140  
Db 3504 TTGATGTGGGTATTTACCTATGTTGGTGCCTTGTATATGCTGCTGACACTACTGATTTTG 3563  
Qy 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db 3564 GCTCTCATTTTCACCTCTTCAGTGTTCCTGTTTATATGAACGGCATCAGGCACAGATAGAT 3623  
Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3624 CATTATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATAATCAACGAAAA 3683  
Qy 181 IleProGlyLeuLysArgLysAlaAsp 189  
Db ATCCCTGGATTGAAGCGCAAGCTGAA 3710

RESULT 18

AAA23454

ID AAA23454 standard; cDNA; 4093 BP.

AC AAA23454;

DT 19-JUN-2000 (first entry)

XX cDNA encoding human secreted protein vb22\_1, SEQ ID NO:63.

XX Human; secreted protein; cancer; tumour; cardiovascular disorder;  
KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;  
KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;  
KW neurodegenerative disease; asthma; contraceptive; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 152..1006

XX /\*tag= b

XX /product= "Clone vb22\_1 ORF2"

XX CDS 1048..3729

XX /\*tag= a

XX /product= "Human secreted protein vb22\_1"

XX WO200011015-A1.

XX 02-MAR-2000.

XX 24-AUG-1999; 99WO-US019351.

XX 24-AUG-1998; 98US-0097638P.

XX 24-AUG-1998; 98US-0097659P.

XX 09-SEP-1998; 98US-0099618P.

XX 28-SEP-1998; 98US-0102092P.

XX 25-NOV-1998; 98US-0109978P.

XX 23-DEC-1998; 98US-0113645P.

XX 23-DEC-1998; 98US-0113646P.

XX 23-AUG-1999; 99US-00379246.

XX (ALPH-) ALPHAGENE INC.

PA

XX Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;  
 XX WPI; 2000-224657/19.  
 XX P-PSDB; AAY95012, AAY95030.  
 XX New secreted or transmembrane proteins and polynucleotides encoding them,  
 XX useful for treating neurodegenerative disorders, autoimmune diseases and  
 XX cancer.  
 XX  
 XX Claim 72; Page 321-322; 357pp; English.  
 XX  
 XX The invention relates to 40 human secreted proteins (AAY94981-Y95020),  
 CC and cDNA sequences encoding them (AAA3423-A23462). The secreted proteins  
 CC of the invention include those that are thought to be only partially  
 CC secreted, i.e., transmembrane proteins. The proteins of the invention may  
 CC exhibit one or more activities selected from the following: cytokine  
 CC activity; cell proliferation; differentiation; immune modulation;  
 CC haematopoiesis regulation; tissue growth activity; activin/inhibin  
 CC activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic  
 CC activity; anti-inflammatory activity; and tumour inhibition activity. The  
 CC proteins may be administered to patients as vaccines, and the nucleotides  
 CC may be used as part of a gene therapy regime. Diseases or conditions that  
 CC may be treated using the proteins or nucleotides of the invention include  
 CC autoimmune diseases; genetic disorders; haemophilia; cardiovascular  
 CC diseases; cancer; bacterial, fungal and viral infections, especially HIV;  
 CC multiple sclerosis; rheumatoid arthritis; pulmonary inflammation;  
 CC Guillain-Barre syndrome; insulin dependent diabetes mellitus; and  
 CC allergic reactions such as asthma and anaemia. They may also be used for  
 CC treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal  
 CC diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease  
 CC and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin  
 CC activity may additionally be useful as contraceptives. Nucleic acid  
 CC sequences of the invention may be used in chromosome mapping, and as a  
 CC source of diagnostic primers and probes. The present sequence represents  
 CC cDNA encoding one of the 40 proteins of the invention  
 XX  
 XX Sequence 4093 BP; 1213 A; 926 C; 928 G; 1026 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1-58e-98 Length: 4093  
 Score: 908.00 Matches: 184  
 Percent Similarity: 98.94% Conservative: 3  
 Best Local Similarity: 97.35% Mismatches: 2  
 Query Match: 98.16% Indels: 0  
 DB: 3 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAA23454 (1-4093)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrClyValValPheGlyAla 20  
 DB 3160 TCAGTTGTTGACCTCTCTGACTGAGAGACATTAAAGAACCTGGAGTGTGTGGTCC 3219  
 QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 3220 AGCCTATTCTGCTGCTTTTCATTCAGCAGTATTTCAGCATTTGTGAGCCTAACAGCCTACATT 3279  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 3280 GCCTTGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAGCT 3339  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 3340 ATCCAGAAATCAGATCAAGGCCACCCATTGAGGCATATCTGGAATCTGAAGTTGCTATA 3399  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 DB 3400 TCTGAGAGTTGTTTTCAGAAAGTACAGTAATCTTCCTTGTTCATGTGAACTGCACGATA 3459  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 3460 AAGGAACCTCAGGCGCCTCTCTTAGTTGATGATTAGTTAGTTCTCTGAAGTTTGCAGTG 3519

QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 DB 3520 TTGATGTGGGTATTTACCTATGTTGGTCCCTTGTAAATGGTCTGACACTACTGATTG 3579  
 QY 141 AlaLeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 DB 3580 GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTAACGGCATCAGGCACAGATAGAT 3639  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 3640 CATTATCTAGGACTTGCATAAATAAGATGTTAAAGATGCTATGCTAAATCAAGCAAAA 3699  
 QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
 DB 3700 ATCCCTGGATTGAAGCGCAAAAGCTGAA 3726  
 RESULT 19  
 ABV94680  
 ID ABV94680 standard; cDNA; 4632 BP.  
 XX  
 AC ABV94680;  
 XX  
 DT 14-JAN-2003 (first entry)  
 XX  
 DE Human pancreatic cancer expressed cDNA SEQ ID NO 53.  
 XX  
 KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;  
 KW cytostatic; tumour; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200260317-A2.  
 PN  
 PD 08-AUG-2002.  
 XX  
 XX 30-JAN-2002; 2002WO-US002781.  
 XX  
 PR 30-JAN-2001; 2001US-0265305P.  
 PR 31-JAN-2001; 2001US-0265682P.  
 PR 09-FEB-2001; 2001US-0267568P.  
 PR 21-MAR-2001; 2001US-0278651P.  
 PR 28-APR-2001; 2001US-0287112P.  
 PR 16-MAY-2001; 2001US-0291631P.  
 PR 12-JUL-2001; 2001US-0305484P.  
 PR 20-AUG-2001; 2001US-0313999P.  
 PR 27-NOV-2001; 2001US-0333626P.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;  
 XX  
 XX WPI; 2002-627435/67.  
 DR P-PSDB; ABP68600.  
 XX  
 XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for  
 PT diagnosing, preventing and/or treating cancer, particularly pancreatic  
 PT cancer.  
 XX  
 PS Claim 1; SEQ ID NO 53; 300pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated polynucleotide (I) comprising: (a)  
 CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)  
 CC complements of (a); (c) sequences consisting of at least 20 contiguous  
 CC residues of (a); (d) sequences that hybridize to (a), under moderately  
 CC stringent conditions; (e) sequences having at least 75% or 90% identity  
 CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-  
 CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer  
 CC in a patient and compositions comprising polypeptides, polynucleotides,  
 CC antibodies, fusion proteins, T cell populations and antigen presenting  
 CC cells expressing the polypeptide are useful in treating pancreatic cancer  
 CC and stimulating an immune response. The polynucleotides can be used as  
 CC probes or primers for nucleic acid hybridisation, in the design and  
 CC preparation of ribozyme molecules for inhibiting expression of the tumour



CC polypeptides and proteins in the tumour cells, in vaccines and for gene  
CC therapy. Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 4632 BP; 1398 A; 1013 C; 1011 G; 1210 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.88e-98 Length: 4632  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 6 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ABV94680 (1-4632)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
Db 3151 TCAGTTGTTGACCTCCTGCTACTGGAGACATTAAGAAGACTGGAGTGGTGTGGTGCC 3210  
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 3211 AGCCTATTCTCGTCTTTCATTGACAGTATTCAGCATTTGAGCGTAACAGCCCTACATT 3270  
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 3271 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCT 3330  
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 3331 ATCCAGAAATCAGATGAAGGCCACCCATTCAAGGCATATCTGGAATCTGGAAGTTGCTATA 3390  
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
Db 3391 TCTGAGGAGTGGTTTCAGAGTACAGTAATCTGCTCTTGTGTCATGTGAACTGCACGATA 3450  
Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3451 AAGGNACTCAGCGCGCTCTTCTTAGTGATGATTTAGTTGATTTCTGAGATTGTCAGTG 3510  
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 3511 TTGATGTGGTATTATACCTATGTTGGTGCCTTGTGTTAATGCTCTGACACTACTGATTTG 3570  
Qy 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db 3571 GCTCTCATTTTCACCTCTTCAGTGTTCCTCTTATTTATGAACGGCATCAGGCACAGATAGAT 3630  
Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3631 CATTATCTAGACTTGCAAAATAGAAATGTTAAGATGCTATGGCTAAATATCAAGCAAAA 3690  
Qy 181 IleProGlyLeuLysArgLysAlaAsp 189  
Db 3691 ATCCCTGGATTGAAGCGCAAGCTGAA 3717

RESULT 20

ADG32772

ID ADG32772 standard; DNA; 4632 BP.

XX AC ADG32772;

XX DT 26-FEB-2004 (first entry)

XX DE Human DNA differentially expressed in patients with SLE SeqID96.

XX KW human; ds; autoimmune; chronic inflammatory disease; SLE;

XX KW systemic lupus erythematosus; rheumatoid arthritis; cholecystitis;

XX KW Sjogren's disease; CREST syndrome; scleroderma; ankylosing spondylitis;

XX KW ulcerative colitis; primary sclerosing cholangitis; appendicitis;

XX KW diverticulitis; primary biliary sclerosis.

OS Homo sapiens.

XX PN WO2003090694-A2.

XX PD 06-NOV-2003.

XX PF 24-APR-2003; 2003WO-US013015.

XX PR 24-APR-2002; 2002US-00131827.

XX PA (EXPR-) EXPRESSION DIAGNOSTICS INC.

XX PI Wohlgenuth J, Fry K, Woodward R, Ly N;

XX DR WPI; 2003-877243/81.

XX PT Diagnosing or monitoring autoimmune and chronic inflammatory diseases,  
XX PT such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative  
XX PT colitis, psoriasis and asthma by detecting the expression level of one or  
XX PT more genes.

XX PS Claim 18; SEQ ID NO 96; 877pp; English.

XX CC This invention relates to novel methods for diagnosing and monitoring  
XX CC autoimmune and chronic inflammatory diseases. Specifically, it refers to  
XX CC the identification of genes that have a clinical utility as diagnostic  
XX CC tools for the management of, in particular, patients with systemic lupus  
XX CC erythematosus (SLE) or rheumatoid arthritis (RA). Accordingly, the  
XX CC present invention describes a method for determining the levels of  
XX CC multiple differentially expressed genes of a patient, in a concerted  
XX CC manner, in order to achieve an improved diagnostic assay with sensitivity  
XX CC and specificity for the disease in question. As such, these genes are  
XX CC useful for the diagnosis of various other inflammatory disorders  
XX CC including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma,  
XX CC ankylosing spondylitis, ulcerative colitis, primary sclerosing  
XX CC cholangitis, appendicitis, diverticulitis, and primary biliary sclerosis.  
XX CC This polynucleotide is a DNA sequence representing human mRNA that is  
XX CC differentially expressed in patients with SLE, used in an exemplification  
XX CC of the invention.

XX SQ Sequence 4632 BP; 1398 A; 1013 C; 1011 G; 1210 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.88e-98 Length: 4632  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 6 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADG32772 (1-4632)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
Db 3151 TCAGTTGTTGACCTCCTGCTACTGGAGACATTAAGAAGACTGGAGTGGTGTGGTGCC 3210

Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 3211 AGCCTATTCTCGTCTTTCATTGACAGTATTCAGCATTTGAGCGTAACAGCCCTACATT 3270

Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 3271 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCT 3330

Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 3331 ATCCAGAAATCAGATGAAGGCCACCCATTCAAGGCATATCTGGAATCTGGAAGTTGCTATA 3390

Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
Db 3391 TCTGAGGAGTGGTTTCAGAGTACAGTAATCTGCTCTTGTGTCATGTGAACTGCACGATA 3450

Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120

Db 3451 AAGGAAGTCTGCTCTCTAGTTGATGATTTAGTCTCTGAAGTTTCAGRG 3510  
121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
3511 TTGATGTGGTATTTACCTATGTTGGTGCCTTTGTTAATGGTCTGACACTACTGATTTG 3570  
141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
3571 GCTCTCATTTCTCTCTAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 3630  
161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
3631 CATTATCTAGGACTTGCAAAATAGAAATGTTAAAGATGCTATGGCTAAATCCAGCAAAA 3690  
181 IleProGlyLeuLysArgLysAlaAsp 189  
3691 ATCCCTGGATTGAGCGCAAGCTGAA 3717

## RESULT 21

ABX34563  
ID ABX34563 standard; cDNA; 4698 BP.

AC ABX34563;

DT 13-FEB-2003 (first entry)

DE Human mddt cDNA SEQ ID 124.

XX MDDT; human; disease detection and treatment molecule polypeptide;  
KW anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;  
KW haemostatic; nephrotropic; antianemic; antipsoriatic; hepatotropic;  
KW gene therapy; protein replacement therapy; cell proliferative disorder;  
KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;  
KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;  
KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;  
KW psoriasis; hepatitis; gene; ss.

OS Homo sapiens.

XX WO200279449-A2.

XX 10-OCT-2002.

XX 27-MAR-2002; 2002WO-US009944.

XX 28-MAR-2001; 2001US-0279619P.

XX 29-MAR-2001; 2001US-0280067P.

XX 29-MAR-2001; 2001US-0280068P.

XX 16-MAY-2001; 2001US-0291280P.

XX 17-MAY-2001; 2001US-0291829P.

XX 17-MAY-2001; 2001US-0291849P.

XX 19-JUN-2001; 2001US-0299428P.

XX 20-JUN-2001; 2001US-0299776P.

XX 20-JUN-2001; 2001US-0300019P.

XX (INCY-) INCYTE GENOMICS INC.

XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;

PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;

PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;

PI Peralta CH, David ME, Lewis SA, Chen AJ, Panzer SR, Harris B;

PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;

XX WPI; 2003-058431/05.

DR P-PSDB; ABU11573.

XX

PT New purified disease detection and treatment molecule proteins and  
PT polynucleotides, useful for diagnosing, treating or preventing cancers  
PT (e.g. leukemia or sarcoma), anaemia, Crohn's disease, AIDS, osteoporosis  
PT or hepatitis.

XX Claim 1; SEQ ID NO 124; 339pp + Sequence Listing; English.

XX This invention describes a novel disease detection and treatment molecule  
CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,  
CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,  
CC antianemic, antipsoriatic and hepatotropic activity. The polynucleotides  
CC and the polypeptides of the invention can be used for gene therapy,  
CC protein replacement therapy and are useful for treating a variety of  
CC diseases or conditions. These polypeptides or polynucleotides are  
CC particularly useful for diagnosing, treating or preventing cell  
CC proliferative disorders (e.g. cancers including adenocarcinoma,  
CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's  
CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's  
CC syndrome, inflammation, osteoporosis, thrombocytopaenia, psoriasis or  
CC hepatitis. ABX3440-ABX34835 encode the MDDT polypeptides represented in  
CC ABU11450-ABU11845, described in the disclosure of the invention. NOTE:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

XX Sequence 4698 BP; 1410 A; 1028 C; 1022 G; 1238 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.91e-98 Length: 4698  
Score: 308.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 8 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ABX34563 (1-4698)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
Db 3155 TCAGTTGTGTACCTCTCTACTGAGAGACATTAGAAAGACTGGAGTGGTGTGGTGC 3214  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 3215 AGCCTATTCTCTGCTCTTTCATTGACAGTATTGACANTTGGAGCGTACAGCCCTACAT 3274  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 3275 GCCTTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCT 3334  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 3335 ATCCAGAAATCAGATGAAGGCCACCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3394  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
Db 3395 TCTGAGGAGTTGGTTTCAGAGTACAGTAACTCTGCTCTTGGTCATGTGACAGTACAGATA 3454  
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3455 AAGGAACCTCAGCGCCTCTCTTCTAGTATGATTTAGTTGATTTCTCTGAAGTTTCAGTG 3514  
QY 121 LeuMetTrpValPheThrTyrValGlyValAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
Db 3515 TTGATGTGGTATTTACCTATGTTGGTGCCTTGTGTTAATGGTCTGACACTACTGATTTTG 3574  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db 3575 GCTCTCATTTCTCTCTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 3634  
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3635 CATTATCTAGGACTTGCAAAATAGAAATGTTAAAGATGCTATGGCTAAATCCAGCAAAA 3694  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
Db 3695 ATCCCTGGATTGAGCGCAAGCTGAA 3721  
RESULT 22  
ADR83534



CC substantially purified and isolated polynucleotides which are co-  
 CC expressed with genes known to be involved in bone remodelling and  
 CC osteoporosis. The invention is used to diagnose disorders associated with  
 CC bone remodelling or osteoporosis. ABS70344-ABS70512 represent human bone  
 CC remodelling genes of the invention  
 XX  
 SQ Sequence 4822 BP; 1441 A; 1046 C; 1073 G; 1247 T; 0 U; 15 Other;

Alignment Scores:  
 Pred. No.: 1,98e-98 Length: 4822  
 Score: 908.00 Matches: 184  
 Percent Similarity: 98.94% Conservative: 3  
 Best Local Similarity: 97.35% Mismatches: 2  
 Query Match: 98.16% Indels: 0  
 DB: Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ABS70449 (1-4822)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 DB 3265 TCAGTTGTTGACCTCTCTGACTGGAGAGACATTAAAGAGACTGGAGTGGTGGTGGC 3324  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 3325 AGCCTATTCCTGCTGCTTCATGACAGTATTCAGCATTTGTGAGCGTAACAGCTACATT 3384  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIlysglyValIleGlnAla 60  
 DB 3385 GCCTTGGCCCTGCTCTCTGACCATCAGCTTAGGATATACAAGGGTGTGATCCAAGCT 3444  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluAlaIle 80  
 DB 3445 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3504  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 DB 3505 TCTGAGAGTTGGTTCAGAGTACAGTATTCCTGCTCTTGGTCATGTGACTGCACGATA 3564  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 3565 AAGGAACCTCAGGCGCTCTCTTAGTGTATGATTTAGTTGATCTCTGAAGTTGCAAGTG 3624  
 QY 121 LeuMetTrpValPheThrValGlyAlaLeuPheAsnGlnLeuThrLeuLeuLeu 140  
 DB 3625 TTGATGTGGGTATTTACCTATGTGTGGTCTGTTTAAATGGTCTGACACTACTGATTTG 3684  
 QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 DB 3685 GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTTATGACGGCATCAGGCACAGATAGAT 3744  
 QY 161 HisTyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 3745 CATTATCTAGGACTTGCAATAGAAATGTTAAAGATGCTATGCTTAAATCCAAAGCAAAA 3804  
 QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
 DB 3805 ATCCCTGGATTGAAGCGCAAGCTGAA 3831

RESULT 24

AD007888

ID AD007888 standard; cDNA; 3492 BP.

XX

AC

XX

AD007888;

01-JUL-2004 (first entry)

XX

Mouse polynucleotide #57.

XX

Mouse; gene; ss; fat cell number; fat cell size; obesity; diabetes;

XX

anorectic; antidiabetic.

XX

Mus sp.

XX

PN US2004071700-A1.  
 XX  
 PD 15-APR-2004.  
 XX  
 PF 09-OCT-2002; 2002US-00267502.  
 XX  
 PR 09-OCT-2002; 2002US-00267502.  
 XX  
 PA (LIFE-) LIFE SCI DEV CORP.  
 XX  
 PI Kim J, Galant R;  
 XX  
 DR WPI; 2004-328526/30.  
 DR P-PSDB; ADO08105.  
 XX  
 PT Identifying compounds that influence fat cell number or size for treating  
 PT or preventing obesity or diabetes by exposing the cell to the agent and  
 PT identifying fat cell number or size relative to cells not exposed to the  
 PT agent.  
 XX  
 PS Claim 1; SEQ ID NO 214; 275pp; English.  
 XX  
 CC The invention relates to a method of identifying compounds that influence  
 CC fat cell number or size comprising providing a cell that expresses a gene  
 CC and an agent, exposing the cell to the agent and identifying fat cell  
 CC number or size relative to cells not exposed to the agent. The method  
 CC also comprises providing an expression vector and an agent, exposing the  
 CC vector to the agent, detecting a change in expression of the gene  
 CC relative to expression of the gene in an expression vector not exposed to  
 CC the agent, treating a subject with the agent and identifying fat cell  
 CC number or size in the subject. The agent comprises an antisense  
 CC oligonucleotide. The subject comprises a mammal, preferably a human. The  
 CC method also comprises providing a polypeptide and an agent, exposing the  
 CC polypeptide to the agent, detecting binding of the agent to the  
 CC subject with the agent and identifying fat cell number or size in the  
 CC subject. The agent comprises an antibody. A method of regulating fat cell  
 CC number or size comprises providing a subject containing fat cells and an  
 CC agent that changes the expression of a gene, and treating the subject  
 CC with the agent under conditions so that fat cell size or number in the  
 CC subject is altered. The method is useful for identifying compounds that  
 CC influence fat cell number or size, for preparing a composition for  
 CC treating or preventing obesity or diabetes. This sequence represents  
 CC mouse cDNA used in the scope of the invention.  
 XX  
 SQ Sequence 3492 BP; 1035 A; 800 C; 817 G; 840 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1,91e-98 Length: 3492  
 Score: 906.50 Matches: 187  
 Percent Similarity: 98.95% Conservative: 1  
 Best Local Similarity: 98.42% Mismatches: 1  
 Query Match: 98.00% Indels: 1  
 DB: Gaps: 12

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADO07888 (1-3492)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValVal---PheGly 19  
 DB 2920 TCAGTTGTTGACCTCTCTGACTGGAGAGACATTAAAGAGACTGGAGTGGTGGT 2979  
 QY 20 AlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr 39  
 DB 2980 GCCAGCTTATTCCTGCTGCTCTGACAGTGTTCAGCATTTGTCAAGTGAAGCGCTAC 3039  
 QY 40 IleAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIlysglyValIleGln 59  
 DB 3040 ATTGCTTGGCCCTGCTCTCTGACTATCAGCTTAGGATATATAAGGGTGTGATCCAA 3099  
 QY 60 AlalleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAla 79  
 DB 3100 GCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTGGAAATCTGAAGTTGCC 3159

QY 80 IleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThr 99  
Db 3160 ATATCAGAGGAATTGGTTCCAGAAATATAGTAATTCCTGCTTGGTCATGTGAACAGCACA 3219  
QY 100 IleLysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAla 119  
Db 3220 ATAAAGAAATGAGCGCTCTCTCTTAGTTGATGATTTAGTTGATTCCTCGAAGTTGCA 3279  
QY 120 ValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeu 139  
Db 3280 GGTGTGATGGGTATTTACTTACGTGGTGCTTGTTCATATGGTTGACACTACTGATT 3339  
QY 140 LeuAlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIle 159  
Db 3340 TTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATATGAACGCGCATCGGCGCAGATA 3399  
QY 160 AspHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAla 179  
Db 3400 GATCATTTATCTAGGACTTGCACAAAGAGCGTTAAGGATGCCATGGCCAAATCCAAAGCA 3459  
QY 180 LysIleProGlyLeuLysArgLysAlaAsp 189  
Db 3460 AAAATCCCTGGATTGAGCGCAAGCAGAA 3489

## RESULT 25

AAF32725/c

ID AAF32725 standard; cDNA; 1758 BP.

XX AAF32725;

AC AAF32725;

XX AAF32725;

DT 23-MAR-2001 (first entry)

XX Human secreted protein gene 27 SEQ ID NO:37.

XX Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;  
XX antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;  
XX cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;  
XX fungicide; ophthalmological; autoimmune disease; rheumatoid arthritis;  
XX hyperproliferative disorder; neoplasm; cardiovascular disorder;  
XX cardiac arrest; cerebrovascular disorder; cerebral ischaemia; infection;  
XX angiogenesis; nervous system disorder; Alzheimer's disease; skin aging;  
XX ocular disorder; corneal infection; wound healing; food additive;  
XX preservative; ss.

XX Homo sapiens.

XX WO200077255-A1.

PN 21-DEC-2000.

PD 01-JUN-2000; 2000WO-US014926.

XX 01-JUN-2000; 2000WO-US014926.

XX 11-JUN-1999; 98US-0138628P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA Rosen CA, Ruben SM, Komatsoulis GA;

PI WPI; 2001-025337/03.

XX P-PSDB; AAB64448.

XX Isolated nucleic acid molecule encoding a human secreted protein is used

XX in preventing, treating or ameliorating a medical condition.

XX Claim 1; Page 495; 593pp; English.

XX The polynucleotide sequences given in AAF32699 to AAF32747 encode the

XX human secreted proteins given in AAB64422 to AAB64470. AAB64471 to

XX AAB64548 represent human secreted polypeptide sequences and proteins

XX homologous to them, which are given in the exemplification of the present

XX invention. Human secreted proteins have activities based on the tissues

XX and cells the genes are expressed in. Examples of activities include:

XX antiarthritic; immunosuppressive; antirheumatic; antiproliferative;

CC cytostatic; cardiant; vasotropic; cerebroprotective; neurotropic;  
CC neuroprotective; antibacterial; virucide; fungicide; and  
CC ophthalmological. The polynucleotides and polypeptides can be used to  
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,  
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used  
CC in diagnosing a pathological condition or susceptibility to a  
CC pathological condition. Disorders which are diagnosed or treated include  
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders  
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,  
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,  
CC infections caused by bacteria, viruses and fungi and ocular disorders  
CC e.g. corneal infection. The polypeptides can also be used to aid wound  
CC healing and epithelial cell proliferation, to prevent skin aging due to  
CC sunburn, to maintain organs before transplantation, for supporting cell  
CC culture of primary tissues, to regenerate tissues and in chemotaxis. The  
CC polypeptides can also be used as a food additive or preservative to  
CC increase or decrease storage capabilities. AAF32690 to AAF32698 and  
CC AAB64421 represent sequences used in the exemplification of the present  
CC invention

XX Sequence 1758 BP; 524 A; 380 C; 348 G; 504 T; 0 U; 2 Other;  
SQ

## Alignment Scores:

Pred. No.:	1.11e-98	Length:	1758
Score:	905.00	Matches:	183
Percent Similarity:	98.94%	Conservative:	4
Best Local Similarity:	96.83%	Mismatches:	2
Query Match:	97.84%	Indels:	0
DB:	4	Gaps:	0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAF32725 (1-1758)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
Db 1580 CGAGTTGTGTACCTCTGTACTGGAGAGACATTAAAGAGCTGGAGTGGTGGTGGC 1521  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 1520 AGCCTATTCCTGCTGCTTCATTGACAGTATTCAGCATTTGAGCGTAACAGCCTACAT 1461  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 1460 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCT 1401  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 1400 ATCCAGAAATCAGATGAGGCCACCCCATTCAGGCGCATATCTGGAATCTGAAAGTTGCTATA 1341  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
Db 1340 TCTGAGGAGTTGGTTTCAGAGTACAGTANTTCTGCTCTTGGTCATGTGACAGTACAGATA 1281  
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 1280 AAGGAACCTCAGCGCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTCAAGTTTCAGTG 1221  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuLeu 140  
Db 1220 TTGATGTGGGTATTTACCTATGTGTGGTCCCTTGTGTTATGTGCTGACACTACTGATTTTG 1161  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db 1160 GCTCTCATTTTCATCTTCAGTGGTTCCTGTTATTTATGAACGCGCATCAGGCACAGATAGAT 1101  
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 1100 CATTATCTAGGACTTGCAAAATGAAGATCTTAAAGATGCTATGGCTAAATCCAAAGCAAAA 1041  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
Db 1040 ATCCCTGGATTGAAGCGCAAGCTGAA 1014

RESULT 26  
AAAF90323  
ID AAF90323 standard; cDNA; 600 BP.  
XX  
AC AAF90323;  
XX  
DT 23-JUL-2001 (first entry)  
XX  
DE Human NOGO-C cDNA.  
XX  
KW NOGO-C; human; chromosome 2p21; neuropathy; spinal injury; brain injury;  
KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;  
KW neuromuscular disorder; psychiatric disorder; developmental disorder;  
KW neuroprotective; nootropic; neuroleptic; antiparkinsonian;  
KW cerebroprotective; neuroleptic; diagnosis; therapy; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200136631-A1.  
XX  
PD 25-MAY-2001.  
XX  
PF 14-NOV-2000; 2000WO-GB004345.  
XX  
PR 15-NOV-1999; 99GB-00026995.  
PR 24-JAN-2000; 2000GB-00001550.  
XX  
PA (SMIK ) SMITHLINE BECHAM PLC.  
XX  
PI Michalovich D, Prinjha R;  
XX  
WPI; 2001-343822/36.  
DR P-PSDB; AAB82348.  
XX  
PT New polypeptide designated NOGO-C is a splice variant of the human NOGO  
PT gene and may be useful in the treatment of neural disorders including  
PT Alzheimer's and Parkinson's diseases.  
XX  
PS Claim 1; Page 25; 25pp; English.  
XX  
CC The present sequence is that of cDNA encoding human NOGO-C (see  
CC AAB82348). NOGO-C is a novel splice variant of the human NOGO gene on  
CC chromosome 2p21. 2 Other splice variants, NOGO-A and NOGO-B, have  
CC previously been identified. The invention provides NOGO-C polypeptides  
CC and polynucleotides, and methods for producing such polypeptides by  
CC recombinant techniques. Also disclosed are methods for utilizing NOGO-C  
CC polypeptides and polynucleotides in the treatment of diseases including  
CC neuropathies, spinal injury, brain injury, stroke, neuronal degeneration,  
CC for example Alzheimer's disease and Parkinson's disease, neuromuscular  
CC disorders, psychiatric disorders and developmental disorders. Also  
CC provided are methods for identifying agonists and agonists for use in  
CC treating conditions associated with NOGO-C imbalance, and diagnostic  
CC assays for detecting diseases associated with inappropriate NOGO-C  
CC activity or levels  
XX  
SQ Sequence 600 BP; 161 A; 113 C; 144 G; 182 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 3.24e-99 Length: 600  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: Gaps: 4

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAF90323 (1-600)

QY 2 valValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 34 GTTGTGACCTCTGCTAGTGGAGAGACATTAAAGACATGGAGTGGTGTGGTGCAGC 93  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

Db 94 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTTGTCAGCGTAAACGCTACATGGC 153  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 154 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGTTGTGATCCAAGCTATC 213  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerClnuValAlaIleSer 81  
Db 214 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAATGCTATATCT 273  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
Db 274 GAGGAGTTGGTTTCAGAGTACAGTAATCTGCTCTTGGTCACTGTGACTGCACGATAAG 333  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 334 GAACTCAGGCGCTCTCTCTAGTATGATGATTTAGTATCTCTGAAGTTGTCAGTGTG 393  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuAla 141  
Db 394 ATGTGGGTATTTACCTATGTTGGTGCCTTGTATTAATGGTCTGACACTACTGATTTGGCT 453  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
Db 454 CTCATTTCACTCTTTCAGTGTCTCTGTTATTAATGAACGCATCAGGCACAGATATCAT 513  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 514 TATCTAGGACTTGCAAATAAGAAATGTTAAAGATGCTATGGCTAAATCCAGCAAAATC 573  
QY 182 ProGlyLeuLysArgLysAlaAsp 189  
Db 574 CCTGGATTGAAGCGCAAAAGCTGAA 597

RESULT 27  
AAAF72983  
ID AAF72983 standard; cDNA; 770 BP.  
XX  
AC AAF72983;  
XX  
DT 24-NOV-2000 (first entry)  
XX  
DE Human NSPH encoding cDNA sequence SEQ ID NO:3.  
XX  
KW Human; neuroendocrine-specific protein; NSPH; NSPA; NSPB; NSPC; ss.  
XX  
OS Homo sapiens.  
XX  
PN CN1253180-A.  
XX  
PD 17-MAY-2000.  
XX  
PF 30-OCT-1998; 98CN-00121473.  
XX  
PR 30-OCT-1998; 98CN-00121473.  
XX  
PA (UYFU-) UNIV FUDAN.  
XX  
PI Yu L, Zhao Y, Zhang H;  
XX  
WPI; 2000-466537/41.  
DR P-PSDB; AAB12805.  
XX  
PT Specific protein of human neuroendocrine, coding sequence and its  
PT preparing process and application.  
XX  
PS Claim 1; Page 14; 21pp; Chinese.  
XX  
CC The present invention relates to a new member of the human neuroendocrine  
CC specific protein family, designated NSPH. The present sequence encodes  
CC the human NSPH protein  
XX  
SQ Sequence 770 BP; 215 A; 136 C; 190 G; 229 T; 0 U; 0 Other;

```
Alignment Scores:
Pred. No.: 4,6e-99 Length: 770
Score: 904.00 Matches: 183
Percent Similarity: 98.94% Conservatives: 3
Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.73% Indels: 0
DB: 3 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x AAA72983 (1-770)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 114 GTTGTGACCTCTCTGACCATGACATTAAGAAGACTGGAGTGGTGTGGTCCAGC 173
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 174 CTATTCTGCTGCTCTTCATTGACGATTAATCAGCATTTGAGCGTAAACAGCCCTACATTGCC 233
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 234 TTGGCCCTGCTCTCTGACCATGACATTAAGAAGACTGGAGTGGTGTGGTCCAGCTATC 293
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 294 CAGAAATCAGATGAAGGCCACCCATTACGGGCATATCTGGAATCTGAAAGTTGCTATATCT 353
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 354 GAGGAGTGGTTCAGAAATGACATGATTAATCTGCTCTTGGTCATGTAAGCTGACGATNAAG 413
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 414 GAATCAGCGGCTCTCTTAGTATGATTTAGTTGATTTCTCTGAAAGTTGCAAGTGTG 473
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 474 ATGTGGGTATTTACCTATGTTGGTGCCTTGTAAATGCTGACACTACTGATTTGGCT 533
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 534 CTCAATTCACCTCTCAGTGTCTCTCTTATTTATGAACGGCATCAGGCGACATAGATCAT 593
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 594 TATCTAGGACTTGCAATTAAGATGTTAAAGATGCTATGGCTAATATCCAGCAAAATC 653
Qy 182 ProGlyLeuLysArgLysAlaAsp 189
Db 654 CTGGATTGAAGCGCAAGCTGAA 677

RESULT 28
AAV23695
ID AAV23695 standard; cDNA; 799 BP.
AC
XX
AC AAV23695;
XX
XX
XX 24-JUL-1998 (first entry)
XX
XX Human NSPLP protein A coding sequence.
DE
DE NSPLP; neuroendocrine-specific protein-like protein; human; gene therapy;
KW neurodegenerative disease; amyotrophic lateral sclerosis; cancer; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT 75..674
XX CDS /*tag= a
XX FT /product= "NSPLPA"
XX
XX
XX PN WO9806841-A2.
XX
```

```
PD 19-FEB-1998.
XX
XX 24-JUL-1997; 97WO-US013469.
XX
PR 12-AUG-1996; 96US-00700607.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Bandman O, Au-Young J, Goli SK, Hillman J;
XX
XX WPI; 1998-159533/14.
XX
XX P-PSDB; AAW53947.
XX
XX Human neuro-endocrine-specific protein-like proteins - useful for
XX diagnosis, monitoring and treatment of cancer and neuro-degenerative
XX disease.
XX
XX Claim 3; Page 38-39; 73pp; English.
XX
XX This sequence encodes a human neuroendocrine-specific protein-like
XX protein (NSPLP) of the invention. Recombinant cells transformed with the
XX DNA are used to express the NSPLP proteins, which are used to treat
XX cancer and neurodegenerative diseases such as amyotrophic lateral
XX sclerosis. Also antisense nucleic acids and antagonists of NSPLP can be
XX used to inhibit activity of the NSPLP proteins. Antibodies specific for
XX NSPLP are used for diagnosis and monitoring treatment of diseases
XX associated with NSPLP expression, in usual immunoassays, and to isolate
XX NSPLP from natural sources. The NSPLP proteins, or their fragments can
XX also be used in drug screening to identify NSPLP antagonists. The nucleic
XX acid can be used diagnostically and for monitoring treatment (in
XX hybridisation or amplification assays); to isolate closely related
XX sequences; in gene therapy for both sense and antisense applications
XX (including use of ribozymes) and for mapping the natural genomic sequence
XX
XX Sequence 799 BP; 218 A; 141 C; 196 G; 242 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.: 4,85e-99 Length: 799
Score: 904.00 Matches: 183
Percent Similarity: 98.94% Conservatives: 3
Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.73% Indels: 0
DB: 2 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x AAV23695 (1-799)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 108 GTTGTGACCTCTCTGACCATGACATTAAGAAGACTGGAGTGGTGTGGTCCAGC 167
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 168 CTATTCTGCTGCTCTTCATTGACGATTAATCAGCATTTGAGCGTAAACAGCCCTACATTGCC 227
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 228 TTGGCCCTGCTCTCTGACCATGACATTAAGAAGACTGGAGTGGTGTGGTCCAGCTATC 287
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 288 CAGAAATCAGATGAAGGCCACCCATTACGGGCATATCTGGAATCTGAAAGTTGCTATATCT 347
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 348 GAGGAGTGGTTCAGAAATGACATTAATCTCTTGGTTCATGTGAAGCTGCACGATAAG 407
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 408 GAATCAGCGGCTCTCTTAGTATGATTTAGTTGATTTCTGAAAGTTGCAAGTGTG 467
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 468 ATGTGGGTATTTACCTATGTTGGTGCCTTGTAAATGCTGACACTACTGATTTGGCT 527
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QY 142 LeuileSerLeuPheSerlleProValilleTyrGluArgHisGlnValGlnleAspHis 161  
 Db 528 CTCATTTCACCTCTCAGTCTCTCTGTTATTATGAACGCATCAGGCACAGATAGATCAT 587  
 QY 162 TyrLeuGlyLeuAlaAsnlySerVallyAspAlaMetAlaAlaSerlleGlnAlaValle 181  
 Db 589 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCCAAGCAAAATC 647  
 QY 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 648 CTGGATTGAAGCGCAAACTGAA 671

RESULT 29  
 AAZ56888  
 ID AAZ56888 standard; DNA; 1122 BP.  
 AC AAZ56888;  
 XX  
 XX 25-APR-2000 (first entry)  
 XX Human MAGI polypeptide variant encoding DNA.  
 DE  
 XX MAGI protein; neuroendocrine-specific protein; neuropathy; human;  
 KW spinal injury; neuronal degeneration; neuromuscular disorder; cancer;  
 KW psychiatric disorder; developmental disorder; inflammatory disorder;  
 KW stroke; cytostatic; cerebroprotective; neuroprotective; variant; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..1122  
 FT CDS /\*tag= a  
 FT /product= "MAGI polypeptide"  
 FT  
 XX WO200005364-A1.  
 PN  
 XX  
 PD 03-FEB-2000.  
 XX  
 XX 21-JUL-1999; 99WO-GB002360.  
 XX  
 PR 22-JUL-1998; 98GB-00016024.  
 PR 19-JUL-1999; 98GB-00016898.  
 XX  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 PA  
 XX  
 XX Michalovich D, Prinjha RK;  
 PI  
 XX  
 XX WPI; 2000-182693/16.  
 DR P-PSDB; AAY56969.  
 DR  
 XX  
 XX Novel polypeptides related to neuroendocrine-specific proteins and  
 PT polynucleotides useful for diagnosis of various diseases and for  
 PT treatment of cancer and neurological disorders.  
 XX  
 XX Claim 5; Page 21-22; 35pp; English.  
 PS  
 XX The invention relates to human MAGI protein, which is similar to  
 CC neuroendocrine-specific protein. The MAGI protein can be expressed by  
 CC standard recombinant methodology. The MAGI polypeptides, polynucleotides  
 CC and antibodies are useful for treating diseases, including neuropathies,  
 CC spinal injury, neuronal degeneration, neuromuscular disorders,  
 CC psychiatric disorders and developmental disorders, cancer, stroke and  
 CC inflammatory disorders. The polynucleotide is also useful for chromosome  
 CC localization and for tissue expression studies. The present sequence  
 CC represents a DNA encoding the human MAGI protein variant  
 XX  
 SQ Sequence 1122 BP; 224 A; 339 C; 316 G; 243 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 7.8e-99 Length: 1122  
 Score: 904.00 Matches: 183  
 Percent Similarity: 98.94% Conservative: 3

Best Local Similarity: 97.34% Mismatches: 2  
 Query Match: 97.73% Indels: 0  
 DB: 3 Gaps: 0  
 US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAZ56888 (1-1122)

QY 2 ValValAspLeuLeuTyrTyrArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 556 GTTGTGTGACCTCTCTACTCTGAGAGACATTAAGAAAGATGGAGTGGTGTGGTGGCCAGC 615  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerlleValSerValThrAlaTyrIleAla 41  
 Db 616 CTATTCCTGCTGCTTCATTGACAGTATTGACCATTTGAGCGTAAACAGCTTACATGGC 675  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 676 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGTATCCAAAGCTATC 735  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 736 CAGAAATCAGATGAAGGCCACCCATTGAGGGCATATCTGGAATCTGAAAGTTGCTATATCT 795  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 796 GAGGAGTTGGTTTCAGAGTACAGTAACTCTGCTCTTGGTCACTGTGAACGACGATAAAG 855  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 856 GAACTCAGCGGCTCTCTCTAGTTAGTATTAGTTAGTTCTCTGAAAGTTTCAGTGTGTTG 915  
 QY 122 MetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
 Db 916 ATGTGGGTATTTACCTATGTTGGTGGCTTTGTTTAAATGGTCTGACACTACTGATTTGGCT 975  
 QY 142 LeuIleSerLeuPheSerIleProValilleTyrGluArgHisGlnValGlnleAspHis 161  
 Db 976 CTCATTTCACCTCTCAGTGTCTCTCTGTTATTATGAACGCATCAGGCACAGATAGATCAT 1035  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerVallyAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 1036 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCCAAGCAAAATC 1095  
 QY 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 1096 CCTGGATTGAAGCGCAAAAGCTGAA 1119

RESULT 30  
 AAF90325  
 ID AAF90325 standard; cDNA; 1122 BP.  
 XX  
 AC AAF90325;  
 XX  
 DT 23-JUL-2001 (first entry)  
 XX  
 XX Human NOGO-B cDNA.  
 XX  
 KW NOGO-B; human; chromosome 2p21; neuropathy; spinal injury; brain injury;  
 KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;  
 KW neuromuscular disorder; psychiatric disorder; developmental disorder;  
 KW neuroprotective; nootropic; neuroleptic; antiparkinsonian;  
 KW cerebroprotective; neuroleptic; diagnosis; therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200136631-A1.  
 PN  
 XX  
 XX 25-MAY-2001.  
 PD  
 XX  
 XX 14-NOV-2000; 2000WO-GB004345.  
 PF  
 XX  
 XX 15-NOV-1999; 99GB-00026995.  
 PR  
 XX 24-JAN-2000; 2000GB-00001550.  
 XX



(SMIK ) SMITHKLINE BEECHAM PLC.

Michalovich D, Prinjha R;

WPI: 2001-343822/36.

P-PSDB; AAB82350.

New polypeptide designated NOGO-C is a splice variant of the human NOGO gene and may be useful in the treatment of neural disorders including Alzheimer's and Parkinson's diseases.

Disclosure; Page 27; 25pp; English.

The present sequence is that of cDNA encoding human NOGO-B (see AAB82350). NOGO-B is a previously known splice variant of the human NOGO gene on chromosome 2p21. The invention relates to a novel NOGO gene splice variant, NOGO-C (see AAF90323). It provides NOGO-C polypeptides and polynucleotides, and methods for producing such polypeptides by recombinant techniques. Also disclosed are methods for utilizing NOGO-C polypeptides and polynucleotides in the treatment of diseases including neuropathies, spinal injury, brain injury, stroke, neuronal degeneration, for example Alzheimer's disease and Parkinson's disease, neuromuscular disorders, psychiatric disorders and developmental disorders. Also provided are methods for identifying agonists and agonists for use in treating conditions associated with NOGO-C imbalance, and diagnostic assays for detecting diseases associated with inappropriate NOGO-C activity or levels.

Sequence 1122 BP; 224 A; 339 C; 316 G; 243 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	7.8e-99	Length:	1122
Score:	904.00	Matches:	183
Percent Similarity:	98.94%	Conservative:	3
Best Local Similarity:	97.34%	Mismatches:	2
Query Match:	97.73%	Indels:	0
DB:	4	Gaps:	0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAF90325 (1-1122)

QY	2	ValValAspLeuLeuTyrTyrArgAspIleLysThrGlyValValPheGlyAlaSer	21
DB	556	GTGTGTGACCTCCTCTACTGAGACACATTAAAGACTGGAGTGGTCTTTGGTGCCAGC	615
QY	22	LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla	41
DB	616	CTATTCTGCTGCTTTCATTGACAGTATTACAGATTGTGAGCTTACAGCTTACATTGCC	675
QY	42	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle	61
DB	676	TTGGCCCTGCTCTCTGTGACCATCAGCTTAGGATATACAAAGGTGTGATCCAGCTATC	735
QY	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer	81
DB	736	CAGAAATCAGATGAGAGGCCACCCATTCAGGCGCATATCTGGAATCTGGAAGTTGCTATATCT	795
QY	82	GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys	101
DB	796	GAGGAGTTGGTTTCAGAGTACAGTAAATTCCTCTGTGTCATGTGAATCGACGATAAAG	855
QY	102	GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu	121
DB	856	GAACCTCAGCGCCTCTCTTAGTTCATGATTAGTTGATTCTCTGAAGTTTGCAGTGTG	915
QY	122	MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla	141
DB	916	ATGTGGGTATTACCTATGTGTGTCCTTGTATATGCTGTGACACTACTGATTGTGCT	975
QY	142	LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis	161
DB	976	CTCATTTTCACCTCTTCAGTGTTCTCTCTTATTATGAACGGCATCAGGCACATAGATCAT	1035
QY	162	TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle	181

Db	1036	TATCTAGGACTTGCAATAGAAATGTTAAAGATGCTATGCTATAAATCCAGCAAAATC	1095
QY	182	ProGlyLeuLysArgLysAlaAsp	189
Db	1096	CCTGGATTGAAGCCAAAGCTGAA	1119
RESULT 31			
AAAX04379			
ID	AAAX04379	standard; DNA; 1213 BP.	
XX	AC	AAAX04379;	
XX	DT	13-APR-1999 (first entry)	
XX	DE	Human secreted protein gene 69 clone HAGFT48.	
XX	KW	Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; de;	
XX	KW	immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;	
XX	KW	inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;	
XX	KW	cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;	
XX	KW	osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;	
XX	KW	endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.	
XX	OS	Homo sapiens.	
XX	PN	W09856804-A1.	
XX	PD	17-DEC-1998.	
XX	PF	11-JUN-1998; 98WO-US012125.	
XX	PR	13-JUN-1997; 97US-0049547P.	
PR	13-JUN-1997; 97US-0049548P.		
PR	13-JUN-1997; 97US-0049549P.		
PR	13-JUN-1997; 97US-0049550P.		
PR	13-JUN-1997; 97US-0049556P.		
PR	13-JUN-1997; 97US-0049606P.		
PR	13-JUN-1997; 97US-0049607P.		
PR	13-JUN-1997; 97US-0049608P.		
PR	13-JUN-1997; 97US-0049609P.		
PR	13-JUN-1997; 97US-0049610P.		
PR	13-JUN-1997; 97US-0049611P.		
PR	13-JUN-1997; 97US-0050901P.		
PR	13-JUN-1997; 97US-0052989P.		
PR	08-JUL-1997; 97US-0051919P.		
PR	18-AUG-1997; 97US-0055984P.		
PR	12-SEP-1997; 97US-0058665P.		
PR	12-SEP-1997; 97US-0058668P.		
PR	12-SEP-1997; 97US-0058669P.		
PR	12-SEP-1997; 97US-0058750P.		
PR	12-SEP-1997; 97US-0058971P.		
PR	12-SEP-1997; 97US-0058972P.		
PR	12-SEP-1997; 97US-0058975P.		
PR	02-OCT-1997; 97US-0060834P.		
PR	02-OCT-1997; 97US-0060844P.		
PR	02-OCT-1997; 97US-0060865P.		
PR	02-OCT-1997; 97US-0061059P.		
PR	02-OCT-1997; 97US-0061060P.		
XX		(HUMA-) HUMAN GENOME SCI INC.	
XX	PI	Moore PA, Shi Y, Rosen CA, Ruben SM, Lafleur DW, Olsen HS;	
PI	PI	Ebner R, Brewer LA, Young P, Greene JM, Ferrie AM, Yu G, Ni J;	
PI	PI	Feng P;	
XX	XX	WPI; 1999-080881/07.	
DR	DR	P-PSDB; AAW78194.	
XX	XX	New isolated human genes and the secreted polypeptides they encode -	

PT useful for diagnosis and treatment of e.g. cancers, neurological  
PT disorders, immune diseases, inflammation or blood disorders.  
XX  
XX  
XX Claim 1; Page 235-236; 380pp; English.

XX This sequence represents a nucleic acid molecule which encodes a secreted  
CC human protein. The gene number, and the clone it is derived from, are  
CC detailed in the descriptor line. The gene can be used to generate fusion  
CC proteins by linking to the gene to a human immunoglobulin Fc portion  
CC (e.g. AAX04302) for increasing the stability of the fused protein as  
CC compared to the human protein only. The invention relates to 86 novel  
CC genes and their fragments (nucleic acid sequences: AAX04311-X04410; amino  
CC acid sequences AAW8126-W8225) which are useful for preventing, treating  
CC or ameliorating medical conditions e.g. by protein or gene therapy. Also,  
CC pathological conditions can be diagnosed by determining the amount of the  
CC new polypeptides in a sample or by determining the presence of mutations  
CC in the new polynucleotides. Specific uses are described for each of the  
CC 86 polynucleotides, based on which tissues they are most highly expressed  
CC in (see AAX04311 for described uses)

XX SQ Sequence 1213 BP; 335 A; 222 C; 297 G; 355 T; 0 U; 4 Other;

Alignment Scores:  
Pred. No.: 8.7e-99 Length: 1213  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: 0 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAX04379 (1-1213)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
DB 248 GTTGTGACCTCTCTGCTGAGAGACATTAAAGACCTGGAGTGGTGTGGTGGCAGC 307  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 308 CTATTCTCTCTCTCTGACAGTATTACAGATTGTGAGCGGTAAACACCTACATTGCC 367  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 368 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGATATATACAGGCTGTGATCCAGCTATC 427  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 428 CAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAACTGTCTATATCT 487  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 488 GAGGAGTTGGTTCAGAAAGTACAGTAATCTCTCTTGGTCATGTGAACCTGCAGCAAG 547  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 548 GAACCTCAGCGCCCTCTCTTAGTTGATGATTAGTTGATCTCTGAAGTTGCAGTTGG 607  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
DB 608 ATGTGGGTATTTACCTATGTTGGTCTGTTTAAATGGTCTGACACTACTGATTTTGGCT 667  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 668 CTCAATTCATCTCTCAGTGTCTCTGTTATTATTAAGACGGCATCAGGCACAGATAGATCAT 727  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 728 TATCTAGGACTTCGAATTAAGATGTTAAAGATGCTTATGGCTAATATCCAAAGCAAAATC 787  
QY 182 ProGlyLeuLysArgLysAlaAsp 189  
DB 788 CTTGGATTGAAGCGCAAAAGCTGAA 811

RESULT 32

ABA05903  
ID ABA05903 standard; cDNA; 1216 BP.  
XX  
XX AC ABA05903;  
XX  
XX DT 04-MAR-2002 (first entry)  
XX DE Human RTN4B encoding cDNA SEQ ID NO 3.  
XX KW Human; RTN4B; gene; ss.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX CDS 5..1126  
XX FT /\*tag= a  
XX FT /product= "RTN4B"  
XX PN CN1311439-A.  
XX PD 05-SEP-2001.  
XX PF 02-MAR-2000; 2000CN-00111791.  
XX PR 02-MAR-2000; 2000CN-00111791.  
XX PA (UYFU-) UNIV FUDAN.  
XX PI Yu L, Fu Q, Zhao Y;  
XX DR WPI: 2002-049934/07.  
XX DR P-PSDB; AAM47954.  
XX Human RTN 4B protein and coding sequence, its preparation and use.  
XX Claim 9; Page 20 (Disclosure); 27pp; Chinese.  
XX The invention relates to human RTN4B protein and coding sequence, useful  
CC for providing a cDNA sequence of human RTN4B. The protein is an isomer of  
CC RTN4 with RTN family members. The present invention also refers to  
CC polypeptide encoded by a nucleotide sequence and manufacturing method and  
CC application of the polypeptide and polynucleotide  
XX SQ Sequence 1216 BP; 256 A; 354 C; 341 G; 265 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 8.73e-99 Length: 1216  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: 0 Gaps: 0  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x ABA05903 (1-1216)  
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
DB 560 GTTGTGACCTCTCTGCTGAGAGACATTAAAGACCTGGAGTGGTGTGGTGGCAGC 619  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 620 CTATTCTCTCTCTCTTATTGACAGTATTACAGATTGTGAGCGGTAAACACCTACATTGCC 679  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 680 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGATATATACAGGCTGTGATCCAGCTATC 739  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 740 CAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAACTGTCTATATCT 799  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101

Db 800 GAGGAGTTGGTTTCAGAGTACAGTAATTCCTCTGTGTCATGTGAACTGCACGATAAAG 859  
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspLeuValPheAlaValLeu 121  
Db 860 GAATCAGCGCGCTCTCTTGTAGTATGATTTAGTTGATTTCTGAAAGTTTGCAGTGTG 919  
Qy 122 MetTrpValPheThrTyValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
Db 920 ATGTGGGTATTTACCTATGTTGGTCCCTGTTTAAATGCTGTGACACTACTGATTTGGCT 979  
Qy 142 LeuLeuSerLeuPheSerIleProValIleTyGluArgHisGlnValGlnIleAspHis 161  
Db 980 CTCATTTTCACCTCTTCAGTGTTCCTGTTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1039  
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaValIleGlnAlaIleVal 181  
Db 1040 TATCTAGACCTTGCANATPAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAATC 1099  
Qy 182 ProGlyLeuLysArgLysAlaAsp 189  
Db 1100 CCTGGATTGAAGCGCAAGCTGAA 1123  
RESULT 33  
ADI62860  
ID ADI62860 standard; cDNA; 1599 BP.  
XX AC ADI62860;  
XX DT 22-APR-2004 (first entry)  
XX DE Human apoptosis-associated cDNA SEQ ID 303.  
XX KW apoptosis; cell death; cytotoxic; neuroprotective; immunosuppressive;  
KW antiarthritis; antiarthritic; dermatologic; antineoplastic; antineoplastic;  
KW hepatocellular; virucide; nontoxic; anticonvulsant; antiparkinsonian;  
KW vasotropic; cerebroprotective; antialcoholic; gene therapy; tumour;  
KW autoimmune disease; degenerative disease; viral infection; leukaemia;  
KW carcinoma; sarcoma; multiple sclerosis; rheumatoid arthritis; diabetes;  
KW lupus; hepatitis; influenza viruses; Alzheimer's disease;  
KW Huntington's disease; Parkinson's disease; reperfusion injury; stroke;  
KW alcoholic liver disease; human; gene; ss.  
XX OS Homo sapiens.  
XX PN WO2003058021-A2.  
XX PD 17-JUL-2003.  
XX PF 13-JAN-2003; 2003WO-EP000270.  
XX PR 11-JAN-2002; 2002DE-01000856.  
XX XX (XANT-) XANTOS BIOMEDICINE AG.  
XX Koenig-Hoffman K, Kazinski M, Schaefer R, Kesper B;  
XX WPI; 2003-542134/51.  
XX New nucleic acids involved in apoptosis, useful for diagnosis and  
XX treatment of e.g. tumors and degenerative disease, also related proteins,  
XX antibodies and modulators.  
XX Claim 1b; SEQ ID NO 303; 517bp; German.  
XX This invention describes novel nucleic acid molecules that are associated  
XX with apoptosis and encode a polypeptide and are derived from a normalised  
XX gene library (embryonic or liver) or clone collections, and the extent of  
XX apoptosis measured by cell death detection assay or the CPRG assay  
XX (measuring loss of membrane integrity). The products of the invention  
XX have cytostatic, neuroprotective, immunosuppressive, antineoplastic,  
XX antiarthritic, dermatologic, antineoplastic, antiparkinsonian, vasotropic,  
XX nontoxic, anticonvulsant, antiparkinsonian, vasotropic, and can be used for gene  
XX cerebroprotective and antialcoholic activity and can be used for gene

CC therapy. The polynucleotides also related vectors, hosts (or their  
CC extracts), encoded polypeptide (or their receptors) and/or agents that  
CC inhibit their activity (including antisense sequences) are used for  
CC treatment or prevention of tumours, autoimmune or degenerative diseases  
CC and viral infections, specifically leukaemia, carcinoma, sarcoma,  
CC multiple sclerosis, rheumatoid arthritis, diabetes, lupus, or infection  
CC with hepatitis or influenza viruses, Alzheimer's, Huntington's or  
CC Parkinson's disease, reperfusion injury, stroke and alcoholic liver  
CC disease. Detection of the polynucleotides and derived polypeptides can  
CC also be used for diagnosis of these diseases. This sequence encodes an  
CC apoptosis-associated protein described in the disclosure of the  
CC invention.  
XX SQ Sequence 1599 BP; 354 A; 452 C; 422 G; 371 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 1.28e-98 Length: 1599  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: Gaps: 0  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADI62860 (1-1599)  
Qy 2 ValValAspLeuLeuTyTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 671 GTTGTTCACCTCTCTGTACTGGAGAGACATTAAGAGACTGGAGTGGTGTGGCCAGC 730  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyIleAla 41  
Db 731 CTATTCCTGCTGCTTTTCATTGACAGTATTACGATTGTGAGCGTAACAGCCTACATGCC 790  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyLysGlyValIleGlnAlaIle 61  
Db 791 TTGSCCTCTGCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAAGCTATC 850  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyTrpLeuGluSerGluValAlaIleSer 81  
Db 851 CAGAAATCAGATGAGGCCACCCATTCAGGCGCATCTCGAATCTGAAGTTGCTATATCT 910  
Qy 82 GluGluLeuValGlnLysTyTrpSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
Db 911 GAGGAGTTGGTTTCAAGAGTACAGTAATTCCTCTGTCATGTGAACCTGCACGATAAAG 970  
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspLeuValPheAlaValLeu 121  
Db 971 GAATCAGCGCGCTCTCTTCTAGTTGATGATTTAGTTGATTTCTCTGAAAGTTTGCAGTGTG 1030  
Qy 122 MetTrpValPheThrTyValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
Db 1031 ATGTGGGTATTTACCTATGTTGGTCCCTTGTAAATGCTGACACTACTGATTTGGCT 1090  
Qy 142 LeuLeuSerLeuPheSerIleProValIleTyGluArgHisGlnValGlnIleAspHis 161  
Db 1091 CTCATTTTCACCTCTTCAGTGTTCCTGTTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1150  
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaValIleGlnAlaIleVal 181  
Db 1151 TATCTAGACCTTGCANATPAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAATC 1210  
Qy 182 ProGlyLeuLysArgLysAlaAsp 189  
Db 1211 CCTGGATTGAAGCGCAAGCTGAA 1234  
RESULT 34  
AAZ36230  
ID AAZ36230 standard; cDNA; 1610 BP.  
XX AC AAZ36230;  
XX DT 22-FEB-2000 (first entry)  
XX

DE CDNA encoding a bone marrow secreted protein designated BMS112.  
XX Bone marrow secreted protein; bone marrow stromal cell; cytokine;  
KW cell proliferation; cell differentiation; hematopoiesis; anaemia;  
KW myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;  
KW erythroid progenitor cell; colony stimulating factor; granulocyte;  
KW monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;  
KW platelet disorder; thrombocytopenia; hematopoietic stem cell;  
KW stem cell disorder; aplastic anaemia; bone differentiation;  
KW paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon;  
KW ligament; nerve; wound healing; tissue repair; burn; incision; ulcer;  
KW bone fracture; cartilage damage; artificial joint; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 132..1253  
FT FT /\*tag= a  
FT FT /product= "bone marrow secreted protein"  
FT polyA\_signal 1516..1521  
FT FT /\*tag= b  
XX  
XX WO9933979-A2.  
XX  
XX 08-JUL-1999.  
XX  
XX 18-DEC-1998; 98WO-US027008.  
XX  
XX 30-DEC-1997; 97US-0068958P.  
XX 24-SEP-1998; 98US-0101603P.  
XX 30-SEP-1998; 98US-0102540P.  
XX  
XX (CHIR ) CHIRON CORP.  
XX  
XX Lin H, Cao L;  
XX  
XX WPI; 2000-038344/03.  
XX P-PSDB; AAY53624.  
XX  
XX New isolated human polynucleotide and secreted proteins can induce  
XX production of other cytokines in certain cell populations.  
XX  
XX Claim 11; Page 72-74; 120pp; English.  
XX  
XX AAZ36228-49 encode bone marrow secreted proteins of human bone marrow  
XX stromal cells. The proteins can exhibit cytokine, cell proliferation, or  
XX cell differentiation activity (either inducing or inhibiting). They can  
XX be used to support colony forming cells or factor-dependent cell lines,  
XX to regulate hematopoiesis, and to treat myeloid or lymphoid cell  
XX deficiencies. In addition, they may be used to support the growth and  
XX proliferation of erythroid progenitor cells, and to treat various  
XX anaemias. They can have colony stimulating factor (CSF) activity and can  
XX be used to support the growth and proliferation of myeloid cells such as  
XX granulocytes, monocytes or macrophages, to prevent or treat myelo-  
XX suppression, to support the growth and proliferation of megakaryocytes  
XX and platelets, thereby allowing prevention or treatment of platelet  
XX disorders such as thrombocytopenia, to support the growth and  
XX proliferation of hematopoietic stem cells, either in place of or in  
XX conjunction with platelet transfusions, to treat stem cell disorders,  
XX such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to  
XX repopulate the stem cell compartment after irradiation or chemotherapy.  
XX They can be used for growth or differentiation of bone, cartilage,  
XX tendon, ligament, or nerve tissue, as well as for wound healing and  
XX tissue repair and replacement, and in the treatment of burns, incisions  
XX and ulcers, to induce cartilage and/or bone growth in circumstances where  
XX bone is not normally formed and thus have an application in healing bone  
XX fractures and cartilage damage or defects, prophylactic use in fracture  
XX reduction and also in the improved fixation of artificial joints  
XX  
XX Sequence 1610 BP; 354 A; 458 C; 426 G; 372 T; 0 U; 0 Other;  
XX  
XX Alignment Scores: 1.29e-98 Length: 1610  
XX Pred. No.: (UYVA-) UNIV VANDERBILT.

Score: 304.00 Matches: 183  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: 3 Gaps: 0  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAZ36230 (1-1610)  
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 687 GTTGTGGACCTCTCTACTGGAGACACATTAAAGAGACTGGAGTGGTGTGGTGGCCAGC 746  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 747 CTATTCTCTGCTCTTTCATTGACAGTATTGAGCATTTGTAGCGGTAAACAGCCACATTGCC 806  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 807 TTGGCCCTGCTCTCTGTGACCATGAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 866  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 867 CAGAAATCAGATGAAGGCCACCCATTCAAGGCATATCTGGAATCTGAAGTTGCTATATCT 926  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
Db 927 GAGGAGTTGGTTTCAAGAGTACAGTAATTTCTGCTCTTTGGTCAATGTCACGATAAAG 986  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 987 GAATCAGCGGCTCTTCTTAGTATGATTTAGTTAGTTCTCTGAAGTTGACAGTGTG 1046  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
Db 1047 ATGTGGTATTATACCTATGTTGGTGGCTTGTAAATGTTCTGACACTACTGATTTGGCT 1106  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
Db 1107 CTCATTTCACTCTTCAGTGTCTCTGTTTATTAAGCGCATCAGGCACAGATAGATCAT 1166  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 1167 TATCTAGGACTTGCATAATAAGAAATGTTAAAGATGCTATGGCTAAATCCACGCAAAATC 1226  
QY 182 ProGlyLeuLysArgLysAlaAsp 189  
Db 1227 CCTGGATTGAAGCGCAAGCTGAA 1250  
RESULT 35  
ADK14166  
ID ADK14166 standard; cDNA; 1785 BP.  
XX  
AC ADK14166;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Human autoimmune disorder gene #62.  
XX  
KW gene; ss; autoimmune disorder; peripheral blood mononuclear cell;  
KW rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;  
KW type 1 (insulin-dependent) diabetes; human.  
XX  
OS Homo sapiens.  
XX  
XX US2003228617-A1.  
XX  
XX 11-DEC-2003.  
XX  
XX 16-MAY-2003; 2003US-00439388.  
XX  
XX 16-MAY-2002; 2002US-0381055P.  
XX  
XX (UYVA-) UNIV VANDERBILT.

XX Anne TW, Olsen NJ;  
PI WPI; 2004-061002/06.  
XX  
XX  
XX Detecting an autoimmune disorder in a subject comprising comparing the  
PT expression level of each gene determined with a standard, where the  
PT comparing detects the presence of an autoimmune disorder in the subject.  
XX  
XX  
XX Claim 10; SEQ ID NO 62; 86pp; English.  
XX  
XX  
XX The invention relates to a method of detecting an autoimmune disorder in  
CC a subject comprising obtaining a biological sample, preferably a  
CC peripheral blood mononuclear cell, from a subject, determining expression  
CC levels of at least two genes in the biological sample, and comparing the  
CC expression level of each gene determined with a standard, where the  
CC comparison detects the presence of an autoimmune disorder in the subject.  
CC The method is useful for detecting or diagnosing an autoimmune disorder,  
CC e.g. rheumatoid arthritis, systemic lupus erythematosus, multiple  
CC sclerosis, or type 1 (insulin-dependent) diabetes. The present sequence  
CC represents one of seventy genes used to detect autoimmune disorders with  
CC the described method.  
XX  
SQ Sequence 1785 BP; 520 A; 316 C; 402 G; 547 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 1.5e-98 Length: 1785  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: 12 Gaps: 0  
  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADK14166 (1-1785)  
  
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
DB 247 GTTGTGACCTCTCTGACCATCAGTAAAGACTGGAGTGGTGTGGTGGCCAGC 306  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 307 CTATTCCTGCTGCTTTCATTCAGCAGTATTCAGCATTGGAGCGTAACAGCCTACATGCC 366  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 367 TTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCTATC 426  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 427 CAGAAATCAGATGAAGGCCACCCATTTCAGGCGCATATCTGGAATCTGAAATGGCTATATCT 486  
QY 82 GluLeuLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 487 GAGGAGTTGGTTTCAAGATACAGTAATTTCTCTTGTGTCATGTGAACCTGCACCAATAAG 546  
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 547 GAATCAGCGCCCTCTTCTTAGTGATGATTTAGTTGATTTCTGGAATTTGCAAGTTGTG 606  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
DB 607 ATGTGGGTATTTACCTATGTTGGTGGCTTTGTTTAAATGCTGTCGACACTACTGATTTGGCT 666  
QY 142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 667 CTCATTTTCACCTTTTCAGTGTTCCTGTTTATTTATGAACGGCATCAGGCACATAGATCAT 726  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 727 TATCTAGGACTTGCATTAAGATGTTAAGATGCTATGGCTTAATCAACAGCAAAATC 786  
QY 182 ProGlyLeuLysArgLysAlaAsp 189  
|||||

Db 787 CTGTGATTGAAGCGCAAAAGCTGAA 810  
RESULT 36  
ABK90133  
ID ABK90133 standard; DNA; 2052 BP.  
XX  
AC ABK90133;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE DNA encoding human NogoB protein.  
XX  
KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;  
KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;  
KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;  
KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;  
KW tissue hypertrophy; central nervous system; axon regeneration; NogoB;  
KW Nogo-associated disease; metastasis; gene; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 67..1188  
FT /\*tag= a  
FT /product= "Human NogoB protein"  
XX  
PN WO200257483-A2.  
XX  
PD 25-JUL-2002.  
XX  
PF 18-JAN-2002; 2002WO-GB000228.  
XX  
PR 18-JAN-2001; 2001GB-00001312.  
XX  
PA (GLAX ) GLAXO GROUP LTD.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
XX  
PI Blackstock WP, Hale RS, Prinjha R, Rowley A;  
XX  
DR WPI; 2002-599722/64.  
DR P-PSDB; ABG30937.  
XX  
PT Identifying modulators of Nogo or BACE activity for treating acute  
PT neuronal injuries, neoplastic or dysproliferative disorders, comprises  
PT providing and monitoring interaction between Nogo and BACE polypeptides.  
XX  
FS Disclosure; Page 50-52; 68pp; English.  
XX  
CC The present invention relates to a new method of identifying modulators  
CC of Nogo function or BACE activity. The method involves providing Nogo and  
CC BACE polypeptides capable of binding with each other, monitoring the  
CC interaction between these polypeptides, and determining if the test agent  
CC is a modulator of Nogo or BACE activity. The method is useful in treating  
CC acute neuronal injuries, such as spinal or head injury, stroke,  
CC peripheral nerve damage, and in neoplastic (e.g. glioblastomas,  
CC neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.  
CC cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue  
CC hypertrophy) of the central nervous system. The BACE polypeptide is  
CC useful in screening methods to identify agents that may act as modulators  
CC of BACE activity and in particular agents that may be useful in treating  
CC Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,  
CC and the polynucleotide encoding the BACE polypeptide are useful in  
CC manufacturing a medicament for the treatment or prevention of disorders  
CC responsive to the modulation of Nogo activity, in alleviating the  
CC symptoms or improving the condition of a patient suffering from this  
CC disorder, in axon regeneration, or in preventing metastasis or spreading  
CC of a cancer. The polynucleotide may also be an essential component in  
CC assays, a probe, in recombinant protein synthesis, and in gene therapy  
CC techniques. The present nucleic acid sequence encodes the human NogoB  
CC protein of the invention  
XX  
SQ Sequence 2052 BP; 511 A; 512 C; 506 G; 523 T; 0 U; 0 Other;

Alignment Scores:			
Pred. No.:	1-82e-98	Length:	2052
Score:	904.00	Matches:	183
Percent Similarity:	98.94%	Conservative:	3
Best Local Similarity:	97.34%	Mismatches:	2
Query Match:	97.73%	Indels:	0
DB:	6	Gaps:	0
US-09-830-972-2_COPY_975_1163 (1-189) x ABK90133 (1-2052)			
QY	2	ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer	21
DB	622	GTGTTGACCTCTCTGTCTGGAGACATTAAGAAGCTGGAGTGTGTTGGTCCAGC	681
QY	22	LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla	41
DB	682	CTATTCTCTGCTGTTTCATGTACAGTATTACAGTATTGAGCGTAAACAGCTTACATTGCC	741
QY	42	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle	61
DB	742	TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGCATATACAGGTTGTATCCNAGCTATC	801
QY	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer	81
DB	802	CAGAAATCAGATGAAGCCACCCATTCAGGCGATATCTGGAATCTGAAGTTGCTATATCT	861
QY	82	GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys	101
DB	862	GAGGAGTTGGTTTCAGAAAGTACAGTAAATCTGCTCTTGGTCAATGGAATGACGAGTAAAG	921
QY	102	GluLeuArgGluPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaValLeu	121
DB	922	GAATCAGGCGCTCTCTTAGTGTATGATGATTTAGTTGATCTCTGAAGTTGCGAGTGTG	981
QY	122	MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuIleAla	141
DB	982	ATGTGGGTATTTACCTATGTTGGTGGCTTGTGTTTAATGGTCTGACACTACTGATTTGGCT	1041
QY	142	LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis	161
DB	1042	CTCATTTCACTCTTCAGTGTCTCTGTATTATGAACGGCATCAGGCACAGATAGATCAT	1101
QY	162	TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle	181
DB	1102	TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAATC	1161
QY	182	ProGlyLeuLysArgIleAlaAsp	189
DB	1162	CTGTGATTGAAGCGCAAGCTGAA	1185
RESULT 37			
ID	ABV94681	ABV94681 standard; cDNA; 2235 BP.	
AC	ABV94681;		
XX			
DT			
XX			
DE	14-JAN-2003 (first entry)		
XX			
XX	Human pancreatic cancer expressed cDNA SEQ ID NO 54.		
KW	Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;		
XX	Cytostatic; tumour; gene; ss.		
OS	Homo sapiens.		
XX			
PN	W0200260317-A2.		
XX			
PD	08-AUG-2002.		
XX			
PF	30-JAN-2002; 2002WO-US0002781.		
XX			
PR	30-JAN-2001; 2001US-0265305P.		
PR	31-JAN-2001; 2001US-0265682P.		

Db 997 GAACCTAGCGGCTCTCTTAGTGTGATGATTTAGTGTGATTTCTCTGAAGTTTCAGCTGTTG 1056  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 1057 ATGTGGGTATTTACCTATGTTGGTGGCTTGTTTAAATGGTCTGACACTACTGATTTGGCT 1116  
 QY 142 LeuileSerLeuPheSerileProValletyrGluArgHisGlnValGlnleAspHis 161  
 Db 1117 CTCATTTCACTCTTCAGTGTCTCTGTATTATTAAGCGCATCAGGCACAGATAGATCAT 1176  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysile 181  
 Db 1177 TATCTAGGACTTGCATAAATAAGATGTTAAAGATGCTATGGCTAAATAATCAAGCAAAAATC 1236  
 QY 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 1237 CCTGGATTGAAGCGCAAGCTGAA 1260  
 RESULT 38  
 AAC64406  
 ID AAC64406 standard; cDNA; 2240 BP.  
 XX  
 AC AAC64406;  
 XX  
 DT 08-FEB-2001 (first entry)  
 XX  
 DE Human Nogo B nucleotide sequence SEQ ID NO:1.  
 XX  
 KW Human; Nogo B; cell stress response; hyperphosphorylated; brain tumour;  
 KW stress-phosphorylated endoplasmic reticulum protein; cytosolic;  
 KW gene therapy; cell growth; cellular stress response; neuron growth;  
 KW regulator of oxidative stress; inhibitor of neurite outgrowth;  
 KW axon regeneration; diagnosis; cancer; identification; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200060083-A1.  
 XX  
 PD 12-OCT-2000.  
 XX  
 PF 07-APR-2000; 2000WO-US009393.  
 XX  
 PR 08-APR-1999; 99US-0128372P.  
 PR 21-JUN-1999; 99US-0140331P.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 XX  
 PI Wei D, Halenbeck R, Williams LT;  
 XX  
 DR WPI; 2000-665007/64.  
 DR P-PSDB; AAB24242.  
 XX  
 PT Novel protein associated with cell stress response useful for modulating  
 PT stress levels, cell growth, diagnosis and treatment of cancer and  
 PT malignant growth and for identifying agonists and antagonists.  
 XX  
 PS Claim 2; Page 63-64; 68pp; English.  
 XX  
 CC The present sequence encodes a human stress-phosphorylated endoplasmic  
 CC reticulum protein, designated Nogo B. Nogo B has cytosolic activity and  
 CC is a modulator of the storage and exchange of calcium, cell growth and  
 CC cellular stress response. It can: regulate oxidative stress; inhibit  
 CC neurite outgrowth, neuron growth and axon regeneration. Nogo B  
 CC polypeptides and polynucleotides are useful for modulating stress levels  
 CC and cellular stress-response, cell growth and viability, diagnosis and  
 CC treatment of cancer, malignant growth and other Nogo B related diseases.  
 CC Nogo B polypeptides are also useful to screen combinatorial libraries to  
 CC identify agonist or antagonist. Antibodies against Nogo B polypeptides  
 CC are useful for affinity chromatography and distinguishing Nogo B  
 CC polypeptides  
 XX  
 SQ Sequence 2240 BP; 570 A; 558 C; 536 G; 576 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 2,06e-98 Length: 2240  
 Score: 904.00 Matches: 183  
 Percent Similarity: 98.94% Conservative: 3  
 Best Local Similarity: 97.34% Mismatches: 2  
 Query Match: 97.73% Indels: 0  
 DB: 3 Gaps: 0  
 US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAC64406 (1-2240)  
 QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 693 GTTGTGTACCTCTCTGCTACTGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGGCCAGC 752  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerileValSerValThrAlaLysileAla 41  
 Db 753 CTATTCTCTGCTGCTTTCATTGACAGTATTGAGCATTTGAGCGTAACAGCCTACATTTGCC 812  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 813 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATATACAGGGTGTGATCCAGCTATC 872  
 QY 62 GlnLysSerAspGluGlyHisPropheArgAlaTyrLeuGluSerGluValAlaLysSer 81  
 Db 873 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAAGTTGCTATATCT 932  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 933 GAGGAGTTGGTTTCAAGATACAGTAATTTCTCTCTTGGTCATGTGAACCTGCACGATAAG 992  
 QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 993 GAACCTAGCGGCTCTCTCTTAGTTGATGATTTAGTGTATCTCTGAAGTTTGCAGTGTG 1052  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 1053 ATGTGGGTATTTACCTATGTTGGTGGCTTGTAAATGGTCTGACACTACTGATTTGGCT 1112  
 QY 142 LeuileSerLeuPheSerileProValletyrGluArgHisGlnValGlnleAspHis 161  
 Db 1113 CTCATTTCACTCTTCAGTGTCTCTGTATTATTAAGCGCATCAGGCACAGATAGATCAT 1172  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysile 181  
 Db 1173 TATCTAGGACTTGCATAAATAAGATGTTAAAGATGCTATGGCTAAATAATCAAGCAAAAATC 1232  
 QY 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 1233 CCTGGATTGAAGCGCAAGCTGAA 1256  
 RESULT 39  
 AAC94408  
 ID AAC94408 standard; cDNA; 1694 BP.  
 XX  
 AC AAC94408;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human full-length cDNA, SEQ ID NO: 3170.  
 XX  
 KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1130094-A2.  
 XX  
 PD 05-SEP-2001.  
 XX  
 PF 07-JUL-2000; 2000EP-00114089.  
 XX  
 PR 08-JUL-1999; 99JP-00194486.  
 PR 11-JAN-2000; 2000JP-00118774.  
 PR 02-MAY-2000; 2000JP-00183765.

XX (HELI-) HELIX RES INST.  
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
XX WPI: 2001-524255/58.  
DR P-PSDB; AAW93484.  
XX 830 Primers useful for synthesizing full length cDNA clones and their use  
PT in genetic manipulation.  
XX Claim 8; SEQ ID NO 3170; 1380pp + Sequence Listing; English.  
XX The invention relates to primers for synthesizing full length cDNA  
CC clones. 830 cDNA molecules encoding a human protein have been isolated  
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have  
CC been determined. Primers for synthesizing the full length cDNA are useful  
CC for clarifying the function of the protein encoded by the cDNA. The full  
CC length clones were obtained by construction of full length enriched cDNA  
CC libraries that were synthesised by the oligo-capping method. The primers  
CC enable the production of the full length cDNA easily without any special  
CC methods. The present sequence is a full length human cDNA of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in CD-ROM format directly  
CC from EPO  
XX  
SQ Sequence 1694 BP; 353 A; 484 C; 469 G; 388 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 4,22e-98 Length: 1694  
Score: 900.00 Matches: 182  
Percent Similarity: 98.40% Conservativeness: 3  
Best Local Similarity: 96.81% Mismatches: 3  
Query Match: 97.30% Indels: 0  
DB: Gaps: 0  
  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAK94408 (1-1694)  
  
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
DB 788 GTTGTGGACCTCTGTTACTGGAGAGACATTAAAGACACTGGAGTGGTGTGGTGCAGC 847  
  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 848 CTATTCCTGCTGCTTTCATTGACAGTATTACAGCATTTGAGCGTAAACGCCCTACATPGCC 907  
  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 908 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGATATACAGGGTGTGATCCAGCTATC 967  
  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 968 CAGAAATCAGATGAAGGCCACCCATTTCAGGCGATATCTGGAATCTCAGTTGCTATCT 1027  
  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 1028 GAGGAGTTGGTTTCAGAAAGTACAGTAATCTCTGCTCTTGGTCATGTGAACGATAAAG 1087  
  
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 1088 GAACCTCAGCGCCCTCTCTTAGTTAGTATGATTAGTTAGTTCTCTGAGTTGCAGTTTG 1147  
  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
DB 1148 ATGTGGGTATTTACCTATGTTGGTGGCTGTTTAAATGGTCTGACACTACTGATTTGGCT 1207  
  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 1208 CTCAITTCATCTCTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCAGATGATCAT 1267  
  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

DB 1268 TATCTAGGACTTGCAATAAGAAATCTTAAAGATGCTATGGCTAAATCCAGCAAAATC 1327  
QY 182 ProGlyLeuLysArgLysAlaAsp 189  
DB 1328 CCTGGATTGAAGCGCAAGACTGAA 1351  
  
RESULT 40  
ADL31137  
ID ADL31137 standard; cDNA; 1694 BP.  
XX AC ADL31137;  
XX DT 20-MAY-2004 (first entry)  
XX DE Full length human cDNA clone SeqID 3170.  
XX KW human; medicine; signal transduction; glycoprotein; transcription;  
XX oligo-capping method; ss; gene.  
XX OS Homo sapiens.  
XX PN EP1396543-A2.  
XX PD 10-MAR-2004.  
XX PF 07-JUL-2000; 2003EP-00025638.  
XX PR 08-JUL-1999; 99JP-00194486.  
PR 11-JAN-2000; 2000JP-00118774.  
PR 02-MAY-2000; 2000JP-00183865.  
PR 07-JUL-2000; 2000EP-00114089.  
XX (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
PI WPI: 2004-204755/20.  
DR P-PSDB; ADL31138.  
XX New oligonucleotide primers (830 cDNAs) useful for synthesizing full  
PT length human cDNAs.  
XX Example 1; SEQ ID NO 3170; 1340pp; English.  
XX This invention relates to a novel primers useful for synthesising full  
CC length cDNA molecules that encode human proteins. Specifically, it refers  
CC to secretory or membrane proteins that are potential therapeutic agents/  
CC target molecules in the field of medicine, and in particular genes  
CC encoding proteins that are associated with signal transduction,  
CC glycoproteins and transcription. The present invention describes a method  
CC for efficiently cloning a full length human cDNA from both the 5' and 3'  
CC ends using the oligo-capping method. This polynucleotide sequence is a  
CC full length human cDNA clone of the invention.  
XX  
SQ Sequence 1694 BP; 353 A; 484 C; 469 G; 388 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 4,22e-98 Length: 1694  
Score: 900.00 Matches: 182  
Percent Similarity: 98.40% Conservativeness: 3  
Best Local Similarity: 96.81% Mismatches: 3  
Query Match: 97.30% Indels: 0  
DB: Gaps: 12  
  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADL31137 (1-1694)  
  
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
DB 788 GTTGTGGACCTCTGTTACTGGAGAGACATTAAAGACACTGGAGTGGTGTGGTGCAGC 847  
  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41



Db 848 CTATTCTGCTGCTTTTCATTGACAGTATTCAGCAATTTGTGAGCGTAACAGCCTACATTGCC 907  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 908 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 967  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 968 CAGAAATCAGATGAAGGCCACCCATTCAAGGCATATCTGGAATCTGGAAGTTGCTATATCT 1027  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 1028 GAGGAGTTGGTTTCAGAGTACAGTAATTTCTGCTCTTGTGTCATGTGAACCTGCACGATAAAG 1087  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 1088 GAACTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAATTTGCGATGTTG 1147  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
 Db 1148 ATGTGGGTATTTACCTATGTTGGTGCCTTGTATATGCTCTGACACTACTGATTTGGCT 1207  
 QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 1208 CTCATTTTCACCTTTCAGTGTTCCTGTTATTTATGAAACGGCATCAGGCACAGATAGATCAT 1267  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaIleIle 181  
 Db 1268 TATCTAGACCTTGCAATTAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAATC 1327  
 QY 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 1328 CCTGGATTGAAGCGCAAGCTGAA 1351  
 RESULT 41  
 ID AAI98079  
 XX AAI98079 standard; cDNA; 1980 BP.  
 AC AAI98079;  
 XX  
 DT 04-DEC-2001 (first entry)  
 DE Human neuroblastoma expressed polynucleotide SEQ ID NO 22.  
 KW Human; neuroblastoma; ss.  
 OS Homo sapiens.  
 XX WO200166733-A1.  
 XX 13-SEP-2001.  
 XX 02-MAR-2001; 2001WO-JP001631.  
 XX 07-MAR-2000; 2000JP-00159195.  
 XX 12-MAY-2000; 2000JP-00140387.  
 XX (CHIB-) CHIBA PREFECTURE.  
 XX (HISM) HISAMITSU PHARM CO LTD.  
 XX Nakagawara A;  
 XX WPI; 2001-602630/68.  
 XX Nucleic acids for prognosis of human neuroblastoma comprise nucleic acids  
 PT expressed by human neuroblastomas.  
 XX Claim 1; Page 69-70; 159pp; Japanese.  
 XX The invention relates to nucleic acids (AAI98058-AAI98161) or their  
 CC homologues expressed by human neuroblastomas useful for detecting genes  
 CC expressed by neuroblastoma and for analysing their structure and  
 CC function. The nucleic acids are useful for the diagnosis and prognosis of

CC neuroblastoma  
 XX SQ Sequence 1980 BP; 601 A; 373 C; 423 G; 583 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 9.15e-98 Length: 1980  
 Score: 898.00 Matches: 182  
 Percent Similarity: 98.41% Conservative: 4  
 Best Local Similarity: 96.30% Mismatches: 3  
 Query Match: 97.08% Indels: 0  
 DB: 4 Gaps: 0  
 US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAI98079 (1-1980)  
 QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysValSerGlyValValPheGlyAla 20  
 Db 1006 TCAGTTGTTGACCTCTCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGGCC 1065  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 1066 AGCCTATTCCAGCTGCTTTTCATTGACAGTATTCAGCAATTTGTGAGCGTAACAGCCTACATT 1125  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 1126 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT 1185  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 1186 ATCAGAAATCAGATGAAGGCCACCCATTTCAGGCGCATATCTGGAATCTGAAAGTTGCTATA 1245  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 Db 1246 TCTGAGGAGTTGGTTTCAGAGTACAGTAATTTCTGCTCTTGTGTCATGTGAACCTGCACGATA 1305  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 1306 AAGGAACCTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGGAGTTGTCAGTG 1365  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 Db 1366 TTGATGTTGGGTATTTACTATGTTGGTCCCTGTTTAAAGTCTGACACTCTGATTTTG 1425  
 QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 1426 GCTCTCATTTTCACCTCTTCAGTGTTCCTGTTTATTATGAACGGCATCAGGCACAGATAGAT 1485  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 1486 CATTATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAA 1545  
 QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
 Db 1546 ATCCCTGGATTGAAGCGCAAGCTGAA 1572  
 RESULT 42  
 ID AAX97587  
 XX AAX97587 standard; DNA; 991 BP.  
 AC AAX97587;  
 XX  
 DT 13-SEP-1999 (first entry)  
 DE Extended human secreted protein coding sequence, SEQ ID NO. 51.  
 KW Secreted protein; human; cytokine; cellular proliferation; cell movement;  
 KW cellular differentiation; immune system regulator; anti-inflammatory;  
 KW haematopoiesis regulator; tissue growth regulator; tumour inhibitor;  
 KW reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;  
 KW genetic disease; ss.  
 OS Homo sapiens.  
 XX WO9931236-A2.  
 XX



```
Pred. No.: 86-98 Length: 994
Score: 895.00 Matches: 182
Percent Similarity: 98.40% Conservative: 3
Best Local Similarity: 96.81% Mismatches: 3
Query Match: 96.76% Indels: 0
DB: 12 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x ADP18854 (1-994)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleValSerValThrGlyValValPheGlyAlaSer 21
DB 68 GTTGTGTACCTCTCTGTACCTGTGGAGACATTAAAGACACTGGAGTGGTGTGGTCCAGC 127
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValIleAla 41
DB 128 CTATTCCTGCTCTTTCATTGACAGTATTACAGTATTGAGCGTAACAGCCTACATTGCC 187
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 188 TTGGCCCTGCTCTCTGTACCATCAGCTTTAGGATATACAGGGTGTGATCCAAAGCTATC 247
QY 62 GlnLysSerAspGlnGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 248 CAGAAATCAGATGAAGGCCACCATTCAGGGCATATCTGGAATCTCAAGTTGCTATATCT 307
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
DB 308 GAGGAGTGGTTCAGAGTACAGTAACTCTGCTCTGTGTCATGTGAACTGCAGATTAAG 367
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 368 GAACCTCAGCGGCTCTCTTAGTGTGATGATTTAGTTGATTTCTCTGAAGTTTCAGTGTG 427
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuAlaIle 141
DB 428 ATGTGGGTATTTACTATGTGGTGGCTGTGTTTAAATGTCGACACTACTGATTTGGCT 487
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
DB 488 CTCATTTTCACTCTTCAGTGTCTCTGTTTATTAAGCGCATCAGCGCAGATAGATCAT 547
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
DB 548 TATCTAGTACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCAAGCAAAATC 607
QY 182 ProGlyLeuLysArgLysAlaAsp 189
DB 608 CTGGATTGAAGCGCAAGCTGAA 631

RESULT 44
ADI31056
ID ADI31056 standard; cDNA; 2610 BP.
XX AC ADI31056;
XX AC ADI31056;
XX 17-JUN-2004 (first entry)
XX DE Human cDNA #382.
XX DE Human; gene; ss; immunological response; immunopathological condition;
KW Crohn's disease; asthma; ulcerative colitis; hyperesoinophilia;
KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
KW acute monocytic leukaemia; antiinflammatory; antistatic; antiulcer;
KW osteopathic; antiarthritic; antirheumatic; cytostatic.
XX OS Homo sapiens.
XX OS US6607879-B1.
XX PN 19-AUG-2003.
XX PD 09-FEB-1998; 98US-00023655.
XX PF
XX
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PR 09-FEB-1998; 98US-00023655.
XX (INCY-) INCYTE CORP.
XX Cocks BG, Stuart SG, Seilhamer JJ;
XX WPI; 2003-895307/82.
XX A composition comprising a plurality of cDNAs, useful for detecting
PT altered expression of genes in an immunological response or for
PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
PT or osteoarthritis.
XX Claim 1; SEQ ID NO 382; 50pp; English.
XX The invention relates to a composition comprising a plurality of cDNAs
CC for detecting the altered expression of genes in an immunological
CC response. The invention also relates to a method of diagnosing or
CC monitoring the treatment of an immunopathological condition in a sample,
CC comprising obtaining nucleic acids from a sample, contacting the nucleic
CC acids of the sample with an array comprising the plurality of cDNAs under
CC conditions to form one or more hybridisation complexes, detecting the
CC hybridisation complexes and comparing the levels of the detected
CC hybridisation complexes with the level of hybridisation complexes
CC detected in a non-diseased sample, where an altered level of the detected
CC hybridisation complexes correlates with the presence of an
CC immunopathological condition. Also disclosed are an expression profile
CC comprising a microarray and a plurality of detectable complexes and a
CC method for identifying a plurality of polynucleotide probes. The cDNAs
CC are useful as hybridisable array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray can be used in
CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,
CC ulcerative colitis, hyperesoinophilia, irritable bowel syndrome,
CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
CC identifying agents for the treatment of the diseases. The microarray may
CC also be used in drug discovery and development, toxicological and
CC carcinogenicity studies, forensics or pharmacogenomics. The composition
CC may also be used in purification of a subpopulation of mRNAs, cDNAs or
CC genomic fragments. This sequence represents a human cDNA of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html.
XX SQ Sequence 2610 BP; 773 A; 434 C; 557 G; 820 T; 0 U; 26 Other;

Alignment Scores:
Pred. No.: 9.4e-97 Length: 2610
Score: 891.00 Matches: 183
Percent Similarity: 98.41% Conservative: 3
Best Local Similarity: 96.83% Mismatches: 2
Query Match: 96.32% Indels: 1
DB: 11 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x ADI31056 (1-2610)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleValSerValThrGlyValValPheGlyAlaSer 21
DB 1311 GTTGTGTACCTCTCTGTACCTGTGGAGACATTAAAGACACTGGAGTGGTGTGGTCCAGC 1370
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValIleAla 41
DB 1371 CTATTCCTGCTCTTTCATTGACAGTATTACAGTATTGAGCGTAACAGCCTACAAATTC 1430
QY 41 aleuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 1431 CTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAAGCTAT 1490
QY 61 eGlnLysSerAspGlnGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 81
DB 1491 CCAGAAATCAGATGAAGGCCACCATTCAGGCATATCTGGATCTGAAGTTGCTATATC 1550
QY 81 rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIlely 101
DB
```

Db 1551 TGAGGAGTTGGTTCAAGTACAGTAATTTCTGCTCTTGGTCATGTGAACGTGACGATATA 1610  
 QY 101 sGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLeuPheAlaValle 121  
 Db 1611 GGAACCTCAGCGCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCACTGTT 1670  
 QY 121 uMetTrpValPheThrTyrrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAl 141  
 Db 1671 GATGTGGTATTTACCTATGTTGGTCCCTGTTTAAATGGTCTGACACTACTGATTTTGGC 1730  
 QY 141 aleuileSerLeuPheSerIleProValIleTyrrGluArgHisGlnValGlnIleAspHi 161  
 Db 1731 TCTCATTTTCACTCTTCAGTGTTCCTGTTTATTAAGCGCATCAGGCACAGATGATCA 1790  
 QY 161 sTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 1791 TTATCTAGGACTTGCATAAAGAAATCTTAAAGATGCTATGGCTAAATCCAGCAAAAT 1850  
 QY 181 eProGlyLeuLysArgLysAlaAsp 189  
 Db 1851 CCCTGGTTTGAAGCGCAAGCTGAA 1875

## RESULT 45

AAV30920

ID AAV30920 standard; cDNA; 2386 BP.

XX AC AAV30920;

XX 14-SEP-1998 (first entry)

XX Human secreted protein BG160\_1 cDNA.

XX BG160\_1; secreted protein; protein factor; human; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 102..2030

XX /\*tag= a

XX sig\_peptide 1863..1899

XX /\*tag= b

XX /\*note= "putative leader/signal peptide"

XX mat\_peptide 1900..2027

XX /\*tag= c

XX W09817687-A2.

XX 30-APR-1998.

XX 24-OCT-1997; 97WO-US019590.

XX 25-OCT-1996; 96US-00740274.

XX 24-OCT-1997; 97US-00740274.

XX (GEMY ) GENETICS INST INC.

XX Jacobs K, McCoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;

XX Spaulding V, Agostino MJ;

XX WPI: 1998-261426/23.

XX P-PSDB; AAW58383.

XX Nucleic acid encoding secreted protein from human cells - useful, e.g. as

XX immuno-modulators, anti-tumour agents, promoters of tissue growth,

XX haemostatic and thrombolytic agents etc.

XX Claim 20; Page 74-75; 114pp; English.

XX CC This cDNA clone, designated BG160\_1, codes for a novel human secreted

XX protein (see AAW58383). It was isolated from a human adult brain cDNA

XX library using methods selective for cDNAs that encode secreted proteins.

XX The clone is deposited in composite clone ATCC 98232; an oligonucleotide

XX (see AAW99725) is designed to isolate the clone from the composite. The

CC predicted AT415\_4 amino acid sequence shows homology to neuroendocrine-  
 CC specific proteins. Novel cDNA clones (see AAV30916-32) coding for human  
 CC secreted proteins (see AAW5880-90) are claimed. These can be used for  
 CC recombinant production of the secreted proteins for analysis,  
 CC characterisation, diagnostic or therapeutic use. They can also be used as  
 CC tissue or mol.wt. markers, for chromosome identification, to identify  
 CC genetic disorders, to isolate new related DNA, as sources of primers for  
 CC PCR, to generate antibodies, and in interaction trap assays. The secreted  
 CC proteins may also have many biological activities, e.g. cytokine,  
 CC immunomodulator, haematopoiesis regulating activity, tissue growth  
 CC activity, activin or inhibin activity, chemotactic or chemokinetic  
 CC activity, haemostatic and thrombolytic activity, receptor/ligand  
 CC activity, antiinflammatory, cadherin and tumour invasion suppressor  
 CC activity, and tumour inhibition activity. The proteins can be expressed  
 CC in vivo from DNA, introduced in gene therapy vectors  
 XX  
 SQ Sequence 2386 BP; 756 A; 450 C; 494 G; 686 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.86e-94 Length: 2386  
 Score: 871.50 Matches: 179  
 Percent Similarity: 96.30% Conservative: 3  
 Best Local Similarity: 94.71% Mismatches: 2  
 Query Match: 94.22% Indels: 5  
 DB: 2 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAV30920 (1-2386)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 Db 1476 TCAGTTTGTGACCTCTCTGCTACTGGAGACATTAAGAGACTGGAGTGGTGTGGTGGC 1535  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 1536 AGCCTATTCTCTGCTTTCATTGACAGTATTTCAGCAITGTGAGCGTAACAGCTACATT 1595  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 1596 GCCTTGGCCCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAGCT 1655  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 1656 ATCCAGAAATCAGATGAGGCCACCCATTTCAGG-----GAAGTTGCTATA 1700  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 Db 1701 TCTGAGGAGTTGGTTTCAGAAATACAGTAAATTCCTCTCTGGTCAATGTAACGACGATA 1760  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 1761 AAGGAACTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTCCTGAAGTTTGAGTG 1820  
 QY 121 LeuMetTrpValPheThrTyrrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 Db 1821 TTGATGTGGTATTTACCTATCTTGGTGCCTTGTATTGTTTAAATGGTCTGACACTACTGATT 1880  
 QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrrGluArgHisGlnValGlnIleAsp 160  
 Db 1881 GCTCTCATTTCACTCTTCAGTGTCTCTGTTTATTTATGAACGGCATCAGGCACAGATAGAT 1940  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 1941 CATTATCTAGGACTTGCATAAATGAAGATGTTAAAGATGCTATGGCTAAATATCCAGCAAAA 2000  
 QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
 Db 2001 ATCCCTGGATTGAGCGCAAGCTGAA 2027  
 RESULT 46  
 ABK90135  
 ID ABK90135 standard; DNA; 1798 BP.  
 XX  
 AC ABK90135;

XX 21-OCT-2002 (first entry)

XX DNA encoding human NogoC protein.

XX Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;

XX stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;

XX neuroblastoma; hyperproliferative disorder; dysproliferative disorder;

XX cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;

XX tissue hypertrophy; central nervous system; axon regeneration; NogoC;

XX Nogo-associated disease; metastasis; gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 215..814

XX /tag= a

XX /product= "Human NogoC protein"

XX WO200257483-A2.

XX 25-JUL-2002.

XX 18-JAN-2002; 2002WO-GB000228.

XX 18-JAN-2001; 2001GB-00001312.

XX (GLAX ) GLAXO GROUP LTD.

XX (SMK ) SMITHKLINE BEECHAM PLC.

XX Blackstock WP, Hale RS, Prinjha R, Rowley A;

XX WPI; 2002-599722/64.

XX P-PSDB; ABG30939.

XX Identifying modulators of Nogo or BACE activity for treating acute

XX neuronal injuries, neoplastic or dysproliferative disorders, comprises

XX providing and monitoring interaction between Nogo and BACE polypeptides.

XX Disclosure; Page 62-64; 68pp; English.

XX The present invention relates to a new method of identifying modulators

XX of Nogo function or BACE activity. The method involves providing Nogo and

XX BACE polypeptides capable of binding with each other, monitoring the

XX interaction between these polypeptides, and determining if the test agent

XX is a modulator of Nogo or BACE activity. The method is useful in treating

XX acute neuronal injuries, such as spinal or head injury, stroke,

XX peripheral nerve damage, and in neoplastic (e.g. glioblastomas,

XX neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.

XX cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue

XX hypertrophy) of the central nervous system. The BACE polypeptide is

XX useful in screening methods to identify agents that may act as modulators

XX of BACE activity and in particular agents that may be useful in treating

XX Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,

XX and the polynucleotide encoding the BACE polypeptide are useful in

XX manufacturing a medicament for the treatment or prevention of disorders

XX responsive to the modulation of Nogo activity, in alleviating the

XX symptoms or improving the condition of a patient suffering from this

XX disorder, in axon regeneration, or in preventing metastasis or spreading

XX of a cancer. The polynucleotide may also be an essential component in

XX assays, a probe, in recombinant protein synthesis, and in gene therapy

XX techniques. The present nucleic acid sequence encodes the human NogoC

XX protein of the invention

XX Sequence 1798 BP; 540 A; 314 C; 392 G; 552 T; 0 U; 0 Other;

XX Alignment Scores:

XX Pred. No.: 1e-93 Length: 1798

XX Score: 864.00 Matches: 182

XX Percent Similarity: 97.88% Conservative: 3

XX Best Local Similarity: 96.30% Mismatches: 3

XX Query Match: 93.41% Indels: 2

XX DB: 6 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ABK90135 (1-1798)

QY 2 ValValAspLeuLeuTyrTyrArgAspIleLeuValThrGlyValValPheGlyAlaSer 21

DB 248 GTTGTGTGACCTCCCTGTACTGGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGGCCAGC 307

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

DB 308 CTATTCTGCTGCTTTCATTGACAGTATTGAGCATTTGAGCGTAACAGCCTACATTGCC 367

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

DB 368 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGGTGTGATCCAAGCTATC 427

QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81

DB 428 CAGAAATCAGATGAAGGCCACCCCATTCAGGGCATATCTGGAATCTGGAAGTTGCTATATCT 487

QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101

DB 488 GAGGAGTTGGTTTCAAGAGTACAGTAATTTCTGCTCTTGGTCTATGTAATGCAAGTAAG 547

QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121

DB 548 GAACTCAGGCGCTCTCTTCTTAGTTGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 607

QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141

DB 608 ATGTGGGTAAATTACCTATGTTGGTGGCTTGTATATGCTGACACTACTGATTTGGCT 667

QY 142 LeuIleSerLeu-PheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHi 161

DB 668 CTCATTTCACTCTCTTCACTGTTCTCTGTTATTTA-GAAGCGCATCAGGCACAGATAGTCA 726

QY 161 sTyrIleGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

DB 727 TTATCTAGGACTTGCMAATAAGAAATGTTAAAGATGCTATGGCTAAATCCCAAGCAAAAT 786

QY 181 eProGlyLeuLysArgLysAlaAsp 189

DB 787 CCTTGGATTGAAGCGCAAAAGCTGAA 811

RESULT 47

ID AAF98399 standard; cDNA; 2386 BP.

XX AAF98399;

XX AAF98399;

XX 07-JUN-2001 (first entry)

DE Human cDNA clone BG160\_1 sequence SEQ ID 41.

XX Human; secreted protein; nutrient; cytokine modulator; proliferation;

XX differentiation; immune system modulator; tissue growth; chemotactic;

XX haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;

XX haematopoiesis.

XX Homo sapiens.

XX WO200119988-A1.

XX 22-MAR-2001.

XX 14-SEP-2000; 2000WO-US025135.

XX 17-SEP-1999; 99US-00398829.

XX (GEMY ) GENETICS INST INC.

XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;

XX Merberg D, Treacy M; Bowman MR, Spaulding V, Agostino MJ;

DR WPI; 2001-244801/25.  
DR P-PSDB; AAB90682.  
XX  
PT Isolated nucleic acids encoding polypeptides, useful for modulating e.g.  
PT cytokine and cell proliferation/differentiation activity, the immune  
PT system and hematopoiesis regulating activity.  
XX  
PS Claim 1; Page 408-409; 557pp; English.  
XX  
CC Human cDNA clones represented in AAF98374 - AAF98489 encode secreted  
CC proteins AAB90667 - AAB90750. The cDNA clones are isolated from various  
CC tissue types, and may be used in the prevention, treatment and diagnosis  
CC of diseases associated with inappropriate protein expression. The  
CC polypeptides and nucleic acids may be used as nutrients or to modulate  
CC cytokine and cell proliferation/differentiation activity and may also be  
CC involved in modulation of the immune system. The cDNA sequences,  
CC proteins, their agonists and/or antagonists exhibit haematopoiesis  
CC regulating activity; tissue growth activity; activin/inhibin activity;  
CC chemotactic/chemokinetic activity; haemostatic and thrombolytic activity;  
CC receptor/ligand activity; anti-inflammatory activity; haematopoiesis  
CC activity; cadherin/tumour suppressor activity; and/or tumour inhibition  
CC activity. Included in the invention are probes represented in AAF98490 -  
CC AAF98572 which are specific for the cDNA clones encoding the secreted  
CC proteins  
XX  
SQ Sequence 2386 BP; 756 A; 448 C; 496 G; 686 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 2-26e-93 Length: 2386  
Score: 862.50 Matches: 178  
Percent Similarity: 95.77% Conservative: 3  
Best Local Similarity: 94.18% Mismatches: 3  
Query Match: 93.24% Indels: 5  
DB: Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAF98399 (1-2386)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLeuThrGlyValValPheGlyAla 20  
Db 1476 TCAGTTGTTGACCTCTGCTGACCATCAGCTTAGGATATACAGGGTGTGATCCAGCT 1535  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 1536 AGCCTATTCTGCTGCTTCTATTGACAGTATTACAGCATTTGTGAGCGTAAACGCTACATT 1595  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60  
Db 1596 GCCTTGCCCTGCTCTCTGTGACCATCAGCTTAGGATATACAGGGTGTGATCCAGCT 1655  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 1656 ATCCAGAAATCAGATGAAGGCCACCCATTCAGG-----GAAGTTGCTATA 1700  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
Db 1701 TCTGAGGAGTGTGTTTCTGAGAGTACAGTAATTCCTCTTGGTATGTGACCTGCAGATA 1760  
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 1761 AAGGAATCAGGCGCTCTCTTAGTTGATGATTTAGTTAGTTCTCTGAAGTTGCAGTG 1820  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
Db 1821 TTGATGTGGGTATTTACCTATGTTGTGCTGCTTTTAAATGGTCTGACACTACTGATTTTG 1880  
QY 141 AlaLeuLysSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db 1881 GCTCTCATTTCTCTCTGAGTGTGTGTTTATTATGACGGCATCAGGCACAGATAGAT 1940  
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 1941 CATTTATAGGACTTCGAAATGAAGATGTTAAAGATGCTTAAAGATGCTTAAATCCAGCAAA 2000

QY 181 lleProGlyLeuLysArgLysAlaAsp 189  
Db 2001 ATCCCTGGATTGAGCGCAAGCTGAA 2027  
RESULT 48  
ABK34580  
ID ABK34580 standard; cDNA; 1514 BP.  
XX  
AC ABK34580;  
XX  
XX 08-MAY-2002 (first entry)  
XX Human cDNA for novel secreted protein, SEQ ID 349.  
XX Human; ss; gene; secreted protein; immune deficiency; viral infection;  
KW bacterial infection; fungal infection; autoimmune disorder; burn;  
KW rheumatoid arthritis; multiple sclerosis; autoimmune thyroiditis;  
KW diabetes; allergy; asthma; neurodegenerative disease; Crohn's disease;  
KW Alzheimer's disease; Parkinson's disease; liver fibrosis; tumour;  
KW coagulation disorder; haemophilia; inflammatory disorder; ulcer;  
KW tissue regeneration; wound healing; haematopoiesis; myeloid deficiency;  
KW lymphoid cell deficiency.  
XX Homo sapiens.  
OS  
XX WO200177290-A2.  
XX 18-OCT-2001.  
XX 29-MAR-2001; 2001WO-US010295.  
XX 06-APR-2000; 2000US-0194941P.  
XX (GENY ) GENETICS INST INC.  
XX  
PI Wong GG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;  
PI Gulukota K, Graham JR;  
XX WPI; 2002-179323/23.  
XX  
PT Six hundred and twenty five polynucleotides derived from a variety of  
PT human tissue sources which encode secreted proteins, useful for treating  
PT immune deficiencies and disorders such as autoimmune disorders.  
XX  
PS Claim 1; Page 173; 339pp; English.  
XX  
CC The invention relates to 625 polynucleotides which have been derived from  
CC a variety of human tissue sources and which encode novel secreted  
CC proteins, their complements and sequences that hybridize to them. Also  
CC included are a vector comprising the polynucleotide, a host cell.  
CC transformed with the vector, the proteins encoded by the polynucleotides,  
CC antibodies that bind to the proteins and identification of modulators of  
CC the proteins or the expression of the polynucleotide. The polynucleotides  
CC can be used as probes for the identification and isolation of full length  
CC cDNA and genomic DNA. The polynucleotides and proteins can also be used  
CC as nutritional supplements. The protein is useful in the treatment of  
CC various immune deficiencies and disorders such as viral infections,  
CC bacterial infections, fungal infections, autoimmune disorders (e.g.  
CC rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis and  
CC diabetes) and allergic reactions and conditions (e.g. asthma). They are  
CC also useful for treating neurodegenerative diseases (e.g. Alzheimer's  
CC disease, Parkinson's disease), liver fibrosis, coagulation disorders  
CC (e.g. haemophilia), inflammatory disorders (e.g. Crohn's disease) and  
CC tumours. They are also useful for tissue regeneration, for wound healing  
CC and in the treatment of burns, incisions and ulcers. The proteins are  
CC also useful for regulating haematopoiesis, for treating myeloid or  
CC lymphoid cell deficiencies. The present sequence is one of the 625 cDNA  
CC sequences encoding a secreted protein  
XX  
SQ Sequence 1514 BP; 455 A; 258 C; 313 G; 488 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 2.03e-91 Length: 1514

Score: 844.00 Matches: 172  
Percent Similarity: 98.87% Conservative: 3  
Best Local Similarity: 97.16% Mismatches: 2  
Query Match: 91.24% Indels: 0  
Dbs: 6 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ABK34580 (1-1514)

QY 13 LysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSer 32  
DB 3 AAGACTGGAGTGGTGGTGGCCAGCCATTCTCTGCTTCATTGACAGTATTCAGC 62

QY 33 IleValSerValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerPheArg 52  
DB 63 ATTGTGAGCGTAACAGCTACATTGCCCTTGGCCCTGCTCTGTGACCATCAGCTTAGG 122

QY 53 IleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAla 72  
DB 123 ATATCAAGGGGTGATCCAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA 182

QY 73 TyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAla 92  
DB 183 TATCTGGAAATCGAAGTGTCTATATCTCAGGAGTGGTTCAGAAATCAGTAATCTGCT 242

QY 93 LeuGlyHisValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeu 112  
DB 243 CTTGGTCATGTGAACATGCACGATGAAGAACTCAGCGCCCTCTCTAGTTGATGATTTA 302

QY 113 ValAspSerLeuLysPheAlaValLeuMetTyrValPheThrTyrValGlyAlaLeuPhe 132  
DB 303 GTTGATTTCTGGAAGTTTGCAGTGTGATGGGTATTTACCTATGTTGGTGGCTTGT 362

QY 133 AsnGlyLeuThrLeuLeuIleLeuAlaLeuLeuSerLeuPheSerIleProValIleTyr 152  
DB 363 AATGTCGTGACACTACTGATTTGGCTCTCATTTCACTTTCAGTGGTCTCTGTTATTTAT 422

QY 153 GluArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerValLysAsp 172  
DB 423 GAACGGCATCAGGCACAGATAGATCATTTATCTAGGACTTGCATAAAGAAATTAAGAT 482

QY 173 AlaMetAlaLysIleGlnAlaLysIleProGlyLeuLysArgLysAlaAsp 189  
DB 483 GCTATGGCTAAATCAAGCAAAAATCCCTGGATTGAAGCGCAAAAGCTGAA 533

RESULT 49  
AAD08386  
ID AAD08386 standard; cDNA; 1683 BP.  
AC AAD08386;  
DT 09-AUG-2001 (first entry)  
XX Human secreted protein-encoding gene 42 cDNA clone HAGFT48, SEQ ID NO:52.  
DE Human; secreted protein; proliferative disorder; cancer; tumour;  
KW foetal abnormality; developmental abnormality; haematopoietic disorder;  
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
KW inflammation; allergy; neurological disorder; Alzheimer's disease;  
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;  
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;  
KW cardiovascular disorder; angiogenic disorder; kidney disorder;  
KW gastrointestinal disorder; pregnancy-related disorder;  
KW endocrine disorder; infection; wound healing; vulnerability; cell culture;  
KW chemotaxis; food additive; gene therapy; binding partner identification;  
XX ss.  
XX Homo sapiens.  
OS  
XX  
FH Key Location/Qualifiers  
FT CDS 830..1192  
FT /\*tag= a  
FT /product= "Human secreted protein precursor"  
FT /note= "CDS does not include start codon"

FT sig\_peptide /partial  
FT 830..898 /\*tag= b  
FT mat\_peptide 899..1189 /\*tag= c  
FT /product= "Mature human secreted protein"  
XX WO200077022-A1.  
XX 21-DEC-2000.  
XX 01-JUN-2000; 2000WO-US015136.  
XX 11-JUN-1999; 99US-0138629P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Rosen CA, Ruben SM, Komatsoulis GA;  
XX P-PSDB; AAE03939.  
XX WPI; 2001-367020/38.  
XX Nucleic acids encoding 50 human secreted polypeptides, useful for preventing, diagnosing and/or treating diseases, e.g. Parkinson's disease, botulism, cancers and Scimitar syndrome.  
XX Claim 1; Page 520; 614pp; English.  
XX AAD08345-AAD08394 represent cDNAs corresponding to 50 human secreted protein genes and AAE03898-AAE03947 represent the proteins they encode.  
XX AAE03948-AAE03996 represent human secreted protein fragments or variants.  
XX The genes and their secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy, or pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 50 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein-encoding cDNA of the invention  
XX  
SQ Sequence 1683 BP; 369 A; 489 C; 464 G; 358 T; 0 U; 3 Other;  
Alignment Scores:  
Pred. No.: 7,61e-80 Length: 1683  
Score: 748.50 Matches: 159  
Percent Similarity: 86.17% Conservative: 3  
Best Local Similarity: 84.57% Mismatches: 3  
Query Match: 80.92% Indels: 24  
Dbs: 4 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAD08386 (1-1683)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
DB 788 GTTGTGACCTCTGTTACTGAGAGACATTAAAGACTGCGAGTGGTGTGTTGGTCCAGC 847

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 848 CTTATCTCTGCTGCTTTTCATTGACAGTATTTCAGCATTTGTGAGCGTAACAGCCTACATTTGCC 907  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 908 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAAGCTATC 967  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 968 CAGAAATCAGATGAGGCCACCCATTCAGGCGATATCTGGAATCTCAAGTTCGTATATCT 1027  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 1028 GAGGAGTTGGTTTCAGAAATGACAGTAATCTGCTCTTTGGTTCATGTGAACCTGCACGATAAAG 1087  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspLeuValAspLeuVal 121  
 Db 1088 GAACTCAGCGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGCT----- 1137  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
 Db 1137 ----- 1137  
 QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 1138 CTTATTTCACTCTTCAGTGTCTGCTGTTATTTATTAAGCGCATCAGGCACAGATAGATCAT 1197  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValIleValIleValIleValIleValIleValIle 181  
 Db 1198 TATCTAGGACTTGCATAATGAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAATC 1257  
 QY 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 1258 CTGGATTGAGCGCAAACTGAA 1281  
 RESULT 50  
 ID ADJ56527 standard; cdna; 1520 BP.  
 XX  
 AC ADJ56527;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Rat cdna differentially expressed in MYCN activated cells SeqID 333.  
 XX  
 KW rat; differential expression; transactivator; proto-oncogene;  
 KW neuroblastoma; small cell lung cancer; cytostatic; gene therapy; ss;  
 KW MYCN activated cell.  
 XX  
 OS Rattus norvegicus.  
 XX  
 PN US2003119009-A1.  
 XX  
 XX 26-JUN-2003.  
 XX  
 XX 25-FEB-2002; 2002US-00084817.  
 XX  
 XX 23-FEB-2001; 2001US-0270784P.  
 XX  
 XX (STUA/) STUART S G.  
 PA (NUCH/) NUCHTERN J G.  
 PA (PLON/) PLON S E.  
 PA (SHOH/) SHOHE J M.  
 XX  
 XX Stuart SG, Nuchtern JG, Plon SE, Shohet JM;  
 PI WPI; 2003-635698/60.  
 XX  
 XX New genes regulated by MYCN activation, useful in gene therapy, other  
 PT particularly for treating a subject with e.g. neuroblastoma or  
 PT cancers, or for diagnosing, staging or monitoring the treatment of the

PT cancer.

XX Claim 1; SEQ ID NO 333; 27pp; English.

XX This invention relates to novel isolated cDNAs that are differentially  
 CC expressed in MYCN activated cells. Specifically, it refers to  
 CC polynucleotide sequences that exhibit differential expression patterns in  
 CC cells activated by the transactivator MYCN, where MYCN is a proto-  
 CC oncogene that is amplified in neuroblastoma cells and is common in small  
 CC cell lung cancers. The present invention describes these cDNA molecules  
 CC as useful for in hybridisation assays to detect expression of nucleic  
 CC acids (or complementary nucleic acids) in a present in a given sample, as  
 CC well as for screening assays by identifying molecules or compounds that  
 CC specifically bind the cDNA as a ligand and modulate function or activity.  
 CC Accordingly, these compositions exhibit cytostatic activity and can also  
 CC be used for gene therapy purposes. This polynucleotide sequence is a cDNA  
 CC that is differentially expressed in MYCN activated cells, given in an  
 CC exemplification of the invention. NOTE: This sequence does not appear in  
 CC the printed specification but has been obtained in electronic format from  
 CC the US Patent Office at  
 CC ftp.sequdata.uspto.gov/sequence.html?DocID=20030119009.

XX Sequence 1520 BP; 398 A; 354 C; 336 G; 432 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.57e-71 Length: 1520  
 Score: 679.00 Matches: 127  
 Percent Similarity: 84.4% Conservative: 31  
 Best Local Similarity: 67.91% Mismatches: 29  
 Query Match: 73.41% Indels: 0  
 DB: 10 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADJ56527 (1-1520)

QY 3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22  
 Db 176 ATTGACCTGTTGTTATTTGGCGGACATCAAGCAGAGCGGCATCGTTTGGAGATTCTCG 235  
 QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
 Db 236 CTGCTGCTCTCTCCCTGACCCAGTTTCAGCGTGTGAGCGTCTGGCCCTACCTGGCCCTG 295  
 QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
 Db 296 GCGGCACCTCAGCCACCACCATCATGTTCCGCATCTCAAGCTCTGTTTACAGCAGTCCAG 355  
 QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
 Db 356 AAACCGACGAGAGGCCACCCCTTTCAAGGCTTACTTGGAGCTTGAGATCACCCCTTCTCAG 415  
 QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102  
 Db 416 GAGCAGATTTCAGAAATGACAGGACTGCTCTGAGTTCACGTGACACAGCACCTTAAGGAA 475  
 QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
 Db 476 CTGAGGAGGCTCTTCTCTGTCAGGACCTGGTGGATTCCTTAATTTGACGTCCTCATG 535  
 QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu 142  
 Db 536 TGGCTCTGACCTACCTGTTGGCGCTCTCTTCAATGGCTGACCTGCTGCTCATGGCTGTG 595  
 QY 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162  
 Db 596 GTTTCATGTTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTT 655  
 QY 163 LeuGlyLeuAlaAsnLysSerValIleValIleValIleValIleValIleValIlePro 182  
 Db 656 CTGGGACTTGTGAGGACTCACAATAATGCTGTTGTGGCAAGATTCAGGCTAAATCCCA 715  
 QY 183 GlyLeuLysArgLysAlaAsp 189  
 Db 716 GCGGCTTAAGAGGACGCTGAG 736



RESULT 51  
 ID ADO07887 standard; cDNA; 2331 BP.  
 XX  
 AC ADO07887;  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Human polynucleotide #66.  
 XX  
 KW Human; gene; ss; fat cell number; fat cell size; obesity; diabetes;  
 KW anorectic; antidiabetic.  
 XX  
 OS Homo sapiens.  
 XX  
 FN US2004071700-A1.  
 XX  
 PD 15-APR-2004.  
 XX  
 PF 09-OCT-2002; 2002US-00267502.  
 XX  
 PR 09-OCT-2002; 2002US-00267502.  
 XX  
 PA (LIFE-) LIFE SCI DEV CORP.  
 XX  
 PI Kim J, Galant R;  
 XX  
 DR WPI; 2004-328526/30.  
 DR P-PSDB; ADO08104.  
 XX  
 PT Identifying compounds that influence fat cell number or size for treating  
 PT or preventing obesity or diabetes by exposing the cell to the agent and  
 PT identifying fat cell number or size relative to cells not exposed to the  
 PT agent.  
 XX  
 PS Claim 1; SEQ ID NO 213; 275pp; English.  
 XX  
 CC The invention relates to a method of identifying compounds that influence  
 CC fat cell number or size comprising providing a cell that expresses a gene  
 CC and an agent, exposing the cell to the agent and identifying fat cell  
 CC number or size relative to cells not exposed to the agent. The method  
 CC also comprises providing an expression vector and an agent, exposing the  
 CC vector to the agent, detecting a change in expression of the gene  
 CC relative to expression of the gene in an expression vector not exposed to  
 CC the agent, treating a subject with the agent and identifying fat cell  
 CC number or size in the subject. The agent comprises an antisense  
 CC oligonucleotide. The subject comprises a mammal, preferably a human. The  
 CC method also comprises providing a polypeptide and an agent, exposing the  
 CC polypeptide to the agent, detecting binding of the agent to the  
 CC subject with the agent and identifying fat cell number or size in the  
 CC subject. The agent comprises an antibody. A method of regulating fat cell  
 CC number or size comprises providing a subject containing fat cells and an  
 CC agent that changes the expression of a gene, and treating the subject  
 CC with the agent under conditions so that fat cell size or number in the  
 CC subject is altered. The method is useful for identifying compounds that  
 CC influence fat cell number or size, for preparing a composition for  
 CC treating or preventing obesity or diabetes. This sequence represents  
 CC human cDNA used in the scope of the invention.  
 XX  
 SQ Sequence 2331 BP; 552 A; 698 C; 649 G; 432 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 2,866-71 Length: 2331  
 Score: 679.00 Matches: 127  
 Percent Similarity: 84.49% Conservative: 31  
 Best Local Similarity: 67.91% Mismatches: 29  
 Query Match: 73.41% Indels: 0  
 DB: 12 Gaps: 0  
 3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22  
 1768 ATTGACCTGTTGTTATTTGGCGGACATCAAGCAGACGGCATCGTGTGGGAGTTTCCTG 1827  
 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
 1828 CTGCTGCTCTTCTCCCTGACCCAGTTCAGCGTGGTGGCGTCTGCTGCTGCTGCTGCTG 1887  
 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
 1888 GCCGACCTCTCAGCCACCATCAGTTCGCGATCTACAAAGTCTGTGTTTACAGCAGTGCGAG 1947  
 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
 1948 AAACCCGACGAGGCCACCTTTCAAGCCCTACTTTGGAGCTTGAGATCACCCCTTTCTCAG 2007  
 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102  
 2008 GAGCAGATTTCAGAAAGTACACGCGACTGCTGCGCTTCTACGTGAACAGCACACTTAAGGAA 2067  
 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
 2068 CTGAGGAGGCTCTCTCTTGTCCAGACCTGTGGATTCCTTAAATTTGCGAGTCTCTGATG 2127  
 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAlaLeu 142  
 2128 TGGCTCCTGACCTAGTTGGCGCTCTCTTCAATGCGCTGACCTGCTGCTGCTGCTG 2187  
 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162  
 2188 GTTTCATGTTTACTCTACCTGATGTATGTTAAGCACCAGGCACAGATTGACCAATAT 2247  
 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaValIleGlnAlaLysIlePro 182  
 2248 CTGGAGCTTGAGGAGCTCACATAAATCTGTTGTGGCAAGATTTCAGCTTAAATTC 2307  
 183 GlyLeuLysArgLysAlaAsp 189  
 2308 GCGCTAAGAGCGCAGCTGAG 2328  
 RESULT 52  
 AAX75770  
 ID AAX75770 standard; DNA; 3202 BP.  
 XX  
 AC AAX75770;  
 DT 22-JUL-1999 (first entry)  
 XX  
 DE Human neuroendocrine-specific protein NSP-A DNA.  
 KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;  
 KW frameshift mutation; age-related disease; neurodegenerative disorder;  
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;  
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;  
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;  
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;  
 KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;  
 KW glial fibrillary acidic protein; GFAP; p53; senaphorin II; HUPF-1;  
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;  
 KW high mobility group protein-C; neuroendocrine specific protein A; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO9845322-A2.  
 XX  
 PD 15-OCT-1998.  
 XX  
 PF 02-APR-1998; 98WO-IB000705.  
 XX  
 PR 10-APR-1997; 97US-0043163P.  
 XX  
 PA (ROYA-) ROYAL NETHERLANDS ACAD AGTS & SCI.  
 PA (UYRO-) UNIV ROTTERDAM ERASMUS.



PR 03-OCT-2000; 2000US-0237604P.  
 PR 03-OCT-2000; 2000US-0237606P.  
 PR 03-OCT-2000; 2000US-0237608P.  
 PR 01-NOV-2000; 2000US-0244867P.  
 PR 01-NOV-2000; 2000US-0245084P.  
 XX (AVAL-) AVALON PHARM.  
 PA Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;  
 PI Soppet DR, Weaver Z;  
 XX WPI; 2002-188264/24.  
 DR  
 XX Screening for anti-neoplastic agent involves exposing cells to a chemical  
 PT agent to be tested for anti-neoplastic activity, and determining a change  
 PT in expression of a gene of a signature gene set.  
 XX  
 PS Claim 1; SEQ ID NO 3237; 44pp; English.  
 XX  
 CC The present invention describes a method (M1) for screening for an anti-  
 CC neoplastic agent. The method involves exposing cells to a chemical agent  
 CC to be tested for anti-neoplastic activity, determining a change in  
 CC expression of at least one gene (I) of a signature gene set, where (I)  
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664  
 CC to ABL70110), or is at least 95% identical to (S), where a change in  
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic  
 CC activity and can be used in gene therapy. M1 can be used for screening an  
 CC anti-neoplastic agent, and can be used for producing a product which is  
 CC the data collected with respect to the anti-neoplastic agent as a result  
 CC of M1, and the data is sufficient to convey the chemical structure and/or  
 CC properties of the agent. M1 can be used in the treatment of cancer such  
 CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,  
 CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell  
 CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous  
 CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms  
 CC tumour  
 XX  
 SQ Sequence 3202 BP; 784 A; 891 C; 825 G; 702 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 4.47e-71 Length: 3202  
 Score: 679.00 Matches: 127  
 Percent Similarity: 84.49% Conservative: 31  
 Best Local Similarity: 67.91% Mismatches: 29  
 Query Match: 73.41% Indels: 0  
 DB: 6 Gaps: 0  
 US-09-830-972-2\_COPY\_975\_1163 (1-189) x ABL64900 (1-3202)  
 Qy 3 ValAspLeuThrTyTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22  
 Db 1890 ATTGACCTGTTGTTATGGCGGACATCAAGCAGCGGCATCGTTGGAGTTCTCTG 1949  
 Qy 23 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
 Db 1950 CTGCTGCTCTCTCCCTCACCAGTTACGCTGGTGGAGCGTGGTCTACCTCGCCCTG 2009  
 Qy 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
 Db 2010 GCCGACCTCTCAGCCACCATCAGTTTCGCGCATCTACAAGTCTGTTTACAGCAGTGCAG 2069  
 Qy 63 LysSerAspGluGlyHisProPheArgAlaTyrIleLeuGluSerGluValAlaIleSerGlu 82  
 Db 2070 ANACCGACGAGGCCACCTTTTCAGGCCCTTCTGAGCTTGAGTACCCCTTCTCAG 2129  
 Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102  
 Db 2130 GAGCAGATTACAGAGTACACGACTCCCTCGAGTTCTACGTTGACAGCACACTTAAGGAA 2189  
 Qy 103 LeuArgLeuPheLeuValAspLeuValAspLeuValAspLeuValAspLeuValMet 122  
 Db 2190 CTGAGGAGGCTCTCTCTTGTCCAGGACCTGGTGGATTCCTTAAAAATTTGCAGTCTGATG 2249

Qy 123 TrpValPheThrTyTrpValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu 142  
 Db 2250 TGGCTCTGACCTAGCTTGGCGCTCTCTCAATGGCCTGACCTGCTCTCATGGCTGTG 2309  
 Qy 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162  
 Db 2310 GTTTCATATGTTTACTCTACCTGTAGTGTATGTTAAGCACCCAGGCACAGATTGACCAATAT 2369  
 Qy 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
 Db 2370 CTGGACTTGTGAGGACTCACATAAATGCTGTTGTGGCAAGATTTCAGGCTAAATCCCA 2429  
 Qy 183 GlyLeuLysArgLysAlaAsp 189  
 Db 2430 GCGCTAAGAGCGCAGCTGAG 2450  
 RESULT 54  
 ADQ18661  
 ID ADQ18661 standard; DNA; 3202 BP.  
 AC ADQ18661;  
 XX  
 DT 26-AUG-2004 (first entry)  
 XX  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1480.  
 XX  
 KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;  
 XX ds.  
 OS Homo sapiens.  
 XX  
 PN WO2004048938-A2.  
 XX  
 PD 10-JUN-2004.  
 XX  
 PF 26-NOV-2003; 2003WO-US038193.  
 XX  
 PR 26-NOV-2002; 2002US-0429739P.  
 XX  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 XX  
 PI Aziz N, Ginsburg WM, Zlotnik A;  
 XX  
 DR WPI; 2004-441208/41.  
 XX  
 PT Early detection of soft tissue sarcoma comprises determining expression  
 PT of a gene in a first soft tissue sample and a normal soft tissue sample  
 PT and comparing the gene expression, also useful in treating soft tissue  
 PT sarcoma.  
 PS  
 XX Example 2; SEQ ID NO 1480; 210pp; English.  
 CC The invention relates to a novel method for detecting soft tissue sarcoma  
 CC which comprises obtaining a first soft tissue sample from an individual  
 CC and a normal soft tissue sample from the same or different individual,  
 CC determining the expression of a gene in both samples and comparing the  
 CC expression of the gene in both soft tissue samples, where a higher level  
 CC of protein expression in the first soft tissue sample indicates the  
 CC presence of soft tissue sarcoma. The method of the invention has  
 CC cytostatic applications and may be useful for detecting soft tissue  
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic  
 CC acid sequences may be useful in diagnostic and screening applications.  
 CC The current sequence is that of a human soft tissue sarcoma-upregulated  
 CC DNA of the invention. The current sequence is not shown within the  
 CC specification per se but was submitted in CD format by the inventor.  
 XX  
 SQ Sequence 3202 BP; 784 A; 891 C; 825 G; 702 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 4.47e-71 Length: 3202  
 Score: 679.00 Matches: 127  
 Percent Similarity: 84.49% Conservative: 31  
 Best Local Similarity: 67.91% Mismatches: 29

Query Match:	73.41%	Indels:	0
DB:	12	Gaps:	0
US-09-830-972-2_COPY_975_1163 (1-189) x ADQ18661 (1-3202)			
Qy	3	ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu	22
Db	1890	ATTGACCTGTTGATTGGCGGACATCAAGCAGCGGCATCGTGTGGGAGTTCTCTG	1949
Qy	23	PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu	42
Db	1950	CTGCTGCTCTCTCCCTGACCCAGTTTCAGCGTGTGAGCGTCTGCTGCTGCTGCTG	2009
Qy	43	AlaLeuLeuSerValThrIleSerPheArgIleTyrIleValSerGlyValIleGlnAlaIleGln	62
Db	2010	GCGCAGCTCTCAGCCACCATCATGTTCCGCATCTACAAGTCTGTTTACAGCAGTGCAG	2069
Qy	63	LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu	82
Db	2070	AAAACCGACGAGGCGACCCCTTTCAAGGCCTACTTGGAGCTTGAGATCACCCCTTTCTCAG	2129
Qy	83	GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu	102
Db	2130	GAGCAGATTCAAGAGTACAGGACTGCTGCTGAGTCTTACGTGACACGACACATTAAGAA	2189
Qy	103	LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet	122
Db	2190	CTGAGGAGGCTCTCTCTGTCAGGACCTGCTGGATTCTTAAATTTGACAGTCTCTGATG	2249
Qy	123	TrpValPheThrValGlyValAlaPheAsnGlyLeuThrLeuLeuLeuAlaLeu	142
Db	2250	TGGCTCTGACCTACCTGCTGGGCTCTCTTCAATGCTGACCCCTGCTGCTGCTGCTG	2309
Qy	143	IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHieTyr	162
Db	2310	GTTTCAATGTTTACTTACTTACTGTTAGTGTATGTAAGCACCAGGACAGATTGACCAATAT	2369
Qy	163	LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro	182
Db	2370	CTGGGACTTGTGAGGACTCACATAAATGCTGTTGTGGCAAGATTCAGGCTAAAATCCCA	2429
Qy	183	GlyLeuLysArgLysAlaAsp	189
Db	2430	GGCGCTAAGAGCAGCGCTGAG	2450
RESULT 56			
ID ADR24525 standard; DNA; 3202 BP.			
AC ADR24525;			
21-OCT-2004 (first entry)			
Breast cancer prognosis marker #386.			
db; breast cancer; prognosis; gene expression; diagnosis.			
Homo sapiens.			
W02004065545-A2.			
05-AUG-2004.			
15-JAN-2004; 2004WO-US001100.			
15-JAN-2003; 2003US-00342887.			
(ROSE-) ROSETTA INPHARMATICS LLC.			
(NECA-) NETHERLANDS CANCER INST.			
Van't Veer LJ, He Y;			
WPI; 2004-593473/57.			



PA (HINZ/) HINZMANN B.  
 PA (DAHL/) DAHL E.  
 PA (ROSE/) ROSENTHAL A.  
 PA (HERM/) HERMANN K.  
 PA (PILA/) PILARSKY C.  
 XX  
 PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;  
 PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;  
 PI Xinzhang L, Staub E;  
 XX  
 XX WPI; 2004-653386/63.  
 XX  
 PT New nucleic acids, and encoded proteins, from prostatic cancer tissue,  
 PT useful for diagnosis, treatment and in screening for specific binding  
 PT agents.  
 XX  
 PS Claim 1; Page 1329; 1607pp; German.  
 XX  
 CC This invention describes novel cytostatic polynucleotide and polypeptide  
 CC sequences which can be used in a method for diagnosing prostatic cancer  
 CC or the risk of developing prostatic cancer. Diagnosis is based on  
 CC determining over transcription or over expression of the sequences in  
 CC prostatic tissue. Screening for inhibitors of the sequences or detection  
 CC substances involves a binding assay, any compounds that bind are  
 CC selected, optionally after deconvolution of mixtures. Detection of a  
 CC predetermined minimum level of the reporter indicates the presence of  
 CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,  
 CC short-interfering RNA or ribozymes; an organic molecule of molecular  
 CC weight below 5000, preferably 300, that binds to the polypeptide; an  
 CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the  
 CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human  
 CC (monoclonal) antibody directed against Ab or any of the above derivatised  
 CC with a reporter group, cell toxin, immunostimulatory molecules and/or  
 CC radioisotope. The polynucleotides are identified in human prostatic  
 CC cancer by differential expression analysis, using DNA microarrays,  
 CC between normal and tumorous tissues, with (over)expression being detected  
 CC by quantitative PCR. Analysis of prostatic cancer samples showed that  
 CC CD24 was upregulated in many of them. Sections of tissue, isolated from  
 CC prostatic cancer patients, or subjects at risk, were incubated  
 CC sequentially with anti-human CD4 murine monoclonal antibodies;  
 CC biotinylated second antibody; streptavidin-conjugated horseradish  
 CC peroxidase and then diaminobenzidine as colour former (brown). The  
 CC samples were counterstained with hemalum (blue). Malignant cells stained  
 CC strongly but non-malignant cells only weakly. In 15 of 63 samples of  
 CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and  
 CC lymph node metastases were also stained. ADR65805-ADR66954 represent the  
 CC polynucleotide and polypeptide sequences used in the method of the  
 CC invention.  
 XX  
 SQ Sequence 3202 BP; 784 A; 891 C; 825 G; 702 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 4,47e-71 Length: 3202  
 Score: 679.00 Matches: 127  
 Percent Similarity: 84.49% Conservative: 31  
 Best Local Similarity: 67.91% Mismatches: 29  
 Query Match: 73.41% Indels: 0  
 DB: 13 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADR66747 (1-3202)

QY 3 valAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22  
 DB 1890 ATTGACCTGTGTATTTGGCGGGACATCAAGCAGCGGCATCGTGTGGGATTCCTCG 1949  
 QY 23 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValLeu 42  
 DB 1950 CTGCTGCTCTTCTCCCTGACCCAGTTCAGCGTGTGAGGTCGTGGCTACCTCGGCCCTG 2009  
 QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaLeu 62  
 DB 2010 GCGGCATCTCAGCCACCATCAGTTTCGCGCATCTACAAAGTCTGTTTACAAAGCAGTGCAG 2069

QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
 DB 2070 AAACCCGACGAAGGCCACCCCTTTCAAGGCTTACTTTGGAGCTTGAGATCATCCCTTTCTCAG 2129  
 QY 83 GlyLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102  
 DB 2130 GAGCAGATTCAAGATACACGGACTGCTCGCAGTTCCTAGCTGACAGCACACTTAAGGAA 2189  
 QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
 DB 2190 CTGAGGAGGCTCTTCTCTTGTCCAGGACCTGTGTGGATTCTCTAAAAATTTTCAGTCTCTGATG 2249  
 QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu 142  
 DB 2250 TGGCTCTGACCTACGTGTGGCGCTCTCTTCAATGGCTGACCTGCTGCTCATGTGCTGTG 2309  
 QY 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162  
 DB 2310 GTTTCATGTTTACTCTACTCTAGTGTATGTTAAGCACCGACGACAGATTGACCAATAT 2369  
 QY 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
 DB 2370 CTGGGACTTGTGAGGACTCACATAAATGCTGTGTGTGGCAAGATTTCAGGCTAAATCCCA 2429  
 QY 183 GlyLeuLysArgLysAlaAsp 189  
 DB 2430 GCGCTAAGAGGACGCTGAG 2450  
 RESULT 58  
 ID ADQ23106 standard; DNA; 3305 BP.  
 XX ADQ23106;  
 AC ADQ23106;  
 XX  
 DT 26-AUG-2004 (first entry)  
 XX  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5926.  
 XX  
 KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;  
 KW ds.  
 OS Homo sapiens.  
 XX  
 PN WO2004048938-A2.  
 XX  
 PD 10-JUN-2004.  
 XX  
 PF 26-NOV-2003; 2003WO-US038193.  
 XX  
 PR 26-NOV-2002; 2002US-0429739P.  
 XX  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 XX  
 PI Aziz N, Ginsburg WM, Zlotnik A;  
 XX  
 DR WPI; 2004-441208/41.  
 XX  
 PT Early detection of soft tissue sarcoma comprises determining expression  
 PT of a gene in a first soft tissue sample and a normal soft tissue sample  
 PT and comparing the gene expression, also useful in treating soft tissue  
 PT sarcoma.  
 XX  
 XX Example 2; SEQ ID NO 5926; 210pp; English.  
 XX  
 CC The invention relates to a novel method for detecting soft tissue sarcoma  
 CC which comprises obtaining a first soft tissue sample from an individual  
 CC and a normal soft tissue sample from the same or different individual,  
 CC determining the expression of a gene in both samples and comparing the  
 CC expression of the gene in both soft tissue samples, where a higher level  
 CC of protein expression in the first soft tissue sample indicates the  
 CC presence of soft tissue sarcoma. The method of the invention has  
 CC cytostatic applications and may be useful for detecting soft tissue  
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic

XX electrophoresis; mass spectrometry; cpg dinucleotide; solid tumour.  
XX  
XX  
XX Homo sapiens.  
XX OS  
XX

Pred. No.:	4,71e-71	Length:	3327
Score:	679.00	Matches:	127
Percent Similarity:	84.49%	Conservative:	31
Best Local Similarity:	67.91%	Mismatches:	29
Query Match:	73.41%	Indels:	0

```

DB:
US-09-830-972-2_COPY_975_1163 (1-189) x ADS99925 (1-3327)
QY 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22
DB 1977 ATTGACCTGTTGATTTGGGGGACATCAAGCAGCGGGATGCTGTTTGGGATGTCCTG 2036

QY 23 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
DB 2037 CTGCTGCTCTCTCCCTGACCCAGTTTCAGCGTGTGAGCGTCTGTCGCTTACCTGCGCCCTG 2096

QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaLeu 62
DB 2097 GCGCGACTCTCAGCCACCATCAGTTTCCGATCTTACAGTCTGTTTACAGCAGTGCAG 2156

QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
DB 2157 AAACCGCAGAGGCCACCTTTTCAGGCTTACTTGAGCTTGAGATCACCTTCTCTCAG 2216

QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102
DB 2217 GAGCAGATTGAGAGTACAGGACTGCTGCTGAGTTTCTGTAACAGCAGCACATTAAAGAA 2276

QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122
DB 2277 CTGAGGAGGCTCTCTCTGTCAGGACCTGGTGGATTCCTTAAATTTTCAGTCTCTGATG 2336

QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeu 142
DB 2337 TGCTCTCCTGACCTACCTGTTGGGCTCTCTCAATGGCTGACCTGCTGCTCATGGCTGTG 2396

QY 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162
DB 2397 GTTTCATGTTTACTCTACTCTGAGTGTATGTTTAAAGCAGCAGATTCACCAATAT 2456

QY 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
DB 2457 CTGGGACTTGTGAGGACTCACATAATGCTGTTGTGGCAAGATTCCAGCTAAATCCCA 2516

QY 183 GlyLeuLysArgLysAlaAsp 189
DB 2517 GCGCTTAAGGCGACGCTGAG 2537

RESULT 60
ID ADB79854
XX ADB79854 standard; DNA; 1502 BP.
XX AC ADB79854;
XX DT 04-DEC-2003 (first entry)
XX DE Rat rS-Rex-s human NSP C homolog coding sequence, SEQ ID 94.
XX KW Analgesic; pain; streptozocin-induced diabetes; rat; gene; ds.
XX OS Rattus norvegicus.
XX PN EP1279744-A2.
XX PD 29-JAN-2003.
XX PF 26-JUL-2002; 2002EP-00255249.
XX PR 27-JUL-2001; 2001GB-00018354.
XX PR 07-FEB-2002; 2002GB-00002910.
XX PA (WARN ) WARNER LAMBERT CO.
XX PI Brooksbank RA, Dixon AK, Lee K, Pinnock RD;
XX DR WPI; 2003-395407/38.
XX DR P-PSDB; ADB79853.

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XX Use of isolated gene sequences and encoded polypeptides that are
PT upregulated in the spinal cord in response to streptozocin-induced
PT diabetes for screening compounds for the treatment of pain, or for
PT diagnosing pain.
XX Claim 1; Page 171; 334pp; English.
XX The present invention relates to nucleotide sequences which are useful in
CC the screening of compounds for the treatment of pain, or for the
CC diagnosis of pain. The nucleotide sequences are up-regulated in the
CC spinal cord in response to streptozocin-induced diabetes. The present
CC sequence is one such nucleotide sequence.
XX Sequence 1502 BP; 348 A; 392 C; 363 G; 399 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 2,046-71 Length: 1502
Score: 678.00 Matches: 126
Percent Similarity: 84.4% Conservative: 32
Best Local Similarity: 67.3% Mismatches: 29
Query Match: 73.3% Indels: 0
DB: 10 Gaps: 0
US-09-830-972-2_COPY_975_1163 (1-189) x ADB79854 (1-1502)
QY 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22
DB 179 ATTGACCTTCTGCTGCGGACATCAAGCAGCGGGATGTTGTTGCGGAGCTCTCTG 238
QY 23 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
DB 239 CTGCTGCTCTCTCTGCTGACCGATTCAGCGTGTGAGCGTCTGCTGCTGCTGCTG 298
QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaLeu 62
DB 299 GCTGCTCTCTGCGCCACCATCAGCTTCCGATCTACAGTCCGTTCTACAGCTGTG 358
QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaLysGlu 82
DB 359 AAACAGATGAGGCTCACCTTTCAAGGCTTACCTGAGCTGAGATCACCTGCTCCAG 418
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102
DB 419 GAGCAGATCCAGAGTACAGACTGCTGCTGAGCTTACGTGAACAGACTCTGAAGAG 478
QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122
DB 479 CTACGGAGGCTCTCTCTGCTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 538
QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeu 142
DB 539 TGCTCTCCTGACCTACCTGTTGGGCTTCTCAATGGCTGACCTGCTGCTGCTGCTG 598
QY 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162
DB 599 GTTTCATGTTTACTCTACTCTGAGTGTATGTTTAAAGCAGCAGATTCACCAATAT 658
QY 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
DB 659 CTGGGACTTGTGAGGACTCACATAACACCGTGTGTCGCAAGATCCAGCTAAATCCC 718
QY 183 GlyLeuLysArgLysAlaAsp 189
DB 719 GCGCGCAGAGGCGACGCTGAG 739
RESULT 61
ID ADO07889
XX ADO07889 standard; cDNA; 2343 BP.
XX AC ADO07889;
XX DT 01-JUL-2004 (first entry)

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XX Mouse polynucleotide #58.  
 DE Mouse; gene; ss; fat cell number; fat cell size; obesity; diabetes;  
 KW anorectic; antidiabetic.  
 XX Mus sp.  
 OS US2004071700-A1.  
 XX 15-APR-2004.  
 PD 09-OCT-2002; 2002US-00267502.  
 XX 09-OCT-2002; 2002US-00267502.  
 XX (LIFE-) LIFE SCI DEV CORP.  
 XX Kim J, Galant R;  
 PI WPI; 2004-328526/30.  
 DR P-PSDB; ADO08106.  
 XX Identifying compounds that influence fat cell number or size for treating  
 PT or preventing obesity or diabetes by exposing the cell to the agent and  
 PT identifying fat cell number or size relative to cells not exposed to the  
 PT agent.  
 XX Claim 1; SEQ ID NO 215; 275pp; English.  
 PS The invention relates to a method of identifying compounds that influence  
 CC fat cell number or size comprising providing a cell that expresses a gene  
 CC and an agent, exposing the cell to the agent and identifying fat cell  
 CC number or size relative to cells not exposed to the agent. The method  
 CC also comprises providing an expression vector and an agent, exposing the  
 CC vector to the agent, detecting a change in expression of the gene  
 CC relative to expression of the gene in an expression vector not exposed to  
 CC the agent, treating a subject with the agent and identifying fat cell  
 CC number or size in the subject. The agent comprises an antisense  
 CC oligonucleotide. The subject comprises a mammal, preferably a human. The  
 CC method also comprises providing a polypeptide and an agent, exposing the  
 CC polypeptide to the agent, detecting binding of the agent to the  
 CC polypeptide or a change in an activity of the polypeptide, treating a  
 CC subject with the agent and identifying fat cell number or size in the  
 CC subject. The agent comprises an antibody. A method of regulating fat cell  
 CC number or size comprises providing a subject containing fat cells and an  
 CC agent that changes the expression of a gene, and treating the subject  
 CC with the agent under conditions so that fat cell size or number in the  
 CC subject is altered. The method is useful for identifying compounds that  
 CC influence fat cell number or size, for preparing a composition for  
 CC treating or preventing obesity or diabetes. This sequence represents  
 CC mouse cDNA used in the scope of the invention.  
 XX SQ Sequence 2343 BP; 536 A; 710 C; 646 G; 451 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 3.8e-71 Length: 2343  
 Score: 678.00 Matches: 126  
 Percent Similarity: 84.49% Conservative: 32  
 Best Local Similarity: 67.38% Mismatches: 29  
 Query Match: 73.30% Indels: 0  
 DB: 12 Gaps: 0  
 US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADO07889 (1-2343)  
 QY 3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValAlaPheGlyAlaSerLeu 22  
 Db 1780 ATTGACCTTCTGTTGGGGGACATCAAGCAGCTGGATTGTTGGGAGCTTCTG 1839  
 QY 23 PheLeuLeuLeuSerLeuValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
 Db 1840 CTGCTGCTTCTTCCCTGACCAGTTTAGCGTTGTGAGCGTGGTTGCTTACCTGCGCCTG 1899

QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
 Db 1900 GCGCCCTCTCTGCCACCATCAGCTTCGCATCTACAAGTCGTTCTACAGCTGTCAG 1959  
 QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
 Db 1960 AAAACAGATGAGGCTCACCCCTTCAAGGCCCTACCTGGAGCTGGAGATCACCTGTCCAG 2019  
 QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102  
 Db 2020 GAGCAGATCCAGAAAGTACACAGACTGCCCTGAGCTGTATGTGAACAGCAGCTCTGAAGGAG 2079  
 QY 103 LeuArgArgLeuPheLeuValAspSerLeuValAspSerLeuLysPheAlaValLeuMet 122  
 Db 2080 CTACGAGGCTTTTCTGCTGGTCCAGACCTGCTGGATTCTTAAATTTGCAGTCTCATG 2139  
 QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeu 142  
 Db 2140 TGGCTCTGACTACCTACGTTGGCGCTCTTCAATGGCTGACCTGCTGCTTATGGCTGTG 2199  
 QY 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162  
 Db 2200 GTTTCGATGTTTACTCTACCTGTTGTGTACCTTAAGCACCAGGCAAGTTGACCAATAT 2259  
 QY 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
 Db 2260 CTGGACTTGTGAGGACTCACAATAACACCTGCTGGCAAGATCCAGGCTAATAATCCCC 2319  
 QY 183 GlyLeuLysArgLysAlaAsp 189  
 Db 2320 GCGCCCAAGAGCGAGCTGTAG 2340  
 RESULT 62  
 ABX43312 ID ABX43312 standard; cDNA; 422 BP.  
 AC ABX43312;  
 XX 20-FEB-2003 (first entry)  
 DE Bovine EST associated with lactation/muscle/fat deposition #8477.  
 KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;  
 KW muscle deposition; fat deposition; genome mapping; gene identification;  
 KW gene analysis; cattle breeding.  
 OS Bos Taurus.  
 XX US2002137139-A1.  
 XX 26-SEP-2002.  
 XX 24-SEP-2001; 2001US-00960352.  
 PR 12-JAN-1999; 99US-0115707P.  
 PR 11-JAN-2000; 2000US-00480902.  
 XX (BYAT/) BYATT J C.  
 PA (MATH/) MATHIALAGAN N.  
 PA (TAON/) TAO N.  
 XX (WARR/) WARREN W C.  
 PI Byatt JC, Mathialagan N, Tao N, Warren WC;  
 XX WPI; 2003-110599/10.  
 XX New nucleic acid associated with lactation, and muscle and fat  
 PT deposition, useful for genome mapping, gene identification and analysis,  
 PT cattle breeding, or for genetically improving cattle.  
 XX Claim 2; SEQ ID NO 8477; 245pp; English.  
 XX The invention relates to a purified nucleic acid molecule associated with

CC lactation or muscle and fat deposition (designated LMPD), derived from  
 CC cattle, and the LMPD nucleic acid can specifically hybridize to a second  
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,  
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are  
 CC ; (1) a transformed cell having a nucleic acid comprising an LMPD nucleic  
 CC acid linked to a promoter and a 3' non-translated sequence that  
 CC functions in the cell to cause termination of transcription and addition  
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and  
 CC (2) determining a level or pattern of a molecule in a bovine cell or  
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any  
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a  
 CC complementary nucleic acid molecule obtained from the bovine cell or  
 CC tissue, where hybridization between the marker nucleic acid and the  
 CC complementary nucleic acid permits the detection of the molecule; and (b)  
 CC detecting the level or pattern of the complementary nucleic acid, where  
 CC the detection of the complementary nucleic acid is predictive of the  
 CC level or pattern of the molecule. The LMPD nucleic acid is used for  
 CC determining a level or pattern of a molecule in a bovine cell or tissue.  
 CC It is useful for genome mapping, gene identification and analysis, cattle  
 CC breeding, preparation of constructs for use in cattle gene expression, or  
 CC for genetically improving cattle. The present sequence is one of the  
 CC 15112 bovine LMPD EST (expressed sequence tag) nucleic acids. Note: The  
 CC present sequence was not shown in the specification but was obtained in  
 CC electronic format from the USPTO web site:  
 CC seqdata.uspto.gov/sequence.html?DocID=200201371139  
 XX  
 SQ Sequence 422 BP; 109 A; 79 C; 94 G; 140 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 7,91e-72 Length: 422  
 Score: 675.00 Matches: 136  
 Percent Similarity: 98.57% Conservative: 2  
 Best Local Similarity: 97.14% Mismatches: 2  
 Query Match: 72.97% Indels: 0  
 DB: Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ABX43312 (1-422)

QY 37 ThrAlaTyrIleAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGly 56  
 Db 2 ACGGCCTACATTGCCCTTGGCCCTGCTCTGTGACTATCAGCTTTAGGATATATAAGGCT 61  
 QY 57 ValIleGlnAlaIleGlnIleSerAspGluGlyHisProPheArgAlaTyrIleGluSer 76  
 Db 62 GTGATCCAGGCTATCAGAAATCTGATGAAGGCCACCCATTGAGGCATATTTGGAACT 121  
 QY 77 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal 96  
 Db 122 GAAGTTGCTATATCTGAGGAGTTGGTTGAGAGTACAGCAATCTGCTCTTGGTCATGTT 181  
 QY 97 AsnSerThrIleLysGluLeuArgArgLeuPheLeuValAspSerLeuValAspSerLeu 116  
 Db 182 AACTGCACAATAAAGAACTCAGACGCCCTCTTCTTAGTTGATCATTTAGTTGATTTCTCG 241  
 QY 117 LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheGlnGlyLeuThr 136  
 Db 242 AAGTTTGCAGTGTGATGTTGGGTATTTACCTATGTTGGTGCCTTGTTCATGCTGCA 301  
 QY 137 LeuLeuIleLeuAlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGln 156  
 Db 302 CTACTAATTTTGGCTCTGATTTCACTTTCAGTGTTCCTGTTATTTATGACGGCATCAG 361  
 QY 157 ValGlnIleAspHisTyrIleGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLys 176  
 Db 362 GCGCAATAGATCATTTATCTGGGACTTGCAATAAGAAATGTAAGATGCTATGGCTAAA 421

RESULT 63

ID ADB85247 standard; DNA; 1473 BP.

XX

AC ADB85247;

XX 04-DEC-2003 (first entry)

XX DE  
 XX KW  
 KW KW  
 KW XX  
 OS  
 PN  
 PD  
 XX  
 PF  
 XX  
 PR  
 PR  
 XX  
 PA  
 PI  
 XX  
 DR  
 DR  
 XX  
 PT  
 PT  
 XX  
 PS  
 XX  
 CC  
 CC  
 CC  
 CC  
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 CC  
 CC  
 CC  
 CC  
 CC  
 CC  
 CC  
 CC  
 CC  
 SQ

Sequence 1473 BP; 357 A; 373 C; 343 G; 400 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 7,32e-70 Length: 1473  
 Score: 665.00 Matches: 126  
 Percent Similarity: 84.4% Conservative: 32  
 Best Local Similarity: 67.3% Mismatches: 29  
 Query Match: 71.8% Indels: 1  
 DB: Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADB85247 (1-1473)

QY 3 ValAspLeuLeuTyrTyrArgAspIleLysTyrGlyValValPheGlyAlaSerLeu 22  
 Db 146 ATTAGCTTCTGTACTGCGGACATCAAGACAGCGGATGTGTTGGGAGCTTCCTG 205  
 QY 23 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
 Db 206 CTGCTGCTCTTCTCTCCCTGACCCAGTTGAGCGTGTGAGCGTCTGCGCTTACCTGGCCCTG 265  
 QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
 Db 266 GCTGCCCTCTCTGCCACCATCATCGCTTCGCAATCAAGTCCGTCTTCAAGCTGGCAG 325  
 QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82

Rat C1-13 protein neuronal-specific gene SEQ ID NO:128.

rat; streptozocin; kinase; phosphatase; ion channel protein; receptor;  
 transporter; G-protein coupled receptor; GPCR; DNA-binding proteins;  
 protease; enzyme; analgesic; gene therapy; pain; diabetes; ds; gene.

Rattus norvegicus.

EP1284297-A2.

19-FEB-2003.

26-JUL-2002; 2002EP-00255228.

27-JUL-2001; 2001GB-00018354.

07-FEB-2002; 2002GB-00002880.

(WARN ) WARNER LAMBERT CO.

Brooksbank RA, Dixon AK, Lee K, Pincock RD;

WPI; 2003-364994/35.

P-PSDB; ADB85246.

Use of gene sequence that is down-regulated in response to streptozocin-induced diabetes, vector, host cell, animal, polypeptide and antibody, in screening of compounds for treating or diagnosing pain.

Claim 1; Page 197; 256pp; English.

The invention relates to a novel isolated gene sequence that is down-regulated in the spinal cord in response to streptozocin-induced diabetes, or comprising, hybridising or having at least 80% sequence identity to a sequence whose expression products are kinases, phosphatases, ion channel proteins, receptors, transporters, G-protein coupled receptor proteins, DNA-binding proteins, proteases or enzymes, given in the specification. A gene of the invention has analgesic activity, and may have a use in gene therapy. The gene sequences, vector, host cell, animal, polypeptide and antibody are useful for screening of compounds for diagnosing or treating pain. The kits are useful for simultaneous, separate or sequential detecting and/or quantifying down-regulation of a gene sequence in the spinal cord of a mammal in response to streptozocin-induced diabetes. The compound or pharmaceutical composition is useful as a medicament for treating or diagnosing pain. The present sequence represents a gene of the invention.

Db 326 AAAACAGATGAGGGTCCACCTTTCAAGGCTACCTGGAGCTGGAGATCACCTGTCCAG 385  
 Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102  
 Db 386 GAGCAGATCCAGAGTACACAGCTGCTGAGCTATACGTGACAGCACTCTGAGGAG 445  
 Qy 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
 Db 446 CTACGAGGCTCTCTTCTGTCACAGACCTAGTGGATTCTTAAATTTGACGCTCTCATG 505  
 Qy 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeu 142  
 Db 506 TGGCTCTGACCTAGCTAGCTGGCGACTCTCAATAGCGCTGACCTGCTGCTATGCTGTG 565  
 Qy 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162  
 Db 566 GTTTCGATCTTACTCTACTCTGCTGTATATGTTAGCACCAGCAGGTTGACCAATAT 625  
 Qy 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
 Db 626 CTGGGACTTGTGAGGACTCACATAAACACCGTTGTGGCAAGATCCAGGCTAAATCCCC 685  
 Qy 183 GlyLeuLysArgLysAlaAsp 189  
 Db 686 GCGGC-AAAGAGCATGCTGAG 705

## RESULT 64

AAH57558

ID AAH57558 standard; cDNA; 3279 BP.

XX AC AAH57558;

XX DT 10-SEP-2001 (first entry)

XX DE Human brain cell specific cDNA sequence SEQ ID NO:398.

XX KW Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung;  
 KW liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;  
 KW metabolic disease; developmental disease; cytostatic; immunomodulatory;  
 KW neuroprotective; gene therapy; cancer; immunopathology; neuropathology.

XX OS Homo sapiens.

XX PN WO200132927-A2.

XX PD 10-MAY-2001.

XX PF 02-NOV-2000; 2000WO-US030396.

XX PR 04-NOV-1999; 99US-0163508P.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Sornasse T, Seilhamer JJ, Watson GA;

XX DR WPI; 2001-291057/30.

XX PT New cell and tissue specific polynucleotides useful for diagnosis,  
 PT prognosis or monitoring of treatments for disorders where the gene is  
 PT associated with a cancer, immunopathology or neuropathology.

XX PS Claim 1; Page 312-313; 327pp; English.

CC AAH57161 to AAH57576 represent cell and tissue specific polynucleotide  
 sequences (I). (I) can have cytosolic, immunomodulatory and  
 CC neuroprotective activities, and can be used in gene therapy. (I) and  
 CC proteins (II) encoded by then are used in high throughput screening  
 CC assays to select DNA molecules, RNA molecules, peptide nucleic acids,  
 CC mimetics, peptides, proteins, agonists, antagonists, antibodies or their  
 CC fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical  
 CC agents. Expression of (I) in a sample indicates the differentiation of  
 CC embryonic stem cells into a tissue selected from brain, heart, kidney,  
 CC liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used

CC to produce an expression profile that defines a metabolic or  
 CC developmental process, treatment, condition, disease or disorder. The  
 CC gene profile can be used for diagnosis, prognosis or monitoring of  
 CC treatments and for investigating a predisposition to a disorder where the  
 CC gene is associated with a cancer, immunopathology or neuropathology

XX SQ Sequence 3279 BP; 814 A; 905 C; 850 G; 710 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 9e-69 Length: 3279  
 Score: 660.00 Matches: 126  
 Percent Similarity: 83.51% Conservative: 31  
 Best Local Similarity: 67.02% Mismatches: 30  
 Query Match: 71.35% Indels: 1  
 DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAH57558 (1-3279)

Qy 3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22  
 Db 1934 ATTGACCTGTTGTTATTTGGCGGACATCAAGCAGACGGCATCGTCTTTGGGAGTTTCCTG 1993  
 Qy 23 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
 Db 1994 CTGCTGCTCTTCTCCCTGACCCAGTTCAAGCTGGTGGAGCTGCTGCTACCTGCGCCTG 2053  
 Qy 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
 Db 2054 GCGGACTCTCAGCCACCATCAGTTTCGCAATCTACAAGTCTGTTTTCACAGCAGTGCAG 2113  
 Qy 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
 Db 2114 AAAACGAGGAGGCCACCTTTCAAGGCTTCTTGGAGCTTGAGATCACCTTCTCTCAG 2173  
 Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102  
 Db 2174 GAGCAGATTCAGAGTACACGCACTGCTGCTGAGTTCTACGTGAACAGCACACTTAAGGAA 2233  
 Qy 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
 Db 2234 CTGAGGAGGCTCTTCTCTTGTCCAGGACCTGCTGGATTCCTTAAATTTGACGCTCTGATG 2293  
 Qy 123 TrpValPheThrTyrValGlyAlaLeuPhe-AsnGlyLeuThrLeuLeuIleLeuAlaLe 142  
 Db 2294 TGGCTCTGACCTAGCTTGGCGCTCTCTTGCATGGCTGACCTGCTGCTCATGCTGT 2353  
 Qy 142 uIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162  
 Db 2354 GGTTCATGTTTACTCTACCTGTAGTGTATGTTAAGCACCAGGCACAGATTGACCAATA 2413  
 Qy 162 rLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePr 182  
 Db 2414 TCTGGACTTGTGAGGACTCACATAAATGCTGTTGTGGCAAGATTGAGGCTAAATCCC 2473  
 Qy 182 oGlyLeuLysArgLysAlaAsp 189  
 Db 2474 AGGCGCTAAGAGGACCGCTGAG 2495

## RESULT 65

ABX46402

ID ABX46402 standard; cDNA; 422 BP.

XX AC ABX46402;

XX DT 21-FEB-2003 (first entry)

XX DE Bovine EST associated with lactation/muscle/fat deposition #11567.

XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;  
 KW muscle deposition; fat deposition; genome mapping; gene identification;  
 XX gene analysis; cattle breeding.

XX OS Bos Taurus.



CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,  
 CC cytotatic and tranquiliser activities. This polynucleotide is a full  
 CC length human cDNA sequence of the invention. NOTE: This sequence is not  
 CC given in the sequence listing of the specification but can be obtained on  
 CC CD-ROM from the European Patent Office, Vienna Sub-office.

XX SQ Sequence 4607 BP; 1428 A; 944 C; 945 G; 1290 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 2,098-64 Length: 4607  
 Score: 625.50 Matches: 114  
 Percent Similarity: 81.05% Conservativity: 40  
 Best Local Similarity: 60.00% Mismatches: 35  
 Query Match: 67.62% Indels: 1  
 DB: 13 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADR06965 (1-4607)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
 Db 2353 TCAGTGCACGATCTGATTCTTCGGAGAGATGGAAGAAGACTGGGTTGTCTTGGCACC 2412  
 Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 2413 ACGCTGATCATGCTGCTTTCCCTGGCAGCTTTTCAGTGTTCATCAGTGTGGTTCTTACCTC 2472  
 Qy 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 2473 ATCTGGCTCTCTCTGTACCATCAGCTTCAGATCTCAAGTCCGTATCAACGCT 2532  
 Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 2533 GTACAGAAGTCAGAGAAGGCCATCATTTCAAAGCTTACCTGGAGTAGACATCTCTG 2592  
 Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 Db 2593 TCCTCAGAAGCTTCCATATATACATGAATGCTGCATGTCATCAACAGGCGCCCTG 2652  
 Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 2653 AAATCATATATTCGCTCTTTCTGGTAGAAGATCTGGTTGACTCTTGAAGCTGGCTGC 2712  
 Qy 121 LeuMetTrpValPheTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 Db 2713 TTCATGTGCTGATGACCTATGTTGGTGTCTGTTTAAAGCAATCACCTCTTAATCTT 2772  
 Qy 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 2773 GCTGAACCTGCTCATTTTCAGTGTCCGATTTGCTATGAGAAGTACAGACCCAGATTGAT 2832  
 Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 2833 CACTATGTTGGATCGCCCGAGATCAGACCAAGTCAATTGTTGAAGATCAAGCAAA 2892  
 Qy 181 IleProGlyLeu---LysArgLysAlaAsp 189  
 Db 2893 CTCCTCGAATCGCCCAAAAAGGACAGAA 2922

RESULT 67

AZ38318

ID AZ38318 standard; cDNA; 708 BP.

XX AC

XX AZ38318;

XX 09-FEB-2000 (first entry)

DE Human transmembrane protein cDNA clone HP02061 coding sequence.

DE HP02061; transmembrane domain; Saos-2; homology;

KW neuroendocrine-specific protein C; antibody; assay reagent;

KW diagnostic marker; primer; probe; antisense; gene therapy; agonist;

KW antagonist; ligand; therapeutic; ds.

XX

OS Homo sapiens.

XX Key Location/Qualifiers  
 CDS 1..708

FT /\*tag= a

FT /product= "Human transmembrane protein HP02061"

FT /note= "No stop codon given in the specification"

XX

PN WO955862-A2.

XX

PD 04-NOV-1999.

XX

PF 27-APR-1999; 99WO-JP002226.

XX

PR 28-APR-1998; 98JP-00119395.

XX

PA (SAGA ) SAGAMI CHEM RES CENT.

PA (PROT-) PROTEGENE INC.

XX

PI Kato S, Kimura T;

XX

DR WPI; 2000-023358/02.

XX

DR P-PSDB; AAY52387.

XX

PT Human proteins with transmembrane domains, involved in control of cell proliferation and differentiation, useful for treating e.g. cancer or inflammation.

XX

PS Claim 3; Page 85; 114pp; English.

XX

CC This sequence represents the coding sequence of human cDNA clone HP02061 which encodes a 26 kD protein with two putative transmembrane domains. The cDNA was isolated from a Saos-2 (human osteosarcoma cell line) cDNA library. The protein has homology with the human neuroendocrine-specific protein C (PIR Accession No. I60904), and may have a similar function. The protein may be used to raise specific antibodies, as assay reagents, as diagnostic tissue markers, for the isolation of cognate receptors, CC ligands and binding proteins, and as biologically active agents. CC Nucleotides encoding the protein may be used as primers and probes or CC antisense molecules, and in gene therapy. Cells transformed with these CC nucleotides may be used to screen for agonists and antagonists which are potentially useful therapeutically

SQ Sequence 708 BP; 158 A; 195 C; 169 G; 186 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3,48e-65 Length: 708

Score: 622.50 Matches: 113

Percent Similarity: 81.05% Conservativity: 41

Best Local Similarity: 59.47% Mismatches: 35

Query Match: 67.30% Indels: 1

DB: 3 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAZ38318 (1-708)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20

Db 139 GCGGTGCACGATCTGATTCTTCGGAGAGATGGAAGAAGACTGGGTTGTCTTGGCACC 198

Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40

Db 199 ACGCTGATCATGCTGCTTTCCCTGGCAGCTTTTCAGTGTTCATCAGTGTGTCTTACCTC 258

Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60

Db 259 ATCTGGCTCTCTCTCTGTCCACCATCAGCTTCAGGATCTCAAGTCCGTATCAACGCT 318

Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80

Db 319 GTACAGAAGTCAGAGAAGGCCATTCATTCAAAGCTTACCTGGAGTAGACATCTCTG 378

Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100

Db 379 TCCTCAGAGCTTTCATTAATACATGAATGCTGCCATGTCACATCAACAGGCGCTG 438  
 QY 101 LysGluLeuArgGluPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 439 AAACATCATTTTCGCTCTCTTCTGGTAGAAGATCTGGTTGACTCCCTTGAAGCTGGCTGC 498  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 Db 499 TTCTGTGGCTGATGACCTATGTTGGTGTGTTTAAACGGAATCACCTCTTAATTCCT 558  
 QY 141 AlaLeuLeuSerLeuPheSerLeuProValIleTyrGluArgHisGlnValGlnLeuLeu 160  
 Db 559 GCTGAACCTCTCATTTTCAGTGTCCGATGTCTATGAGAAGATCAAGCCAGATTGAT 618  
 QY 161 HistyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 619 CACTATGTTGGCATGCCCGGAGATCAGACCAAGTCAATGTTGAAAAAGATCCAAGCAAAA 678  
 QY 181 IleProGlyLeu---LysArgLysAlaAsp 189  
 Db 679 CTCCTTGAATCGCCAAAAAAGGCAGAA 708

## RESULT 68

ADK67496

ID ADK67496 standard; cDNA; 711 BP.

XX AC

XX ADK67496;

XX DT 06-MAY-2004 (first entry)

XX DE

XX ds; neuroprotective; gene therapy; BACE1 activity; RTN4; RTN3;

XX KW

XX KW amyloidosis; Alzheimer's disease.

XX OS

XX OS Homo sapiens.

XX FH

XX FT CDS Location/Qualifiers

XX FT 1..711

XX FT /\*tag= a

XX FT /product= "RTN-3 protein"

XX FT

XX PN

XX WO2003088926-A2.

XX XX

XX 30-OCT-2003.

XX XX

XX 08-APR-2003; 2003WO-US008829.

XX PF

XX 17-APR-2002; 2002US-0373284P.

XX PR

XX (PHAA ) PHARMACIA &amp; UPJOHN CO.

XX PA

XX Yan R, Lu Y;

XX PI

XX WPI; 2003-854033/79.

XX DR

XX F-PSDB; ADK67497.

XX XX

XX New polypeptide having BACE1 activity, useful in preparing a composition

XX PT for treating amyloidosis or Alzheimer's disease.

XX PS

XX Claim 2; SEQ ID NO 1; 42pp; English.

XX XX

XX The invention relates to an isolated polypeptide having BACE1 activity.

XX CC The protein is RTN4 or RTN3 protein. The polypeptide is useful in

XX CC preparing a composition for treating amyloidosis or Alzheimer's disease.

XX CC

XX This sequence corresponds to the RTN-3 gene.

XX XX

XX SQ Sequence 711 BP; 161 A; 196 C; 168 G; 186 T; 0 U; 0 Other;

XX

XX Alignment Scores:

XX Pred. No.: 3.5e-65

XX Score: 622.50

XX Percent Similarity: 81.05%

XX Length: 711

XX Matches: 113

XX Conservative: 41

Best Local Similarity: 59.47% Mismatches: 35  
 Query Match: 67.30% Indels: 1  
 DB: 10 Gaps: 1  
 US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADK67496 (1-711)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
 Db 139 GCGGTGCACGATCTCTATTTCTGGAGAGATGTGAAGAAGACTGGGTTGTCTTTGGCACC 198  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 199 ACGCTGATCATGCTGCTTTCCTGCGACCTTTCAGTGTTCATGTCAGTGTGGTTCTTACCTC 258  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 259 ATCTCTGGCTCTCTCTCTGTCCATCAGTTCAGGATCTACAAGTCCGTCTCATCAAGCT 318  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 319 GTACAGAAAGTCAGAGAAGGCCATCCATTCAAAGCTTACCTGAGCTAGACATTACTCTG 378  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 Db 379 TCCTCAGAAAGCTTTCATAATATACATGAATGCTGCCATGGTGCACATCAACAGGCGCTG 438  
 QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 439 AAACATCATTTTCGCTCTCTCTGTGTAAGATCTGTTGACTCTCTTGAAGCTGGCTGTC 498  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 Db 499 TTCATGTGGCTGATGACCTATGTTGGTGTGTTTTAACGGAATCACCTCTCTAATTCCT 558  
 QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 559 GCTGAACCTGCTCATTTTCAGTGTCCGATGTCTATGAGAAGTACAAGCCAGATTGAT 618  
 QY 161 HistyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 619 CACTATGTTGGCATGCCCGGAGATCAGACCAAGTCAATGTTGAAAAAGATCCAAGCAAAA 678  
 QY 181 IleProGlyLeu---LysArgLysAlaAsp 189  
 Db 679 CTCCTTGAATCGCCAAAAAAGGCAGAA 708

## RESULT 69

AAH34853

ID AAH34853 standard; cDNA; 1330 BP.

XX AC

XX AAH34853;

XX XX

XX 03-SEP-2001 (first entry)

XX DT

XX Human colon cancer antigen encoding cDNA SEQ ID NO:1935.

XX DE

XX Human; colon cancer; colon cancer antigen; diagnosis; detection;

XX KW

XX colorectal carcinoma; chromosome 11; ss.

XX OS

XX Homo sapiens.

XX XX

XX WO200122920-A2.

XX XX

XX 05-APR-2001.

XX PD

XX 28-SEP-2000; 2000WO-US026524.

XX PF

XX 29-SEP-1999; 99US-0157137P.

XX PR

XX 03-NOV-1999; 99US-0163280P.

XX XX

XX (HUMA-) HUMAN GENOME SCI INC.

XX PA

XX Ruben SM, Barash SC, Birse CE, Rosen CA;

XX PI

```
XX WPI; 2001-235357/24.
DR P-PSDB; AAG75448.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers.
XX
PS Claim 1; Page 3443; 9803pp; English.
XX
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
CC proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene therapy
CC and vaccine production. N and P may be used in the prevention, diagnosis
CC and treatment of diseases associated with inappropriate P expression. For
CC example, N and P may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of P by expressing inactive proteins or to
CC supplement the patient's own production of P. Additionally, N may be used
CC to produce the colon cancer-associated P, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the proteins. N and P
CC can be used in the prevention, diagnosis and treatment of colorectal
CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
CC sequences used in the exemplification of the present invention. N.B.
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC time of publication, meaning no sequences are present for SEQ ID NO:1027
CC to 1052, 7921 and 7922
XX
SQ Sequence 1330 BP; 329 A; 334 C; 294 G; 372 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 8,41e-65 Length: 1330
Score: 622.50 Matches: 113
Percent Similarity: 81.05% Conservative: 41
Best Local Similarity: 59.47% Mismatches: 35
Query Match: 67.30% Indels: 1
Gaps: 4

US-09-830-972-2_COPY_975_1163 (1-189) x AAH34853 (1-1330)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
DB 297 GCGGTGCGACGATCTGATTTCTGGAGAGATGTGAAGAAGACTGGGTGTCTTGGCACC 356
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 357 AGCTGATGATGCTGCTTCTCCCTGGCAGCTTTCAGTGATCATGAGTGGTGTCTTACCTC 416
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
DB 417 ATCCCTGGCTCTTCTCTGTCCACCATCAGCTTCAGGATCTCAAGTCCGTCATCCAGCT 476
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 477 GTACAGAAGTCAGAGAAGGCCATCCATTCAAGGCTACCTGGAGCTAGACATTAATCTGTG 536
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
DB 537 TCCTCAGAGGCTTCCATAATACATGATGATGCTGCTGATGCTGATCAAGAGGCGCTG 596
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
DB 597 AAACCTCATTTTCGTCCTCTTCTGCTAGAGATCTGGTTGACTCTCTTGAAGCTGGCTGC 656
QY 121 LeuMetTrpPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
DB 657 TTCATGTGCTGATGACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 716
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
DB 717 GCTGAACCTGCTCATTTTTCAGTGTCCGATGTCTATGAGAAAGTCAACAGCCACCATGAT 776
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaAlaLys 180

Db 777 CACTATGTGGCATGCGCCGAGATCAGACCAAGTCAATTTGTTGAAAAGATCCCAAGCAAAA 836
QY 181 IleProGlyLeu---LysArgLysAlaAsp 189
Db 837 CTCCTCGAATGCGCAAAAAGGAGGAGAA 866

RESULT 70
AAH60810
ID AAH60810 standard; DNA; 1656 BP.
XX
AC AAH60810;
XX
DT 09-AUG-1999 (first entry)
XX
DE Human secreted protein encoding DNA (clone yb8-1).
XX
KW Secreted protein; kidney; lung; brain; blood; testis; bone marrow;
KW nutritional activity; cytokine; cell proliferation; immune stimulation;
KW hematopoiesis regulation; tissue growth; thrombolytic; gene therapy;
KW anti-inflammatory; tumour invasion; ss.
XX
OS Homo sapiens.
XX
PN WO9926961-A1.
XX
PD 03-JUN-1999.
XX
PF 24-NOV-1998; 98WO-US025149.
XX
PR 26-NOV-1997; 97US-0066804P.
PR 23-NOV-1998; 98US-00197886.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M, Agostino MJ, Steininger RJ, Wong GG, Clark HF;
PI Fechtel K;
XX
DR WPI; 1999-357809/30.
DR P-PSDB; AAY17228.
XX
PT New polynucleotides encoding secreted proteins.
XX
PS Claim 39; Page 125-126; 133pp; English.
XX
CC The invention relates to secreted proteins (AAY17219-228) encoded by
CC polynucleotides obtained from human fetal kidney, adult lung, adult
CC kidney, adult brain, adult blood, adult testes, and fetal brain and
CC murine adult bone marrow cDNA libraries. The secreted protein nucleic acid
CC sequences (X6801-811) correspond to clones bd306-7, gj283-6, fk317-3,
CC k213-2x, na316-1, nf93-20, np164-1, pe204-1, yal-1 and yb-1, (all clones
CC are deposited as ATCC 98599); The PNs and proteins are predicted to have
CC biological activities which would make them suitable for treating,
CC preventing or ameliorating medical conditions in humans and animals,
CC although no supporting data is given. Suggested activities include
CC nutritional activity, cytokine and cell proliferation/differentiation
CC activity, immune stimulating (e.g. as vaccines) or suppressing activity,
CC hematopoiesis regulating activity, tissue growth activity, activin/
CC inhibin activity, chemotactic/chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, cadherin/tumour invasion suppressor activity, and tumour
CC inhibition activity. The PNs are also stated to be useful for gene
CC therapy
XX
SQ Sequence 1656 BP; 473 A; 389 C; 340 G; 454 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.14e-64 Length: 1656
Score: 822.50 Matches: 113
Percent Similarity: 81.05% Conservative: 41
Best Local Similarity: 59.47% Mismatches: 35
Query Match: 67.30% Indels: 1
```

```
DB: 1 2 Gaps: 1
US-09-830-972-2_COPY_975_1163 (1-189) x AAX60810 (1-1656)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 165 GGGTGCAGATCTGATTTCTGGAGAGATGTGAAGAGACTGGGTGTTCTTTGGCACC 224
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 225 ACGTGTATCATGCTGCTTTCCCTGGCAGCTTTTCAGTGTCTCATCAGTGTGGTTCCTTACCTC 284
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 285 ATCTCGGCTCTTCTCTGTCCACCATCAGCTTCAGGATCTACAGTCCGCTCATCCAGCT 344
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 345 GTACAGAGTCAAGAGGCCATCCATTCAAAGCCTACTCGACGTAGACATTACTCTG 404
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 405 TCCTCAGAGCTTCCATATACATGATGCTGCCATGTGCACATCAACAGGGCCCTG 464
QY 101 LysGluLeuArgGluLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 465 AAATCATATTATTCCTCTCTCTGTAGAGATCTGTTGACTCCTTGAAGCTGGCTGTC 524
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuLeuLeuLeu 140
Db 525 TTCATGTGCTGATGACCTATGTTGTGCTGTTTAAACGGAATCACCTTCTAATCTT 584
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 585 GCTGAAGTCTCATTTTCAGTGTCCGATGTCTATGAGAGTACAAAGACCCAGATTGAT 644
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 645 CACTATGTGGTATCCCGCAGATCAGACCAAGTCAATTTGTTCAAAGATCCAAAGCAAA 704
QY 181 IleProGlyLeu--LysArgLysAlaAsp 189
Db 705 CTCCTTGGATCGCCAAAAGGCGAGAA 734
RESULT 71
AAS59216
ID AAS59216 standard; cDNA; 1656 BP.
AC AAS59216;
XX
XX
XX 16-JAN-2002 (first entry)
XX
XX Human cDNA encoding a secreted protein yb8_1.
XX
XX Human; secreted protein; ss; antiinflammatory; immunosuppressive;
KW nootropic; neuroprotective; antiarthritic; antimicrobial; vulnerary;
KW cytotatic; antidiabetic; virucide; antiinfertility; anticonvulsant;
KW vasotropic; antiparkinsonian; immunostimulant; dermatological;
KW antirheumatic; antitumor; antiulcer; osteopathic; tranquiliser;
KW cerebroprotective; cytokine; cell proliferation; cell differentiation;
KW immune deficiency; severe combined immunodeficiency; SCID; tumour;
KW autoimmune disorder; multiple sclerosis; rheumatoid arthritis;
KW graft-versus-host disease; myeloid deficiency; wound healing; ulcer;
KW periodontal disease; osteoporosis; osteoarthritis; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; infection; cardiac disease;
KW stroke; sepsis; inflammatory bowel disease; contraceptive; immunogen;
KW food supplement.
XX
XX Homo sapiens.
XX
XX WO200175068-A2.
XX
XX 11-OCT-2001.
```

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XX PF 22-MAR-2001; 2001WO-US009369.
XX PR 30-MAR-2000; 2000US-00539330.
XX PR 04-DEC-2000; 2000US-00729674.
XX PA (GENY) GENETICS INST INC.
XX
XX Jacobs K, McCoey JM, Lavallie E, Collins-Racie LA, Evans C;
XX Treacy M, Agostino MJ, Steininger RJ, Spaulding V, Wong GG, Clark H;
XX Pechtel K, Merberg D;
XX
XX WPI: 2001-639363/73.
XX P-PSDB; AAU38998.
XX
XX Secreted human proteins, useful as vaccine for treating various diseases
XX such as autoimmune disorders (e.g. multiple sclerosis), and nervous
XX system disorders (e.g. stroke).
XX
XX Claim 13; Page 471; 619pp; English.
XX
XX The invention relates to novel human secreted proteins, the nucleic acids
XX encoding them. The protein may exhibit cytokine, cell proliferation or
XX cell differentiation activity or may induce production of other cytokines
XX in certain cell populations and may exhibit immune stimulating or immune
XX suppressing activity, which is useful for the treatment of various immune
XX deficiencies and disorders e.g. severe combined immunodeficiency (SCID),
XX autoimmune disorders e.g. multiple sclerosis, systemic lupus
XX erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation.
XX The proteins are also useful in the treatment of diseases and disorders
XX including tissue, skin and organ transplantation and in graft-versus-host
XX diseases (GVHD), in the induction of tumour immunity, myeloid or lymphoid
XX cell deficiencies, wound healing and tissue repair, in the treatment of
XX burns, incisions and ulcers; as well as in treatment of periodontal
XX disease, osteoporosis or osteoarthritis, mediated by inflammatory
XX processes, diseases of the peripheral nervous system, Alzheimer's,
XX Parkinson's disease, Huntington's disease, amyotrophic lateral
XX sclerosis, and Sny-Drager syndrome, infections, infarction of cardiac and
XX central nervous system vessel e.g. stroke, sepsis, inflammatory bowel
XX disease, ulcers, bone regeneration. The protein, having active- or
XX inhibin-related activities is useful as a contraceptive based on the
XX ability of inhibits to decrease fertility in female mammals and decrease
XX spermatogenesis in male mammals. The proteins and nucleic acids are also
XX useful as food supplements. The present sequence encodes a secreted
XX protein of the invention
XX
XX Sequence 1656 BP; 473 A; 389 C; 340 G; 454 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.: 1,148-64 Length: 1656
Score: 622.50 Matches: 113
Percent Similarity: 81.05% Conservative: 41
Best Local Similarity: 59.47% Mismatches: 35
Query Match: 67.30% Indels: 1
DB: 4 Gaps: 1
US-09-830-972-2_COPY_975_1163 (1-189) x AAS59216 (1-1656)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 165 GGGTGCAGATCTGATTTCTGGAGAGATGTGAAGAGACTGGGTGTTCTTTGGCACC 224
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 225 ACGTGTATCATGCTGCTTTCCCTGGCAGCTTTTCAGTGTCTCATCAGTGTGGTTCCTTACCTC 284
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 285 ATCTCGGCTCTTCTCTGTCCACCATCAGCTTCAGGATCTACAGTCCGCTCATCCAGCT 344
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 345 GTACAGAGTCAAGAGGCCATCCATTCAAAGCCTACTCGACGTAGACATTACTCTG 404
```



QY 81 SerGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAsnSerThrile 100  
 DB TCTCAGAGCTTTCATTAATACATGATGCTGCGCATGCTCAACAGGCGCTG 464  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 DB AAACCTCAATATTCGTCCTCTTCTGCTAGAGATCTGTTGATCTCTTGAAGCTGCTGTC 524  
 QY 121 LeuMetTTPValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 DB TTTATGTCGCTGATGACCTATGTTGCTGCTGTTTAAACGGAATCACCTTCTTAATCTT 584  
 QY 141 AlaLeuLeuSerPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 DB GCTGACGCTCATTTTCAGTGTCCGATGCTATGAGAGTACAGACCCAGATTGAT 644  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB CACTATGTTGGCATCGCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAGCAAAA 704  
 QY 181 IleProGlyLeu--LysArgLysAlaAsp 189  
 DB CTCCTGGAATGCGCAAAAAGGACAGAA 734  
 RESULT 72  
 ID ABA90885  
 AC ABA90885 standard; cDNA; 1656 BP.  
 XX ABA90885;  
 DT 14-FEB-2002 (first entry)  
 DE Human polynucleotide SEQ ID NO 19.  
 KW Human; clone bd306-7; clone yb8-1; ATCC number 98599; gene therapy;  
 KW immune disorder; bacterial infection; fungal infection; cancer; tumour;  
 KW autoimmune disorder; systemic lupus erythematosus; wound; ulcer; inhibin;  
 KW osteoporosis; osteoarthritis; nervous system disorder; neuropathy;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; activin;  
 KW haemophilia; cardiac infarction; stroke; sepsis; arthritis; vulnerability;  
 KW ischaemia-reperfusion injury; inflammatory bowel disease; chemotactic;  
 KW Crohn's disease; cytostatic; anti-inflammatory; immunomodulator;  
 KW neuroprotective; haemostatic; thrombolytic; anti-inflammatory; ss.  
 XX Homo sapiens.  
 OS  
 XX  
 XX US2001039335-A1.  
 XX  
 XX 08-NOV-2001.  
 XX  
 XX 04-DEC-2000; 2000US-00729674.  
 XX  
 XX 26-NOV-1997; 97US-0126425P.  
 XX 04-DEC-1997; 97US-0067454P.  
 XX 20-DEC-1997; 97US-0068379P.  
 XX 02-JAN-1998; 98US-0070346P.  
 XX 07-JAN-1998; 98US-0070643P.  
 XX 08-JAN-1998; 98US-0070755P.  
 XX 13-JAN-1998; 98US-0071304P.  
 XX 22-JAN-1998; 98US-0072134P.  
 XX 30-JAN-1998; 98US-0073095P.  
 XX 18-FEB-1998; 98US-0075038P.  
 XX 23-NOV-1998; 98US-00197886.  
 XX 30-MAR-2000; 2000US-00539330.  
 XX  
 XX (JACO/) JACOBS K.  
 XX (MCCO/) MCCOY J M.  
 XX (LAVA/) LAVALLIE E R.  
 XX (COLL/) COLLINS-RACIE L A.  
 XX (EVAN/) EVANS C.  
 XX (MERB/) MERBERG D.  
 XX (TREA/) TREACY M.

PA (AGOS/) AGOSTINO M J.  
 PA (STEI/) STEININGER R J.  
 PA (SPAU/) SPAULDING V.  
 PA (WONG/) WONG G G.  
 PA (CLAR/) CLARK H.  
 XX (FECH/) FECHTEL K.  
 PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;  
 PI Merberg D, Treacy M, Agostino MJ, Steininger RJ, Spaulding V;  
 PI Wong GG, Clark H, Fechtel K;  
 XX WPI; 2002-040725/05.  
 DR P-PSDB; ABB55707.  
 XX  
 PT New secreted proteins and encoding polynucleotides, useful in gene  
 PT therapies, particularly for preventing or treating autoimmune disorders,  
 PT cancer, graft-versus-host disease, wound, osteoporosis, stroke or  
 PT inflammations.  
 XX  
 PS Claim 13; Page 191-192; 349pp; English.  
 XX  
 CC The invention relates to isolated polynucleotides (ABA90876-ABA90968 and  
 CC ABA90980) and encoded proteins (ABB55698-ABB55800), especially  
 CC polynucleotides SEQ ID NO 1 (ABA90876) and SEQ ID NO 19 (ABA90885) and  
 CC proteins SEQ ID NO 2 (ABB55698) and SEQ ID NO 20 (ABB55707) contained in  
 CC clones bd306-7 and yb8-1 respectively and the clones bd306-7 and yb8-1  
 CC are deposited with the American Type Culture Collection (ATCC) with  
 CC accession number 98599. The polynucleotides and encoded polypeptides have  
 CC cytostatic, anti-inflammatory, immunomodulator, vulnerary,  
 CC neuroprotective, activin, inhibit, chemotactic, haemostatic, thrombolytic  
 CC and anti-inflammatory activity and acting as cytokine modulators,  
 CC haematopoiesis regulators, tissue growth modulators and/or cadherin  
 CC suppressors. The polypeptides and polynucleotides are useful in gene  
 CC therapies, particularly for preventing, treating or ameliorating any of  
 CC the following diseases: immune deficiency and disorders; e.g. bacterial  
 CC or fungal infections, autoimmune disorders, cancer, systemic lupus  
 CC erythematosus or graft-versus-host disease; myeloid or lymphoid cell  
 CC deficiencies; wound, burns, incisions and ulcers, osteoporosis or  
 CC osteoarthritis; central and peripheral nervous system diseases and  
 CC neuropathies, e.g. Alzheimer's, Parkinson's disease, Huntington's  
 CC disease, amyotrophic lateral sclerosis or Shy-Drager syndrome;  
 CC haemophilia, cardiac infarction or stroke; inflammations, shock, sepsis  
 CC or systemic inflammatory response syndrome, ischaemia-reperfusion injury,  
 CC endotoxin lethality, arthritis, inflammatory bowel disease or Crohn's  
 CC disease; or tumours or cancers, pemphigus vulgaris or pemphigus foliaceus  
 XX  
 SQ Sequence 1656 BP; 473 A; 389 C; 340 G; 454 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.14e-64 Length: 1656  
 Score: 622.50 Matches: 113  
 Percent Similarity: 81.05% Conservative: 41  
 Best Local Similarity: 59.47% Mismatches: 35  
 Query Match: 67.30% Indels: 1  
 DB: 6 Gaps: 1  
 US-09-830-972-2\_COPY\_975\_1163 (1-189) x ABA90885 (1-1656)  
 QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 DB 165 CGCGTGCACGATCTCAATTTCTCGAGAGATGCTGAAGAAGACTGGGTTTGTCTTTGGCACC 224  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 225 ACGCTGATCATGCTGCTTCTCCCTGGCAGCTTTCAGTGTTCATGCTGCTTCTTACCTC 284  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 285 ATCTGCGCTCTTCTCTGTCACCATCAGCTTCAGGATCTACAGTCCGTCATCAAGCT 344  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 345 GTACAGAAGTCAGAAGAAGGCCATCCATTCCTCAAGCTACCTGGACGTAGACATTACTCTG 404

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 DB 405 TCCTCAGAGCTTCCATAATACATGAATGTCGCATCAACACAGGCGCCCTG 464  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 465 AAATCATATTATTCGCTCTCTTCGAGAGAGATCTGGTTCATCTCTGAGCTGCTGTC 524  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 DB 525 TTCTATGCTGCTGATGACCTATGTTGCTGCTGTTTTTAACGGAATCACCTCTTAATTCCT 584  
 QY 141 AlaLeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 DB 585 GCTGAACCTCTCATTTTCATGTCCTCCGATGTCATGAGAGATACCAAGACCCAGATTGAT 644  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 645 CACTATGTTGGATCCGCCGAGATCAGACCAAGTCAATGTTGMAAAGATCCAGCAAAA 704  
 QY 181 IleProGlyLeu---LysArgLysAlaAsp 189  
 DB 705 CTCCTCGGAATGCCCAAAAAGGCGAGAA 734  
 RESULT 73  
 AAZ36240  
 ID AAZ36240 standard; cDNA; 1668 BP.  
 AC  
 XX AAZ36240;  
 DT 22-FEB-2000 (first entry)  
 DE cDNA encoding a bone marrow secreted protein designated BMS240.  
 KW Bone marrow secreted protein; bone marrow stromal cell; cytokine;  
 KW cell proliferation; cell differentiation; hematopoiesis; anaemia;  
 KW myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;  
 KW erythroid progenitor cell; colony stimulating factor; granulocyte;  
 KW monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;  
 KW platelet disorder; thrombocytopenia; hematopoietic stem cell;  
 KW stem cell disorder; aplastic anaemia; bone differentiation;  
 KW paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon;  
 KW ligament; nerve; wound healing; tissue repair; burn; incision; ulcer;  
 KW bone fracture; cartilage damage; artificial joint; ss.  
 XX Homo sapiens.  
 OS  
 XX  
 FH Location/Qualifiers  
 FT 99..809  
 FT /\*tag= a  
 FT /product= "bone marrow secreted protein"  
 FT poly\_a\_signal  
 FT 1626..1631  
 FT /\*tag= b  
 XX  
 XX WO9933979-A2.  
 XX  
 XX 08-JUL-1999.  
 XX  
 XX 18-DEC-1998; 98WO-US027008.  
 XX  
 XX 30-DEC-1997; 97US-0068958P.  
 XX 24-SEP-1998; 98US-0101603P.  
 XX 30-SEP-1998; 98US-0102540P.  
 XX  
 XX (CHIR ) CHIRON CORP.  
 XX  
 XX Lin H, Cao L;  
 XX  
 XX WPI; 2000-038344/03.  
 DR P-PSDB; AAY53634.  
 XX  
 XX New isolated human polynucleotide and secreted proteins can induce

PT production of other cytokines in certain cell populations.

XX Claim 11; Page 98-100; 120pp; English.

XX AAZ36228-49 encode bone marrow secreted proteins of human bone marrow  
 CC stromal cells. The proteins can exhibit cytokine, cell proliferation, or  
 CC cell differentiation activity (either inducing or inhibiting). They can  
 CC be used to support colony forming cells or factor-dependent cell lines,  
 CC to regulate hematopoiesis, and to treat myeloid or lymphoid cell  
 CC deficiencies. In addition, they may be used to support the growth and  
 CC proliferation of erythroid progenitor cells, and to treat various  
 CC anaemias. They can have colony stimulating factor (CSF) activity and can  
 CC be used to support the growth and proliferation of myeloid cells such as  
 CC granulocytes, monocytes or macrophages, to prevent or treat myelo-  
 CC suppression, to support the growth and proliferation of megakaryocytes  
 CC and platelets, thereby allowing prevention or treatment of platelet  
 CC disorders such as thrombocytopenia, to support the growth and  
 CC proliferation of hematopoietic stem cells, either in place of or in  
 CC conjunction with platelet transfusions, to treat stem cell disorders,  
 CC such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to  
 CC repopulate the stem cell compartment after irradiation or chemotherapy.  
 CC They can be used for growth or differentiation of bone, cartilage,  
 CC tendon, ligament, or nerve tissue, as well as for wound healing and  
 CC tissue repair and replacement, and in the treatment of burns, incisions  
 CC and ulcers, to induce cartilage and/or bone growth in circumstances where  
 CC bone is not normally formed and thus have an application in healing bone  
 CC fractures and cartilage damage or defects, prophylactic use in fracture  
 CC reduction and also in the improved fixation of artificial joints  
 XX  
 SQ Sequence 1668 BP; 435 A; 414 C; 349 G; 470 T; 0 U; 0 Other;

# Alignment Scores:

Pred. No.: 1.16e-64 Length: 1668  
 Score: 622.50 Matches: 113  
 Percent Similarity: 81.05% Conservative: 41  
 Best Local Similarity: 59.47% Mismatches: 35  
 Query Match: 67.30% Indels: 1  
 DB: 3 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAZ36240 (1-1668)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 DB 237 GCGGTGCGAGATCTGATTTCTGAGAGATGTGAAGAGACTGGTGTCTTTGGCACC 296  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 297 ACGCTGATCATGCTGCTTTCCCTGGCAGCTTTTCAGTGTGTCAGTGTGTTCTTACCTC 356  
 QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 357 ATCTGGGCTTCTCTCTGTCCACATCAGCTTCAGATCTACAGATCCGTGTCATCCAGCT 416  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 417 GTACAGAGTCAAGAGAGGCCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCTG 476  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 DB 477 TCCTCAGAAGCTTTCCATAAATTACATGAATGTGTCATGTGTCACATCAACAGGCGCCCTG 536  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 537 AAATCATATTATTCGCTCTCTTCGAGAGAGATCTGGTTCATCTCTGAGCTGCTGTC 596  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 DB 597 TTCTATGCTGCTGATGACCTATGTTGCTGCTGTTTTTAACGGAATCACCTCTTAATTCCT 656  
 QY 141 AlaLeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 DB 657 GCTGAACCTCTCATTTTCATGTCCTCCGATTTGTTCTATGAGAGATACCAAGACCCAGATTGAT 716

QY 161 HistTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 717 CACTATGTTGGCATCGCCGAGATCAGACCAAGTCAATTGTTGAAAGATCCAGCAAAA 776  
 QY 181 IleProGlyLeu---LysArgLysAlaAsp 189  
 Db 777 CTCCTGGAATCGCCCAAAAAAAGGCAGAA 806

## RESULT 74

AAZ38319  
 ID AAZ38319 standard; cDNA; 1759 BP.

XX  
 AC AAZ38319;

DT 09-FEB-2000 (first entry)

XX Human transmembrane protein cDNA clone HP02061.

DE HP02061; transmembrane domain; Saos-2; homology;  
 KW neuroendocrine-specific protein C; antibody; assay reagent;  
 KW diagnostic marker; primer; probe; antisense; gene therapy; agonist;  
 KW antagonist; ligand; therapeutic; ds.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH 142..852  
 CDS /\*tag= a

FT /product= "Human transmembrane protein HP02061"

XX WO9955862-A2.

XX 04-NOV-1999.

XX 27-APR-1999; 99WO-JP002226.

XX 28-APR-1998; 98JP-00119395.

XX (SAGA ) SAGAMI CHEM RES CENT.

XX (PROT-) PROTEGENE INC.

XX Kato S, Kimura T;

XX WPI; 2000-023358/02.

XX P-PSDB; AAY52387.

XX Human proteins with transmembrane domains, involved in control of cell proliferation and differentiation, useful for treating e.g. cancer or inflammation.

XX Claim 4; Page 92-94; 114pp; English.

XX This sequence represents the human cDNA clone HP02061 which encodes a 26 kD protein with two putative transmembrane domains. The cDNA was isolated from a Saos-2 (human osteosarcoma cell line) cDNA library. The protein has homology with the human neuroendocrine-specific protein C (PIR Accession No. I60904), and may have a similar function. The protein may be used to raise specific antibodies, as assay reagents, as diagnostic tissue markers, for the isolation of cognate receptors, ligands and binding proteins, and as biologically active agents. Nucleotides encoding the protein may be used as primers and probes or antisense molecules, and in gene therapy. Cells transformed with these nucleotides may be used to screen for agonists and antagonists which are potentially useful therapeutically

SQ Sequence 1759 BP; 454 A; 433 C; 376 G; 496 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.25e-64 Length: 1759  
 Score: 622.50 Matches: 113  
 Percent Similarity: 81.05% Conservative: 41  
 Best Local Similarity: 59.47% Mismatches: 35  
 Query Match: 67.30% Indels: 1

Db US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAZ38319 (1-1759)  
 Gaps: 1  
 QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 Db 280 GCGGTGCACGATCTGATTTCTGGAGAGATGTGAAGAGACTGGGTTTGTCTTTGGCACC 339  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 340 ACGTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTCATCAGTGGTTCCTTACCTC 399  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 400 ATCTGGCTCTTCTCTGTCTGTCACCATCAGCTTCAGGATCTACAAAGTCGTCATCCAAGCT 459  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 460 GTACAGAAGTCAGAAGAAGGCCATCCATTCAAGCTACCTGGAGCTAGACATTACTCTG 519  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 Db 520 TCCTCAGAAGCTTCCCATATTATGATGATCTGCCATGTGGTCACATCAACAGGCCCTG 579  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 580 AAACCTATTATTCGTCCTCTTCTGCTAGAGATCTGGTGTGACTCTTGAAGCTGGCTGTC 639  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 Db 640 TTCATGTGGCTGATGACCTATGTTGGTCTGTTTAAACGGAATCACCTTCTAATTCCT 699  
 QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 700 GCTGAACCTGCTCATTTTCAGTGTCCGATGTCATGAGAAGTGAAGACCCAGATTGAT 759  
 QY 161 HistTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 760 CACTATGTTGGCATCGCCGAGATCAGACCAAGTCAATTGTTGAAAGATCCAGCAAAA 819  
 QY 181 IleProGlyLeu---LysArgLysAlaAsp 189  
 Db 820 CTCCTGGAATCGCCCAAAAAAAGGCAGAA 849

## RESULT 75

AAV59748

ID AAV59748 standard; DNA; 1766 BP.

XX AC

XX AAV59748;

XX DT 19-JAN-1999 (first entry)

XX Human secreted protein gene 92 clone HAUBL57.

DE Human; secreted protein; fusion protein; gene therapy; protein therapy;  
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
 KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;  
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX Homo sapiens.

XX OS

XX WO9839448-A2.

XX PD 11-SEP-1998.

XX PF 06-MAR-1998; 98WO-US004493.

XX PR 07-MAR-1997; 97US-0038621P.

XX PR 07-MAR-1997; 97US-0040161P.

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PR 07-MAR-1997; 97US-0040162P.
PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040335P.
PR 07-MAR-1997; 97US-0040336P.
PR 07-MAR-1997; 97US-0040337P.
PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043568P.
PR 11-APR-1997; 97US-0043569P.
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043578P.
PR 11-APR-1997; 97US-0043580P.
PR 11-APR-1997; 97US-0043669P.
PR 11-APR-1997; 97US-0043670P.
PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.
PR 11-APR-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047582P.
PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
PR 23-MAY-1997; 97US-0047585P.
PR 23-MAY-1997; 97US-0047586P.
PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
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PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048640P.
PR 06-JUN-1997; 97US-0048641P.
PR 13-JUN-1997; 97US-0049610P.
PR 16-JUL-1997; 97US-0051926P.
PR 16-JUL-1997; 97US-0052874P.
PR 18-AUG-1997; 97US-0055724P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056633P.
PR 22-AUG-1997; 97US-0056636P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056642P.
PR 22-AUG-1997; 97US-0056644P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
PR 22-AUG-1997; 97US-0056864P.
PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.
PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056883P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056885P.
PR 22-AUG-1997; 97US-0056886P.
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PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.
PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057659P.
PR 05-SEP-1997; 97US-0057669P.
PR 12-SEP-1997; 97US-0057761P.
PR 12-SEP-1997; 97US-0058785P.
PR 02-OCT-1997; 97US-0061060P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
PI Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PB, Greene JM;
PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI Moore PA, Shi Y, Iaffeur DW, Li Y, Zeng Z, Kyaw H;
XX
XX WPI; 1998-506364/43.
XX P-PSDB; AAW74963.
XX
XX New isolated human genes and the secreted polypeptide(s) they encode -
XX useful for diagnosis and treatment of e.g. cancers, neurological
XX disorders, immune diseases, inflammation or blood disorders.
XX
XX Claim 1; Page 473-474; 721pp; English.
XX
XX This sequence represents a nucleic acid molecule designated Gene 92 from
XX the human cDNA clone HAUBL57 (deposited as clone ATCC 97897 and ATCC
XX 209043) which encodes a secreted human protein. The gene can be used to
XX generate fusion proteins by linking to the gene to a human immunoglobulin
XX Fc portion (e.g. AAV59502) for increasing the stability of the fused
XX protein as compared to the human protein only. The invention relates to
XX 186 novel genes and their fragments (nucleic acid sequences: AAV59511-
XX V59812; amino acid sequences AAW74731-W5026) which are useful for
XX preventing, treating or ameliorating medical conditions e.g. by protein
XX or gene therapy. Also, pathological conditions can be diagnosed by
XX determining the amount of the new polypeptides in a sample or by
XX determining the presence of mutations in the new polynucleotides.
XX Specific uses are described for each of the 186 polynucleotides, based on
XX which tissues they are most highly expressed in (see AAV59511 for
XX described uses)
XX
XX Sequence 1766 BP; 463 A; 437 C; 383 G; 481 T; 0 U; 2 Other;
SQ
Alignment Scores:
Pred. No.: 1.25e-64 Length: 1766
Score: 622.50 Matches: 113
Percent Similarity: 81.05% Conservative: 41
Best Local Similarity: 59.47% Mismatches: 35
Query Match: 67.30% Indels: 1
DB: 2 Gaps: 1
US-09-830-972-2_COPY_975_1163 (1-189) x AAV59748 (1-1766)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 287 GCGGTGCACGATCTGATTTCTTCTGGAGAGATGTGAAGAGACTGGGTTTCTCTTGGCACC 346
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QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 347 ACCTGATCATGCTCTTCCCTGGCAGCTTTCAGTGTTCATGCTGGTTCCTACCTC 406
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60
Db 407 ATCTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGT 466
QY 61 IleGlnIleSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 467 GTACAGAAGTCAGAGAAGGCCATCCATTCAAGGCTACCTCGAGCTAGACATTACTCTG 526
QY 81 SerGluGluLeuValGlnIleTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 527 TCCTCAGAAAGCTTCCATAATTACATGAATGCTGCATGTCACATCAACAGGCCCTG 586
QY 101 LysGluLeuArgArgPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 587 AAACCTCATATTTCGCTCTCTTCTGGTAGAAGATCTGGTTGACTCCTTGAAGCTGGCTGTC 646
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuIleLeu 140
Db 647 TTCATGTGCTGATGACCTATGTTGGTGTGCTTTTAAACGGATCACCTTCTTAATCTT 706
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 707 GCTGAAGTCTCATTTTCAGTGTCCGATGTCTATGAGAGTACAAACCCAGATTGAT 766
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 767 CACTATGTTGGCATCGCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAAA 826
QY 181 IleProGlyLeu--LysArgLysAlaAsp 189
Db 827 CTCCTTGAATGCCCAAAAAAGGCAGAA 856
RESULT 76
ID ABS73741 standard; cDNA; 1766 BP.
XX AC ABS73741;
XX DT 15-JAN-2003 (first entry)
XX DE Human cDNA #2 for novel secreted protein gene 92.
XX KW Human; ss; gene; secreted protein; autoimmune disease; chemotaxis;
KW rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;
KW liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn;
KW nervous system disorders; Alzheimer's disease; infection;
KW ocular disorder; corneal infection; wound healing; tissue regeneration;
KW epithelial cell proliferation; organ transplantation; food additive;
XX KW preservative; nutritional.
XX OS Homo sapiens.
XX PN US6420526-B1.
XX PD 16-JUL-2002.
XX PF 08-SEP-1998; 98US-00149476.
XX PR 07-MAR-1997; 97US-0038621P.
XX PR 07-MAR-1997; 97US-0040161P.
XX PR 07-MAR-1997; 97US-0040162P.
XX PR 07-MAR-1997; 97US-0040163P.
XX PR 07-MAR-1997; 97US-0040333P.
XX PR 07-MAR-1997; 97US-0040334P.
XX PR 07-MAR-1997; 97US-0040336P.
XX PR 07-MAR-1997; 97US-0040626P.
XX PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-00433568P.
PR 11-APR-1997; 97US-0043569P.
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043578P.
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PR 11-APR-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047492P.
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PR 23-MAY-1997; 97US-0047502P.
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PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 13-JUN-1997; 97US-0048974P.
PR 08-JUL-1997; 97US-0049610P.
PR 16-JUL-1997; 97US-0051926P.
PR 18-AUG-1997; 97US-0055724P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056633P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
PR 22-AUG-1997; 97US-0056864P.
PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.
PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
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PR 22-AUG-1997; 97US-0056884P.  
 PR 22-AUG-1997; 97US-0056886P.  
 PR 22-AUG-1997; 97US-0056887P.  
 PR 22-AUG-1997; 97US-0056888P.  
 PR 22-AUG-1997; 97US-0056889P.  
 PR 22-AUG-1997; 97US-0056892P.  
 PR 22-AUG-1997; 97US-0056893P.  
 PR 22-AUG-1997; 97US-0056894P.  
 PR 22-AUG-1997; 97US-0056903P.  
 PR 22-AUG-1997; 97US-0056908P.  
 PR 22-AUG-1997; 97US-0056910P.  
 PR 22-AUG-1997; 97US-0056911P.  
 PR 05-SEP-1997; 97US-0057650P.  
 PR 05-SEP-1997; 97US-0057669P.  
 PR 12-SEP-1997; 97US-0057761P.  
 PR 02-OCT-1997; 97US-0061060P.  
 PR 06-MAR-1998; 98WO-US004493.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC;  
 PI Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;  
 PI Perrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;  
 PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;  
 XX  
 DR WPI; 2002-634796/68.  
 DR P-PSDB; ABG95423.  
 XX

PT New isolated human secreted protein for diagnosing, preventing, treating  
 PT or ameliorating medical conditions and used as a food additive or  
 PT preservative.

PS Example 1; SEQ ID NO 254; 129pp; English.

XX The invention relates to an isolated protein that is one of 186 human  
 CC secreted proteins, given in the specification, encoded by one of 309 cDNA  
 CC sequences also given in the specification. The protein is used in a  
 CC pharmaceutical composition used to prevent, treat or ameliorate a medical  
 CC condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs,  
 CC chickens or sheep. Disorders which are diagnosed or treated include  
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders  
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,  
 CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,  
 CC infections caused by bacteria, viruses and fungi and ocular disorders  
 CC e.g. corneal infection. The polypeptides can also be used to aid wound  
 CC healing and epithelial cell proliferation, to prevent skin aging due to  
 CC sunburn, to maintain organs before transplantation, for supporting cell  
 CC culture of primary tissues, to regenerate tissues and in chemotaxis. The  
 CC polypeptides can also be used as a food additive or preservative to  
 CC increase or decrease storage capabilities, fat content, lipid, protein,  
 CC carbohydrate, vitamins, minerals, cofactors and other nutritional  
 CC components. The present sequence represents a cDNA derived from a gene  
 CC encoding one of the novel human secreted proteins of the invention. Note:  
 CC This sequence did not form part of the printed specification, but was  
 CC obtained in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=642052681  
 XX

SQ Sequence 1766 BP; 463 A; 437 C; 383 G; 481 T; 0 U; 2 Other;

Alignment Scores:  
 Pred. No.: 1,25e-64 Length: 1766  
 Score: 622.50 Matches: 113  
 Percent Similarity: 81.05% Conservative: 41  
 Best Local Similarity: 59.47% Mismatches: 35  
 Query Match: 67.30% Indels: 1  
 DB: 6 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ABS73741 (1-1766)

QY 1-SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20

Db 287 GCGGTGCGAGTCTGATTTCTGGAGAGATGTGAAGAAGACTGGTGTCTTTGGACC 346  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 347 ACGCTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTTCATCAGTGTGGTTCTTACCTC 406  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 407 ATCCTGGGCTCTTCTCTCTGTCCACCATCAGCTTCAGGATCTACAGTCCGTCTATCCAAGCT 466  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 467 GTACAGAAGTCAGAGAAGGCCATCCATTCAAAGCTACCTGGAGCTAGACATCTCTG 526  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 Db 527 TCCTCAGAAGCTTTTCCATAATTACATGAATGCTGCCATGTCACATCAACAGGCCCTG 586  
 QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 587 AAACATCATTTATTCGTCTCTTCTGTGAAGATCTGTTGACTCTCTTGAAGCTGCTGTC 646  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 Db 647 TTCATGTGCTGATGACCTATGTTGCTGCTGTTTAAACGGATCACCCTCTTAATCTT 706  
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 Db 707 GCTGAACGTCTCATTTTCAGTGTCCGATTTGCTATGAGAAGTACAAGACCCAGATTGAT 766  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 767 CACTATGTCGATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCCAAGCAAA 826  
 QY 181 IleProGlyLeu---LysArgLysAlaAsp 189  
 Db 827 CTCCTTGAATCGCCAAAAGGAGCAAA 856  
 RESULT 77  
 ID ACD82884 standard; cDNA; 1766 BP.  
 XX ACD82884;  
 AC ACD82884;  
 XX  
 DT 22-SEP-2003 (first entry)  
 XX  
 DE cDNA sequence #244 containing coding region of a human secreted protein.  
 XX  
 KW Human; secreted protein; hyperproliferative disorder; leukaemia;  
 KW breast cancer; wound; reproductive disorder; blood-related disorder;  
 KW haemophilia; thrombocytopaenia; immunodeficiency; thymic hypoplasia;  
 KW Wiskott-Aldrich syndrome; autoimmune disorder; multiple sclerosis;  
 KW graft-versus-host disease; Hashimoto's thyroiditis; allergy; asthma;  
 KW viral infection; bacterial infection; fungal infection; AIDS; sepsis;  
 KW renal disorder; kidney failure; cardiovascular disorder; cytostatic;  
 KW angina pectoris; cerebral ischaemia; congenital heart defect;  
 KW respiratory disorder; neurological disorder; Alzheimer's disease;  
 KW Parkinson's disease; inflammation; Crohn's disease; vulvovaginitis;  
 KW immunosuppressive; antibacterial; haemostatic; thrombolytic;  
 KW anticoagulant; neuroprotective; thyromimetic; antiallergic;  
 KW antiasthmatic; virucide; fungicide; anti-HIV; nephroretropic; antiangiinal;  
 KW cerebroprotective; cardiant; nootropic; antiparkinsonian;  
 KW antiinflammatory; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003049618-A1.  
 XX  
 PD 13-MAR-2003.  
 XX  
 PF 16-MAR-2001; 2001US-00809391.  
 XX

PR 07-MAR-1997; 97US-0038621P.  
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 PR 06-JUN-1997; 97US-0048974P.  
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 PR 08-JUL-1997; 97US-0051928P.  
 PR 16-JUL-1997; 97US-0052874P.  
 PR 18-AUG-1997; 97US-0055724P.  
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 PR 05-SEP-1997; 97US-0057761P.  
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 PR 09-OCT-1997; 97US-0061660P.  
 PR 06-MAR-1998; 98MO-US004493.  
 PR 08-SEP-1998; 98US-00149476.  
 PR 17-MAR-2000; 2000US-0190068P.  
 XX  
 PA (RUBE/) RUBEN S M.  
 PA (ROSE/) ROSEN C A.  
 PA (SOPP/) SOPPET D R.  
 PA (CART/) CARTER K C.  
 PA (BEDN/) BEDNARIK D P.  
 PA (ENDR/) ENDRESS G A.  
 PA (YUGG/) YU G.  
 PA (NIJJ/) NI J.  
 PA (FENG/) FENG P.  
 PA (YOUN/) YOUNG P E.  
 PA (GREE/) GREENE J M.  
 PA (FERR/) FERRIE A M.  
 PA (DUAN/) DUAN D R.  
 PA (HUJJ/) HU J.  
 PA (FLOR/) FLORENCE K A.  
 PA (OLSE/) OLSEN H S.  
 PA (FISC/) FISCHER C L.  
 PA (EENE/) EENER R.  
 PA (BREW/) BREWER L A.  
 PA (MOOR/) MOORE P A.  
 PA (SHIY/) SHI Y.  
 PA (LAPL/) LAPLEUR D W.  
 PA (LIYY/) LI Y.  
 PA (ZENG/) ZENG Z.  
 PA (KYAW/) KYAW H.  
 XX  
 PI Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;  
 PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;  
 PI Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;  
 PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;  
 XX WPI: 2003-521800/49.  
 DR P-PSDB; ABO34617.  
 XX  
 PT New genes and its encoded prostate cancer antigen proteins, useful for  
 PT preventing, treating, ameliorating or diagnosing e.g. prostate cancers,  
 PT thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral  
 PT ischemia.  
 XX  
 PS Claim 4; SEQ ID NO 254; 260pp; English.  
 XX  
 CC The present invention relates to the isolation of novel human secreted  
 CC proteins and the polynucleotide sequences encoding them. The invention

CC also discloses vectors, host cells, antibodies, and recombinant methods  
CC for producing human secreted proteins. The polypeptide and polynucleotide  
CC sequences for the secreted proteins are useful for preventing, treating,  
CC ameliorating or diagnosing medical conditions such as hyperproliferative  
CC disorders (e.g. leukemia or breast cancers), wounds, reproductive  
CC disorders, blood-related disorders (e.g. haemophilia or  
CC thrombocytopaenia), immunodeficiencies (e.g. Wiskott-Aldrich syndrome or  
CC thymic hypoplasia), autoimmune disorders (e.g. graft-versus-host disease,  
CC multiple sclerosis or Hashimoto's thyroiditis), allergies (e.g. asthma),  
CC viral or bacterial or fungal infections (e.g. AIDS or sepsis), renal  
CC disorders (e.g. kidney failure), cardiovascular disorders (e.g. angina  
CC pectoris, cerebral ischaemia or congenital heart defects), respiratory  
CC disorders, neurological disorders (e.g. Alzheimer's disease or  
CC Parkinson's disease), and inflammations (e.g. Crohn's disease). The  
CC polynucleotide or polypeptide may also be used as vaccine adjuvants.  
CC ACD82641-ACD82950 encode human secreted proteins or their fragments.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from the  
CC USPTO web site at [seqdata.uspto.gov/paipatIDentry.html](http://seqdata.uspto.gov/paipatIDentry.html)

XX SQ Sequence 1766 BP; 463 A; 437 C; 383 G; 481 T; 0 U; 2 Other;

## Alignment Scores:

Pred. No.:	1-25e-64	Length:	1766
Score:	622.50	Matches:	113
Percent Similarity:	81.05%	Conservative:	41
Best Local Similarity:	59.47%	Mismatches:	35
Query Match:	67.30%	Indels:	1
DB:	9	Gaps:	1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ACD82884 (1-1766)

QY	1	SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla	20
DB	287	CGGTCACGATCTGATTTCTCGAGAGATTCAGAGACATGGGTTCTCTTGGCC	346
QY	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
DB	347	ACGCTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTCTCAGTGTGTTCTTACCTC	406
QY	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
DB	407	ATCTGGCTCTTCTCTCTGCACCATCAGCTTCAGGATCTACAGTCCGTCATCCAAGCT	466
QY	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
DB	467	GTACAGAGTCAGAGAGAGCCATCCATTCAGAGCTTACCTGACCTAGACATTAATCTG	526
QY	81	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle	100
DB	527	TCCTCAGAGCTTTCATTAATACATGATGCTGCATCATCAACAGGCGCCCTG	586
QY	101	LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal	120
DB	587	AAACTCATTTCTCTCTCTGAGAGATCTGTTGACTCTCTTGAAGCTGGCTGTC	646
QY	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu	140
DB	647	TTCATGTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	706
QY	141	AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp	160
DB	707	GCTGAAGTCTCATTTCTGAGTGTCCGATGTTCTATGAGAGATGACAGCCAGATGAT	766
QY	161	HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys	180
DB	767	CATATGTTGGCATCCCGGAGATCAGACCAAGTCAATGTTCAAAAGATCCAGCAAAA	826
QY	181	IleProGlyLeu---LysArgLysAlaAsp	189
DB	827	CTCCCTGGAATCGCCAAAAAAGGAGAA	856

RESULT 78

AD122969  
ID AD122969 standard; cDNA; 1766 BP.  
XX  
AC AD122969;  
DT 22-APR-2004 (first entry)  
XX  
DE cDNA encoding novel human secreted protein seq id 254.  
XX  
KW cytostatic; gene therapy; cancer; human; secreted protein; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2003175858-A1.  
PD  
PF 18-SEP-2003.  
XX  
PF 18-JUN-2001; 2001US-00882171.  
XX  
PR 07-MAR-1997; 97US-0038621P.  
PR 07-MAR-1997; 97US-0040162P.  
PR 07-MAR-1997; 97US-0040163P.  
PR 07-MAR-1997; 97US-0040333P.  
PR 07-MAR-1997; 97US-0040334P.  
PR 07-MAR-1997; 97US-0040336P.  
PR 07-MAR-1997; 97US-0040628P.  
PR 11-APR-1997; 97US-0043311P.  
PR 11-APR-1997; 97US-0043312P.  
PR 11-APR-1997; 97US-0043313P.  
PR 11-APR-1997; 97US-0043314P.  
PR 11-APR-1997; 97US-0043315P.  
PR 11-APR-1997; 97US-0043568P.  
PR 11-APR-1997; 97US-0043569P.  
PR 11-APR-1997; 97US-0043576P.  
PR 11-APR-1997; 97US-0043578P.  
PR 11-APR-1997; 97US-0043580P.  
PR 11-APR-1997; 97US-0043669P.  
PR 11-APR-1997; 97US-0043670P.  
PR 11-APR-1997; 97US-0043671P.  
PR 11-APR-1997; 97US-0043672P.  
PR 11-APR-1997; 97US-0043674P.  
PR 23-MAY-1997; 97US-0047492P.  
PR 23-MAY-1997; 97US-0047500P.  
PR 23-MAY-1997; 97US-0047501P.  
PR 23-MAY-1997; 97US-0047502P.  
PR 23-MAY-1997; 97US-0047503P.  
PR 23-MAY-1997; 97US-0047581P.  
PR 23-MAY-1997; 97US-0047582P.  
PR 23-MAY-1997; 97US-0047583P.  
PR 23-MAY-1997; 97US-0047584P.  
PR 23-MAY-1997; 97US-0047585P.  
PR 23-MAY-1997; 97US-0047586P.  
PR 23-MAY-1997; 97US-0047587P.  
PR 23-MAY-1997; 97US-0047588P.  
PR 23-MAY-1997; 97US-0047589P.  
PR 23-MAY-1997; 97US-0047590P.  
PR 23-MAY-1997; 97US-0047592P.  
PR 23-MAY-1997; 97US-0047593P.  
PR 23-MAY-1997; 97US-0047594P.  
PR 23-MAY-1997; 97US-0047595P.  
PR 23-MAY-1997; 97US-0047596P.  
PR 23-MAY-1997; 97US-0047597P.  
PR 23-MAY-1997; 97US-0047598P.  
PR 23-MAY-1997; 97US-0047599P.  
PR 23-MAY-1997; 97US-0047600P.  
PR 23-MAY-1997; 97US-0047601P.  
PR 23-MAY-1997; 97US-0047612P.  
PR 23-MAY-1997; 97US-0047613P.  
PR 23-MAY-1997; 97US-0047614P.  
PR 23-MAY-1997; 97US-0047615P.  
PR 23-MAY-1997; 97US-0047617P.  
PR 23-MAY-1997; 97US-0047618P.  
PR 23-MAY-1997; 97US-0047632P.







PS Claim 3; SEQ ID NO 254; 142pp; English.

XX The invention relates to isolated nucleic acid molecules and the human  
CC secreted proteins (SPs) they encode. The proteins and nucleic acids may  
CC be used in the prevention, diagnosis and treatment of diseases associated  
CC with inappropriate SP expression e.g. cancer, haematopoietic disorders,  
CC endocrine disorders, diseases of the immune system, inflammatory  
CC disorders and many others. Full details of disorders that may be  
CC prevented, diagnosed and/or treated by the above methods are given in the  
CC specification. The nucleic acid molecules may be used to produce their  
CC proteins. The nucleic acid and its complementary sequences may also be  
CC used as DNA probes in diagnostic assays to detect and quantitate the  
CC presence of similar nucleic acids in samples, and therefore which  
CC patients may be in need of restorative therapy. The SPs may also be used  
CC as antigens in the production of antibodies against the proteins and in  
CC assays to identify modulators of SP expression and activity. The anti-SP  
CC antibodies and antagonists may also be used to down regulate expression  
CC and activity. The anti-SP antibodies may also be used as diagnostic  
CC agents for detecting the presence of the proteins in samples (e.g. by  
CC enzyme linked immunosorbent assay (ELISA)). The present sequence  
CC represents a human secreted protein CDNA.

XX  
SQ Sequence 1766 BP; 463 A; 437 C; 383 G; 481 T; 0 U; 2 Other;

#### Alignment Scores:

Pred. No.: 1.25e-64 Length: 1766  
Score: 622.50 Matches: 113  
Percent Similarity: 81.05% Conservative: 41  
Best Local Similarity: 59.47% Mismatches: 35  
Query Match: 67.30% Indels: 1  
DB: 12 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADH73971 (1-1766)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
DB 287 GCGGTGCAGATCTGATTTCTGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCACC 346  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 347 ACGCTGATCATGCTGCTTCCCTGGCAGCTTTTCAGTGTCTCATGTTGGTTCCTTACCTC 406  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
DB 407 ATCTCGCTCTTCTCTGTCCACCATCAGCTTCAGGATCTCAAGTCGTCATCCAGCT 466  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
DB 467 GTACAGAAGTCAGAAGAAGGCCCATCCATTCAAAGCTTACCTGGAGCTAGACATTA 526  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
DB 527 TCTCAGAGCTTTCATAATTACATGATGTCGTCATGTCGATCAACAGAGGCCCTG 586  
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
DB 587 AAATCATTTATTCGCTCTCTCTGCTAGAGATCTGTTGACTCTCTTGAAGCTGCTGC 646  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
DB 647 TTCATGTGGCTGATGACCTATGTTGGTGTCTGTTTAAACGGAATCACCCTCTTAATCTT 706  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
DB 707 GCTGAACGTCTCATTTTACGTCTCCGATTTGTCTATGAGAGATCAACAGCCAGATTGAT 766  
QY 161 HistyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
DB 767 CACTATGTTGGCATCGCCGAGATCAGACCAAGTCAATTGTTGAAAGATCCAGCAAAA 826  
QY 181 IleProGlyLeu---LysArgLysAlaAsp 189  
DB 827 TCTCCCTGGAATCGCCAAAAAAGGCAGAA 856

#### RESULT 80

ADM36177  
ID ADM36177 standard; DNA; 1911 BP.  
XX  
AC ADM36177;  
DT 03-JUN-2004 (first entry)  
XX  
DE Human RTN3 isoform VI coding sequence, SEQ ID 60.  
XX  
KW Neuroprotective; Myotropic; neuromuscular disease; RTN3; reticulon 3;  
XX amyotrophic lateral sclerosis; ALS; myopathy; human; gene; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 124..834  
FT /\*tag= a  
FT /product= "RTN3 isoform VI"  
XX  
FN WO2004001069-A2.  
XX  
PD 31-DEC-2003.  
XX  
PF 20-JUN-2003; 2003WO-PRO001910.  
XX  
PR 25-JUN-2002; 2002PR-00007846.  
XX  
PA (UWPA-) UNIV PASTEUR LOUIS.  
XX  
PI Dupuis L, Di Scala F, De Tapia M, Larmet Y, Loeffler J;  
PI Gonzales De Aguilar J, Boutillier AL, Gaidon C, Rene F;  
XX  
DR WPI; 2004-071743/07.  
DR P-PSDB; ADM36178.  
XX  
PT Diagnosing, prognosing and monitoring neuromuscular disease, particularly  
PT amyotrophic lateral sclerosis, comprises detecting modulation of the  
PT reticulon 3 gene.  
XX  
PS Claim 17; SEQ ID NO 60; 116pp; French.  
XX  
CC The present invention relates to a method for diagnosing, or evaluating  
CC progression of, a neuromuscular disease. The method comprises detecting  
CC modulation of the expression of a product (I) of the RTN (reticulon)3  
CC gene. Differential expression of RTN3 is a specific marker of  
CC neuromuscular disease, allowing early diagnosis from readily available  
CC muscle biopsies. The method is also useful for determining the efficacy  
CC of treatment. The method is used to diagnose (also to evaluate  
CC progression or therapy of) neuromuscular disorders, specifically  
CC amyotrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies  
CC specific for isoforms of RTN3 or oligonucleotides (antisense sequences or  
CC small interfering RNA) that can block/reduce expression of these isoforms  
CC are useful for treating neuromuscular diseases and (ii) cells that  
CC express RTN3 are useful in screening for therapeutic agents. The present  
CC sequence is a RTN3 DNA sequence used to illustrate the invention.  
XX  
SQ Sequence 1911 BP; 488 A; 463 C; 406 G; 554 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 1.4e-64 Length: 1911  
Score: 622.50 Matches: 113  
Percent Similarity: 81.05% Conservative: 41  
Best Local Similarity: 59.47% Mismatches: 35  
Query Match: 67.30% Indels: 1  
DB: 12 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADM36177 (1-1911)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
DB 262 GCGGTGCAGATCTGATTTCTGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCACC 321

```
QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 322 AGCGTGATGCTGCTGCTCCCTCGGACGCTTTTCAGTGTCTCATCAGTGTGCTTTCTTACCTC 381
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60
Db 382 ATCTCTGGCTTCTCTCTGTCCACATCAGCTTCAGGATCTACAGTCCCTCATCAAGCT 441
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 442 GTACAGAACTCAGAGAGAGCCATCCATTCAAGGCTACTCGACGTAGACATTACTCTG 501
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 502 TCTCAGAAAGCTTTCATTAATACATGAATGCTGCTGATGCTGATGCTGATGCTGATGCTG 561
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspLeuValAspLeuValAspLeuVal 120
Db 562 AAATCATATTGCTGCTCTCTCTGTTGAGAGATCTGTTGATCTCTTGAAGCTGGCTGTC 621
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db 622 TTCATGTGCTGATGACCTATGTTGCTGCTGTTTAAACGGAATCACCTCTCAATCTT 681
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 682 GTGGAATCTCTATTTTCAGTGTCCGATGCTGATGATGCTGATGATGATGATGATGATGAT 741
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 742 CACTATGTTGGATCGCCGAGATCAGACCAAGTCAATGTTGTAAGAAAGATCCAGCAAAA 801
QY 181 IleProGlyLeu---LysArgLysAlaAsp 189
Db 802 CTCCTCGGAATCGCCCAAAAAGAGGCGAGAA 831
RESULT 81
ABA09204
ID ABA09204 standard; cDNA; 1915 BP.
XX
AC ABA09204;
XX
DT 11-JAN-2002 (first entry)
XX
DE Human neuroendocrine-specific protein-like homologue cDNA, SEQ ID NO:980.
XX
KW Human; cytokine; cell proliferation; tissue growth; immunomodulator; growth factor;
KW haematopoiesis regulation; tumour; tumour; tumour; tumour; tumour; tumour;
KW inhibin; chemotaxis; chemokinesis; thrombolytic; oncogenesis;
KW proliferation; metastasis; cancer; tumour; tumour; tumour; tumour; tumour;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytosolic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnary; antiulcer; ss.
XX
OS Homo sapiens.
XX
PN WO200157188-A2.
XX
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US003800.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-FEB-2000; 2000US-00560875.
XX
PA (HYSE-) HYSEQ INC.
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XX Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-457740/49.
XX P-PSDB; ABB11960.
XX Human proteins and DNA encoding sequences useful for preventing, treating
XX or ameliorating a medical condition in a mammalian subject e.g. arthritis
XX and cancer.
XX Claim 1; Page 838; 1963pp; English.
XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
XX sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
XX invention also relates to vectors and recombinant host cells comprising a
XX nucleotide of the invention, methods of producing the novel polypeptides,
XX antibodies against the polypeptides, methods of detecting the nucleotides
XX or polypeptides in a sample, and methods of identifying compounds which
XX bind to polypeptides of the invention. Although novel, many of the
XX polypeptides of the invention have homology to known proteins, thereby
XX giving an insight into their probable biological activities, and hence
XX potential therapeutic applications. The polypeptides of the invention may
XX have various activities, including cytokine, cell proliferation or cell
XX differentiation activities; stem cell growth factor activity;
XX haematopoiesis regulatory activity; tissue growth activity;
XX immunomodulatory activity; activin- or inhibin-related activities;
XX chemotactic or chemokinetic activities; haemostatic, thrombotic or
XX thrombolytic activities; receptor or ligand activities; or may be
XX involved in oncogenesis, cancer cell proliferation or metastasis.
XX Depending on their biological activities, polypeptides and nucleotides of
XX the invention are useful for preventing, treating or ameliorating medical
XX conditions, e.g., by protein or gene therapy. Such conditions include
XX cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
XX disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
XX proliferative retinopathy, atherosclerosis, coronary heart disease,
XX arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
XX vascular growth. Polypeptides involved with tissue regeneration and
XX repair (or nucleic acids encoding them) may be used to promote wound
XX healing (e.g., of burns, incisions and ulcers), while those with
XX immunomodulatory activities may be used in the treatment of viral,
XX bacterial and fungal infections in addition to immune disorders.
XX Polypeptides with growth factor activity may be used in cell cultures to
XX promote cell growth. For example, such polypeptides may be used to
XX manipulate stem cells in culture to give rise to neuroepithelial cells
XX that can be used to augment or replace cells damaged by illness,
XX CC autoimmune disease or accidental damage. The polypeptides and nucleotides
XX may also be used in the diagnosis of the above conditions, and in drug
XX screening techniques. The present sequence represents a cDNA encoding a
XX novel human polypeptide of the invention
XX
XX Sequence 1915 BP; 492 A; 463 C; 411 G; 549 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 1.4e-64 Length: 1915
XX Score: 622.50 Matches: 113
XX Percent Similarity: 81.05% Conservative: 41
XX Best Local Similarity: 59.47% Mismatches: 35
XX Query Match: 67.30% Indels: 1
XX DB: 4 Gaps: 1
XX
XX US-09-830-972-2_COPY_975_1163 (1-189) x ABA09204 (1-1915)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
Db 287 GCGGTGCGACGATCTGATTTCTGCGAGAGATGTGAAGAACTGGGTTTCTTTGGCACC 346
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 347 ACGTGATCATCTGCTTCTTCCCTGCGACGTTTCAGTGTATCAGTGTGTTCTTACCTC 406
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60
Db 407 ATCTCTGGCTTCTCTCTGTCCACATCAGCTTCAGGATCTACAGTCCCTCATCAAGCT 466
```

Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 467 GTACAGAGTCAAGAGAGGCAATCCATTCAAGGCTACCTGGAGTACATTAATCTG 526  
 Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 Db 527 TCCTCAGAAGCTTTCCATAATTTACATGAATGTCGCATGTCACATCAACAGGCGCCCTG 586  
 Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 587 AAATCATATTGCTGCTCTTCTGTGAGAGATCTGGTGTGATCTCTGAAGCTGGCTGTC 646  
 Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 Db 647 TTCATGTGCTGATGACCTATGTTGGTCTGTTTAAAGGAAATCACCTCTTAATCTT 706  
 Qy 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 707 GCTGAATGCTCATTTTCAGTGTCCGATTTGCTATGAGAAAGTACAGACCCAGATTGAT 766  
 Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 767 CACTATGTTGGATCGCCGAGATCAGACCAAGTCAATTTGTGAAGAGATCCAGCAAA 826  
 Qy 181 IleProGlyLeu---LysArgLysAlaAsp 189  
 Db 827 CTCCTGGAATGCCCAAAAAGGAGCAAA 856

RESULT 82  
 ID AAF93902 standard; cDNA; 2530 BP.  
 AC AAF93902;  
 XX  
 XX 23-MAY-2001 (first entry)  
 XX  
 DE Human cDNA encoding a membrane or secretory protein clone PSEC0103.  
 KW Human; secretory protein; membrane protein; vaccine; gene therapy;  
 KW rheumatoid arthritis; diabetes; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1067182-A2.  
 XX  
 PD 10-JAN-2001.  
 XX  
 PF 07-JUL-2000; 2000EP-00114090.  
 XX  
 PR 08-JUL-1999; 95JP-00194179.  
 PR 11-JAN-2000; 2000JP-00118775.  
 PR 02-MAY-2000; 2000JP-00183766.  
 XX  
 PA (HELI-) HELIX RES INST.  
 XX  
 PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;  
 XX WPI; 2001-093989/11.  
 DR P-PSDB; AAB88475.  
 XX

Nucleic acids encoding secretory proteins/membrane proteins, useful in gene therapy or as candidate target molecules in drug development.

XX Claim 1; SEQ ID NO 317; 609pp + Sequence Listing; English.

XX This invention relates to nucleic acid sequences AAF93744 - AAF93916  
 CC which encode human secretory or membrane proteins represented by AAB88317  
 CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and  
 CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the  
 CC invention. The invention also includes methods for the production of  
 CC antibodies directed against the proteins, and cDNA sequences, which can  
 CC be used in vaccines. The polynucleotide sequences can be used in gene

CC therapy. The polynucleotide sequences and the proteins they encode may be  
 CC used in the prevention, treatment and diagnosis of diseases associated  
 CC with inappropriate secretory protein/membrane protein expression. The  
 CC nucleic acids and complementary sequences may also be used as DNA probes  
 CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect  
 CC and quantitate the presence of similar nucleic acid sequences in samples.  
 CC They may also be used to study the expression and function of secretory  
 CC proteins/membrane polypeptides and their role in metabolism. The  
 CC polypeptides may be used as antigens in the production of antibodies  
 CC against them and in assays to identify modulators (agonists and  
 CC antagonists) of expression and activity. The antibodies and antagonists  
 CC may also be used as therapeutic agents to down regulate expression and  
 CC activity. The antibodies may also be used as diagnostic agents for  
 CC detecting the presence of the polypeptides in samples (e.g. by enzyme  
 CC linked immunosorbent assay (ELISA)). Examples of diseases which may be  
 CC treated include rheumatoid arthritis and diabetes

XX SQ Sequence 2530 BP; 665 A; 577 C; 534 G; 754 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 2,07e-64 Length: 2530  
 Score: 622.50 Matches: 113  
 Percent Similarity: 81.05% Conservative: 41  
 Best Local Similarity: 59.47% Mismatches: 35  
 Query Match: 67.30% Indels: 1  
 DB: 5 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AAF93902 (1-2530)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
 Db 276 GCGGTGCAGCATCTGATTTCTCGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCACC 335  
 Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 336 ACGCTGATCATGTGCTGCTTCCCTGGCAGCTTTCAGTGTCTCATGTGGTGTCTTACCTC 395  
 Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 396 ATCTGTGCTCTTCTCTCTGCACCATCAGCTTCAGGATCTACAAAGTCCGTCATCCAGCT 455  
 Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 456 GTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCTTACCTGGAGTACATTAATCTG 515  
 Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 Db 516 TCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGTGGTCACATCAACAGGCGCCCTG 575  
 Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 576 AAATCATATTGCTGCTCTTCTGTGAGAGATCTGGTGTGATCTCTGAAGCTGGCTGTC 635  
 Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 Db 636 TTCATGTGCTGATGACCTATGTTGGTCTGTTTAAAGGAAATCACCTCTTAATCTT 695  
 Qy 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 696 GCTGAATGCTCATTTTCAGTGTCCGATTTGCTATGAGAAAGTACAGACCCAGATTGAT 755  
 Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 756 CACTATGTTGGATCGCCGAGATCAGACCAAGTCAATTTGTGAAGAGATCCAGCAAA 815  
 Qy 181 IleProGlyLeu---LysArgLysAlaAsp 189  
 Db 816 CTCCTGGAATGCCCAAAAAGGAGCAAA 845

RESULT 83  
 ADL02184  
 ID ADL02184 standard; cDNA; 2559 BP.  
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AC ADL02184;  
 XX 06-MAY-2004 (first entry)  
 XX Human neuroendocrine specific protein linked gene, hNSPL1, cDNA.  
 DE ss; gene; human; neuroendocrine specific protein linked gene; hNSPL1;  
 KW glia cell; tumour; nervous system disease.  
 XX Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FT CDS 137..847  
 FT /\*tag= a  
 FT /product= "hNSPL1"  
 XX  
 XX CN1408868-A.  
 PN  
 XX  
 XX 09-APR-2003.  
 XX  
 XX 25-SEP-2001; 2001CN-00141445.  
 XX  
 XX 25-SEP-2001; 2001CN-00141445.  
 XX  
 XX (PREC-) PRECLINICAL MEDICINE INST CHINESE ACAD.  
 XX  
 XX Yuan J, Qiang B, Peng X;  
 PI WPI; 2003-713650/68.  
 DR P-PSDB; ADL02185.  
 DR  
 XX Gene NSPL1 with expression difference in human normal neuroglia cell and  
 PT neuroglia cell tumor.  
 XX  
 XX Disclosure; Page 7-8; 34pp; Chinese.  
 XX  
 XX The present invention relates to human neuroendocrine specific protein  
 CC linked gene, hNSPL1, highly expressed in human nerve system. The protein  
 CC is located in the endoplasmic reticulum membrane of cell, is highly  
 CC expressed in normal nerve cell and has obvious difference in expression  
 CC inside glia cell and inside glia cell tumour. It may have important  
 CC effect in maintaining the physiological function of nerve system and in  
 CC some nerve system disease occurrence. The present sequence represents  
 CC human neuroendocrine specific protein linked gene, hNSPL1, cDNA.  
 XX  
 XX  
 SQ Sequence 2559 BP; 694 A; 577 C; 533 G; 755 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 2,11e-64 Length: 2559  
 Score: 622.50 Matches: 113  
 Percent Similarity: 81.05% Conservative: 41  
 Best Local Similarity: 59.47% Mismatches: 35  
 Query Match: 67.30% Indels: 1  
 DB: 10 Gaps: 1  
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 QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 Db 275 GCGGTGCACGATCTGATTCTTCGAGAGATGTGAAGAGACTGGGTTCCTTTGGCACC 334  
 QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 335 ACGCTGATCATGTGCTTCCTCCCTGGCAGCTTCCTCAGTGTTCATGCTGTGTTCTTACCTC 394  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 395 ATCTGGCTTCTCTCTGTCCACCATCAGCTTCAGGATCTACAGTCCGCTCATCCAGCT 454  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 455 GTACAGAAGTCAGAAGAAGCCATCCATTCAAAGCCTACTGTGACGTAGACATTACTCTG 514

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 Db 515 TCCTCAGAGCTTTCATAATTACATGAATGCTCCATGGTGCCATCAACAGGGCCCTG 574  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 575 AAACATATATTCGTCCTCTTCTGCTAGAGATCTGGTTGACTCTTGAAGCTGGCTGC 634  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 Db 635 TTCATGTGGCTGATGACCTATGTTGGTGTCTTTTAAACGGAATCACCTCTTAATTCCT 694  
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 QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 755 CACTATGTGGCATCGCCCGAGATCAGACCAAGTCAATTTGTTGAAAAGATCCACAGCAAA 814  
 QY 181 IleProGlyLeu---LysArgLysAlaAsp 189  
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 RESULT 84  
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 ID AAV59749 standard; DNA; 2664 BP.  
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 XX AAV59749;  
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 XX 19-JAN-1999 (first entry)  
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 KW Human; secreted protein; fusion protein; gene therapy; protein therapy;  
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
 KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;  
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO9839448-A2.  
 XX  
 XX 11-SEP-1998.  
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 XX 06-MAR-1998; 98WO-US0004493.  
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XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC,
PI Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM,
PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA,
PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX WPI: 1998-506364/43.
XX P-PSDB; AAW74964.
XX
XX New isolated human genes and the secreted polypeptide(s) they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX
XX Claim 1; Page 475-476; 721pp; English.
XX
XX This sequence represents a nucleic acid molecule designated Gene 92 from
CC the human cDNA clone HAU6L57 (deposited as clone ATCC 97897 and ATCC
CC 209043) which encodes a secreted human protein. The gene can be used to
CC generate fusion proteins by linking to the gene to a human immunoglobulin
CC Fc portion (e.g. AAV59502) for increasing the stability of the fused to
CC protein as compared to the human protein only. The invention relates to
CC 186 novel genes and their fragments (nucleic acid sequences: AAV59511-
CC V59812; amino acid sequences AAW74731-W75026) which are useful for
CC preventing, treating or ameliorating medical conditions e.g. by protein
CC or gene therapy. Also, pathological conditions can be diagnosed by
CC determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 186 polynucleotides, based on
CC which tissues they are most highly expressed in (see AAV59511 for
CC described uses)
XX
XX SQ Sequence 2664 BP; 707 A; 605 C; 566 G; 779 T; 0 U; 7 Other;

Alignment Scores:
Pred. No.: 2.23e-64 Length: 2664
Score: 622.50 Matches: 113
Percent Similarity: 81.05% Conservative: 41
Best Local Similarity: 59.47% Mismatches: 35
Query Match: 67.30% Indels: 1
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US-09-830-972-2_COPY_975_1163 (1-189) x AAV59749 (1-2664)

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QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 322 ACGCTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTTCATCAGTGTGGTTCCTACCTC 381
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
DB 382 ATCTGGCTCTTCTCTGTCCATCATCAGTTCAGGATCTACAGATCGCTCATCCAAGCT 441
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 442 GTACAGAAAGTCAGAAAGAGGCCATCCATTCAAAGCTACCTGGAGTACATTACTCTG 501
QY 81 SerGluGluLeuValGlnLysTy-SerAenSerAlaLeuGlyHisValAasnSerThrIle 100
DB 502 TCCTCAGAAAGCTTCCATAATTACATGATGCTGCCATGCTGTCATCATCAACAGGCCCTG 561
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
DB 562 AAACATATTTCGTCTCTTTCTGTGTAAGATCTGGTTGACTCTCTTGAAGCTGGCTGTC 621
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QY 121 LeuMetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
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QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
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QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
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Db 802 CTCCTGGAATGCCAAAAAAGGCAGAA 831  
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ID ABS73742 standard; cDNA; 2664 BP.  
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AC ABS73742;  
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DT 15-JAN-2003 (first entry)  
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KW Human; ss; gene; secreted protein; autoimmune disease; chemotaxis;  
KW rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;  
KW liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;  
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn;  
KW nervous system disorders; Alzheimer's disease; infection;  
KW ocular disorder; corneal infection; wound healing; tissue regeneration;  
KW epithelial cell proliferation; organ transplantation; food additive;  
KW preservative; nutritional.  
XX  
OS Homo sapiens.  
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PN US6420526-B1.  
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PD 16-JUL-2002.  
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PR 16-JUL-1997; 97US-0052874P.  
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PR 22-AUG-1997; 97US-0056879P.  
PR 22-AUG-1997; 97US-0056880P.  
PR 22-AUG-1997; 97US-0056881P.  
PR 22-AUG-1997; 97US-0056882P.  
PR 22-AUG-1997; 97US-0056884P.  
PR 22-AUG-1997; 97US-0056886P.  
PR 22-AUG-1997; 97US-0056887P.  
PR 22-AUG-1997; 97US-0056888P.  
PR 22-AUG-1997; 97US-0056889P.  
PR 22-AUG-1997; 97US-0056892P.  
PR 22-AUG-1997; 97US-0056893P.  
PR 22-AUG-1997; 97US-0056894P.  
PR 22-AUG-1997; 97US-0056903P.  
PR 22-AUG-1997; 97US-0056908P.  
PR 22-AUG-1997; 97US-0056909P.  
PR 22-AUG-1997; 97US-0056910P.  
PR 22-AUG-1997; 97US-0056911P.  
PR 05-SEP-1997; 97US-0057650P.  
PR 05-SEP-1997; 97US-0057659P.  
PR 05-SEP-1997; 97US-0057761P.  
PR 12-SEP-1997; 97US-0058785P.  
PR 09-OCT-1997; 97US-0061660P.  
PR 06-MAR-1998; 98WO-US004493.  
PR 08-SEP-1998; 98US-00149476.  
PR 17-MAR-2000; 2000US-0190068P.  
XX  
PA (RUBE/) RUBEN S M.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (CART/) CARTER K C.  
PA (BEDN/) BEDNARIK D P.  
PA (ENDR/) ENDRESS G A.  
PA (YUGG/) YU G.  
PA (NIJJ/) NI J.  
PA (FENG/) FENG P.  
PA (YOUN/) YOUNG P E.  
PA (GREE/) GREENE J M.  
PA (FERR/) FERRIE A M.  
PA (DUAN/) DUAN D R.  
PA (HUJJ/) HU J.  
PA (FLOR/) FLORENCE K A.  
PA (OLSE/) OLSEN H S.  
PA (FISC/) FISCHER C L.  
PA (EBNE/) EBNER R.  
PA (BREW/) BREWER L A.  
PA (MOOR/) MOORE P A.  
PA (SHLY/) SHI Y.  
PA (LAFLE/) LAFLEUR D W.  
PA (LIYY/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (KYAW/) KYAW H.  
XX  
PI Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;  
PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;  
PI Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;  
PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;  
XX WPI: 2003-521800/49.  
DR P-PSDB; ABO34618.  
XX  
XX New genes and its encoded prostate cancer antigen proteins, useful for  
PT preventing, treating, ameliorating or diagnosing e.g. prostate cancers,  
PT thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral  
PT ischemia.  
XX  
PS Claim 4; SEQ ID NO 255; 260pp; English.  
XX  
CC The present invention relates to the isolation of novel human secreted  
CC proteins and the polynucleotide sequences encoding them. The invention  
CC also discloses vectors, host cells, antibodies, and recombinant methods  
CC for producing human secreted proteins. The polypeptide and polynucleotide  
CC sequences for the secreted proteins are useful for preventing, treating,  
CC ameliorating or diagnosing medical conditions such as hyperproliferative  
CC disorders (e.g. leukaemia or breast cancers), wounds, reproductive  
CC disorders, blood-related disorders (e.g. haemophilia or  
CC thrombocytopaenia), immunodeficiencies (e.g. Wiskott-Aldrich syndrome or  
CC multiple sclerosis or Hashimoto's thyroiditis) allergies (e.g. asthma),  
CC viral or bacterial or fungal infections (e.g. AIDS or sepsis), renal  
CC disorders (e.g. kidney failure), cardiovascular disorders (e.g. angina  
CC pectoris, cerebral ischaemia or congenital heart defects), respiratory  
CC disorders, neurological disorders (e.g. Alzheimer's disease or  
CC Parkinson's disease), and inflammations (e.g. Crohn's disease). The  
CC polynucleotide or polypeptide may also be used as vaccine adjuvants.  
CC ACD82641-ACD82950 encode human secreted proteins or their fragments.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from the  
CC USPTO web site at [seqdata.uspto.gov/paipaDIDEntry.html](http://seqdata.uspto.gov/paipaDIDEntry.html)  
XX

SQ Sequence 2664 BP; 707 A; 605 C; 566 G; 779 T; 0 U; 7 Other;

**Alignment Scores:**

Pred. No.:	2,238-64	Length:	2664
Score:	622.50	Matches:	113
Percent Similarity:	81.05%	Conservative:	41
Best Local Similarity:	59.47%	Mismatches:	35
Query Match:	67.30%	Indels:	1
DB:	9	Gaps:	1

US-09-830-972-2 COPY 975 1163 (1-189) x ACD82885 (1-2664)

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Db	262	CGGGTCACGAGTCTGATTTTTCTTGGAGAGATGTGAAGAGACTGGGTGTGTCTTTGGCACC	321	
Qy	40	21	SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	322	ACGCTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTTCATCATGTGGTTCCTTACCTC	391	
Qy	60	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
Db	382	ATCCTGGCTCTTCTCTGTCAACATCAGCTTCAGGATCTACAAGTCCGTATCCCAAGCT	441	
Qy	80	61	IleGlnIysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
Db	442	GTACAGAGTTCAGAGAAGGCCATCCATTCAAAGCTACCTGGAGCTAGTAACTTACTCTG	501	
Qy	100	81	SerGluGluLeuValGlnIlystYrSerAsnSerAlaLeuGlyHisValAsnSerThrIle	100
Db	502	TCCTCAGAGCTTTCATTAATTACATGATGCTGCATGTGGTGCATCAACAGGGCCCTG	561	
Qy	120	101	LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal	120
Db	562	AAACTCATTTATTCGTCCTCTTCTGGTAGAAGATCTGGTTGACTCTCTTGAAGCTGGCTGTC	621	
Qy	140	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
Db	622	TTCATGTGGCTGATGACCTTATGTTGGTGCTGTTTTTAACGGGAATCACCCCTTCTAATTCCT	681	
Qy	160	141	AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp	160
Db	682	GCTGAACCTGCTCATTTTCAGTGTCGCCGATGTCTATGAGAAGTACAAGCCAGATGAT	741	
Qy	180	161	HisTyrLeuGlyLeuAlaAsnIlysserValIlyAspAlaMetAlaIlyIleGlnAlaLys	180
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RESULT 87

ADI22970  
ID ADI22970 standard; cDNA; 2664 BP.

AC ADI22970;

DT 22-APR-2004 (first entry)

DE CDNA encoding novel human secreted protein seq id 255.

KW cytostatic; gene therapy; cancer; human; secreted protein; gene; ss.

OS Homo sapiens.

AA  
PN  
US2003175858-A1.

18-SEP-2003.

18-JUN-2001: 2001US-00882171.

AA 07-MAR-1997; 97US-0038621P.

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PR	07-MAR-1997,	97TUS-00403336P,
PR	07-MAR-1997,	97TUS-00403344P,
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PR	23-MAY-1997,	97TUS-00476334P,
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XX OS Homo sapiens.  
XX PN US2003225248-A1.  
XX PD 04-DEC-2003.  
XX PF 10-JUN-2002; 2002US-00164861.  
XX PR 07-MAR-1997; 97US-0038621P.  
XX PR 07-MAR-1997; 97US-0040161P.  
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XX PR 23-MAY-1997; 97US-0047633P.  
XX PR 06-JUN-1997; 97US-0048964P.  
XX PR 06-JUN-1997; 97US-0048974P.  
XX PR 13-JUN-1997; 97US-0049610P.  
XX PR 08-JUL-1997; 97US-0051926P.  
XX PR 16-JUL-1997; 97US-0052874P.  
XX PR 18-AUG-1997; 97US-0055724P.  
XX PR 22-AUG-1997; 97US-0056630P.  
XX PR 22-AUG-1997; 97US-0056631P.  
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PR 22-AUG-1997; 97US-0056662P.  
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PR 22-AUG-1997; 97US-0056845P.  
PR 22-AUG-1997; 97US-0056862P.  
PR 22-AUG-1997; 97US-0056864P.  
PR 22-AUG-1997; 97US-0056872P.  
PR 22-AUG-1997; 97US-0056874P.  
PR 22-AUG-1997; 97US-0056875P.  
PR 22-AUG-1997; 97US-0056876P.  
PR 22-AUG-1997; 97US-0056877P.  
PR 22-AUG-1997; 97US-0056878P.  
PR 22-AUG-1997; 97US-0056879P.  
PR 22-AUG-1997; 97US-0056880P.  
PR 22-AUG-1997; 97US-0056881P.  
PR 22-AUG-1997; 97US-0056882P.  
PR 22-AUG-1997; 97US-0056884P.  
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PR 22-AUG-1997; 97US-0056888P.  
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PR 22-AUG-1997; 97US-0056892P.  
PR 22-AUG-1997; 97US-0056893P.  
PR 22-AUG-1997; 97US-0056894P.  
PR 22-AUG-1997; 97US-0056903P.  
PR 22-AUG-1997; 97US-0056908P.  
PR 22-AUG-1997; 97US-0056909P.  
PR 22-AUG-1997; 97US-0056910P.  
PR 22-AUG-1997; 97US-0056911P.  
PR 05-SEP-1997; 97US-0057650P.  
PR 05-SEP-1997; 97US-0057669P.  
PR 05-SEP-1997; 97US-0057761P.  
PR 12-SEP-1997; 97US-0058785P.  
PR 02-OCT-1997; 97US-0061060P.  
PR 06-MAR-1998; 98WO-US004493.  
PR 08-SEP-1998; 98US-00149476.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;  
PI Endres GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;  
PI Duan R, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;  
PI Brewer LA, Moore PA, Shi Y, Lafleur DM, Li Y, Zeng Z, Kyaw H;  
XX WPI; 2004-131264/13.  
XX P-PSDB; ADH74281.  
XX Isolated nucleic acid molecules encoding human secreted proteins, useful  
PT for preventing, diagnosing and treating disorders associated with  
PT aberrant expression and activity.  
XX Claim 3; SEQ ID NO 255; 142pp; English.  
XX The invention relates to isolated nucleic acid molecules and the human  
CC secreted proteins (SPs) they encode. The proteins and nucleic acids may  
CC be used in the prevention, diagnosis and treatment of diseases associated  
CC with inappropriate SP expression e.g. cancer, haematopoietic disorders,  
CC endocrine disorders, diseases of the immune system, inflammatory  
CC disorders and many others. Full details of disorders that may be  
CC prevented, diagnosed and/or treated by the above methods are given in the  
CC specification. The nucleic acid molecules may be used to produce their  
CC proteins. The nucleic acid and its complementary sequences may also be  
CC used as DNA probes in diagnostic assays to detect and quantitate the  
CC presence of similar nucleic acids in samples, and therefore which  
CC patients may be in need of restorative therapy. The SPs may also be used  
CC as antigens in the production of antibodies against the proteins and in  
CC assays to identify modulators of SP expression and activity. The anti-SP  
CC antibodies and antagonists may also be used to down regulate expression  
CC and activity. The anti-SP antibodies may also be used as diagnostic  
CC agents for detecting the presence of the proteins in samples (e.g. by  
CC enzyme linked immunosorbent assay (ELISA)). The present sequence

```
CC represents a human secreted protein cDNA.
XX
SQ Sequence 2664 BP; 707 A; 605 C; 566 G; 779 T; 0 U; 7 Other;

Alignment Scores:
Pred. No.: 2,23e-64 Length: 2664
Score: 622.50 Matches: 113
Percent Similarity: 81.05% Conservativeness: 41
Best Local Similarity: 59.47% Mismatches: 35
Query Match: 67.30% Indels: 1
DB: 12 Gaps: 1

US-09-830-972-2_COPY_975_1163 (1-189) x ADH73972 (1-2664)
QY 1 SerValValAspLeuLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
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QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
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Db 322 AGCCTGATCATGCTGCTTTCCCTGGCAGCTTTTCAGTGTCTCATGTTGGTTTCTTACCTC 381

QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
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Db 382 ATCTGGCTCTTCTCTGTCCATCAGTCTTCAGGATCTACAGTCCGTCTATCCAGCT 441

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 442 GTACAGAAGTCAAGAAGGCCATCCATTCAAAGCCCTACCTGGACGTAGACATTACTCTG 501

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 502 TCCTCAGAAGCTTTCATTAATTACATGAATGTGCGCATGTGCACATCAACAGGCCCTG 561

QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
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QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
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QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
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RESULT 89
ADQ24047
ID ADQ24047 standard; DNA; 2768 BP.
XX
AC ADQ24047;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6867.
XX
KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
XX
OS da.
XX
OS Homo sapiens.
XX
XX WO2004048938-A2.
XX
PD 10-JUN-2004.
XX
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 Db 800 CACTATGTTGGATCCCGAGATCAGACCAATGTTGTTGAAAAGATCCAGCAAAA 859  
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 DT 04-DEC-2003 (first entry)  
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 XX  
 KW Toxic; toxin; gene expression profile; hepatotoxicity; liver;  
 KW drug screening; toxicity assay; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2003064624-A2.  
 XX  
 PD 07-AUG-2003.  
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 PF 31-JAN-2003; 2003WO-US003194.  
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 PR 31-JAN-2002; 2002US-00060087.  
 PR 15-MAR-2002; 2002US-0364045P.  
 PR 15-MAR-2002; 2002US-0364055P.  
 PR 30-DEC-2002; 2002US-0436643P.  
 XX  
 PA (GENE-) GENE LOGIC INC.  
 XX  
 PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;  
 XX WPI; 2003-689530/65.  
 DR  
 PT Predicting a toxic effect of a compound, useful in identifying toxicity  
 PT markers in liver tissues or cells for drug screening and toxicity assays,  
 PT comprises preparing gene expression profile of tissue or cells exposed to  
 PT the compound.  
 XX  
 PS Claim 1; SEQ ID NO 3915; 1156pp; English.  
 XX  
 CC The present invention relates to a method for predicting a toxic effect  
 CC of a compound. The method comprises preparing a gene expression profile  
 CC of a tissue or cell sample exposed to the compound, and comparing the  
 CC gene expression profile to a database comprising SEQ ID 1-4925, where  
 CC differential expression of the gene indicates at least one toxic effect.  
 CC The method is useful for predicting at least one toxic effect of a  
 CC compound, predicting hepatotoxicity or the progression of a toxic effect  
 CC of a compound, identifying an agent that modulates the onset or  
 CC progression of a toxic response, predicting the cellular pathways that a  
 CC compound modulates in a cell, and identifying an agent that modulates at  
 CC least one activity of a protein. The method and compositions of the  
 CC present invention using a database of genes having liver toxin-induced  
 CC differential expression, are useful in identifying toxicity markers in  
 CC liver tissues or cells for drug screening and toxicity assays. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 2773 BP; 699 A; 653 C; 632 G; 789 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 2.36e-64 Length: 2773  
 Score: 622.50 Matches: 113  
 Percent Similarity: 81.05% Conservative: 41

Best Local Similarity: 59.47% Mismatches: 35  
 Query Match: 67.30% Indels: 1  
 DB: 10 Gaps: 1  
 US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADB58889 (1-2773)  
 QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
 Db 267 GCGGTGCATGATCTGATTTCTGGCGAGATGTGAAGAGACTGGGTGTCTTTGGCACC 326  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 327 ACGCTGATCATGCTCTCTCTGCGAGCTTTCACTGTATCATGATGTGCTCTTACCTC 386  
 QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 387 ATCTTGGCTCTACTCTCTGTCCATCAGCTTCAGAGTCTACAGTCTGTCTATCCAGCT 446  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 447 GTGCAGAGTTCAGAGAGAGGACATCCATTCAAGGCTACCTGGATGTGGACATTACACTG 506  
 QY 81 SerGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAenSerThrIle 100  
 Db 507 TCCTCAGAAGCTTTCCACAGCTACATGAATGCTGCAATGGTGCATGTCAACAAGGCCCTC 566  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspPheLeuValAspSerLeuLysPheAlaVal 120  
 Db 567 AAATCATATTCTGCTCTTTCTGTGTAAGACTTGGTTGACTCTCTTGAAGCTGGCTGTC 626  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 Db 627 TTCATGTGGCTGATGATCACCCTAGCTCGGTCTCTGTTTAAACGGAATTACCTCTGATTCTC 686  
 QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 687 GCCGAGCTGCTGGTTCCTCAGCGTCCCAATGCTATGAGAAGATATAAGACACAGATTGAC 746  
 QY 161 HistTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 747 CACTATGTTGGGATTTGCCCGGATCAGACCAAGTCAATTGTTGAAAAGATCCAGCAAG 806  
 QY 181 IleProGlyLeu---LysArgLysAlaAsp 189  
 Db 807 CTTCCTGGAATCGCCAAAAGGCGAGAA 836  
 RESULT 91  
 ID ADM36171 standard; DNA; 1968 BP.  
 XX  
 AC ADM36171;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Human RTN3 isoform III coding sequence, SEQ ID 54.  
 XX  
 KW Neuroprotective; Myotropic; neuromuscular disease; RTN3; reticulum 3;  
 KW amyotrophic lateral sclerosis; ALS; myopathy; human; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PH Key Location/Qualifiers  
 FT CDS 124..891  
 FT /\*tag= a  
 FT /product= "RTN3 isoform III"  
 XX  
 PN WO2004001069-A2.  
 XX  
 PD 31-DEC-2003.  
 XX  
 PF 20-JUN-2003; 2003WO-FR001910.  
 XX  
 PR 25-JUN-2002; 2002FR-00007846.

XX (UYPA-) UNIV PASTEUR LOUIS.  
PA Dupuis L, Di Scala F, De Tapia M, Larmet Y, Loeffler J;  
PI Gonzales De Aguilar J, Boutillier AL, Gaiddon C, Rene F;  
XX WPI; 2004-071743/07.  
DR P-PSDB; ADM36172.  
XX  
XX Diagnosing, prognosing and monitoring neuromuscular disease, particularly  
PT amyotrophic lateral sclerosis, comprises detecting modulation of the  
PT reticulon 3 gene.  
XX  
XX Claim 35; SEQ ID NO 54; 116pp; French.  
XX  
XX The present invention relates to a method for diagnosing, or evaluating  
CC progression of, a neuromuscular disease. The method comprises detecting  
CC modulation of the expression of a product (I) of the RTN (reticulon)3  
CC gene. Differential expression of RTN3 is a specific marker of  
CC neuromuscular disease, allowing early diagnosis from readily available  
CC muscle biopsies. The method is also useful for determining the efficacy  
CC of treatment. The method is used to diagnose (also to evaluate  
CC progression or therapy of) neuromuscular disorders, specifically  
CC amyotrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies  
CC specific for isoforms of RTN3 or oligonucleotides (antisense sequences or  
CC small interfering RNA) that can block/reduce expression of these isoforms  
CC are useful for treating neuromuscular diseases and (ii) cells that  
CC express RTN3 are useful in screening for therapeutic agents. The present  
CC sequence is a RTN3 DNA sequence used to illustrate the invention.  
XX  
XX Sequence 1968 BP; 496 A; 482 C; 411 G; 579 T; 0 U; 0 Other;  
SQ

Alignment Scores:  
Pred. No.: 1.92e-64 Length: 1968  
Score: 621.50 Matches: 113  
Percent Similarity: 80.95% Conservative: 40  
Best Local Similarity: 59.79% Mismatches: 35  
Query Match: 67.19% Indels: 1  
DB: 12 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADM36171 (1-1968)

QY 2 ValValAspLeuLeuThrPheArgAspIleLeuLeuThrGlyValValPheGlyAlaSer 21  
DB 322 GTGCAGCATGCTGATTTCTGGAGAGATGTGAAGAGACTGGGTTGCTTTGGCCACCG 381

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 382 CTGATCATGCTGCTTTCCCTGGCAGCTTTTCAGTGTCTCATGCTGGTGTCTTACCTCATC 441

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAlaIle 61  
DB 442 CTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAAGCTGTA 501

QY 62 GlnIleSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 502 CAGAAGTCAAGAAGAGCCATCCATTCAGGCTCTCTGAGCGTAGACATTCTCTGTC 561

QY 82 GluGluLeuValGlnIleYstYrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 562 TCAGAGCTTTCATTAATACATGAATGTCGTCATGTCACATCAACAGGCGCTGAAA 621

QY 102 GluLeuArgGluLeuPheLeuValAspLeuValAspSerLeuLeuLysPheAlaValLeu 121  
DB 622 CTCAATTATTCGCTCTCTCTGGTAGAGATCTGTTGACTCTCTGAAGCTGGCTGCTTC 681

QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuLeuLeuIleAla 141  
DB 682 ATGTGCTGATGACCTATGTGTGCTGCTTTTAAACGGAATCACCTTCTTAATCTTGT 741

QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 742 GAACTGCTCATTTTCAGTGTGCCGATTGTCTATGAGAAGTACAAGACCCAGAGTTGATCAC 801

QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysPheAlaMetAlaLysIleGlnAlaLysIle 181  
DB 802 TATGTTGGCATGCGCCGAGATCAGACCAAGTCAATTGTTGAAAGATCCAGCAAACTC 861

QY 182 ProGlyLeu--LysArgLysAlaAsp 189  
DB 862 CCTGGAATCGCCCAAAAAAAGGACGAA 888

RESULT 92  
ADQ84465  
ID ADQ84465 standard; cDNA; 2250 BP.  
XX AC ADQ84465;  
XX  
XX 07-OCT-2004 (first entry)  
XX Human tumour-associated antigenic target (TAT) cDNA sequence #1279.  
XX human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;  
KW cancer; cell proliferative disorder; gene; ss.  
XX Homo sapiens.  
XX WO2004060270-A2.  
XX  
XX 22-JUL-2004.  
XX  
XX 15-OCT-2003; 2003WO-US029126.  
XX  
XX 18-OCT-2002; 2002US-0418988P.  
XX  
XX (GETH ) GENENTECH INC.  
XX (WUTD/) WU T D.  
XX (ZHOU/) ZHOU Y.  
XX Wu TD, Zhou Y;  
XX  
XX WPI; 2004-534300/51.  
XX  
XX New nucleic acid molecule and encoded polypeptide, for diagnosing,  
PT preventing or treating cell proliferative disorders such as cancer.  
XX  
XX Claim 1; SEQ ID NO 1279; 5504pp; English.  
XX  
XX The present invention describes an isolated tumour-associated antigenic  
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide  
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of  
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%  
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-  
CC (c). Also described: (1) an expression vector comprising the above  
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)  
CC a process for producing a polypeptide; (4) an isolated polypeptide  
CC comprising: (a) an amino acid sequence encoded by any of the above  
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-  
CC length coding region of the above nucleotide sequences; or (c) a sequence  
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide  
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)  
CC an isolated antibody that binds to the above polypeptide; (7) a process  
CC for producing the antibody; (8) an isolated oligopeptide that binds to  
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)  
CC binding organic molecule that binds to the above polypeptide; (10) a  
CC composition of matter comprising the above (chimeric) polypeptide,  
CC antibody, oligopeptide or TAT binding organic molecule, in combination  
CC with a carrier; (11) an article of manufacture comprising a container and  
CC the composition of matter contained within the container; (12) methods of  
CC inhibiting the growth of a cell that expresses the above protein, where  
CC the growth of the cell is at least in part dependent upon a growth  
CC potentiating effect of the above protein; (13) a method of  
CC therapeutically treating a mammal having a cancerous tumour comprising  
CC cells that express the above protein; (14) a method of determining the  
CC presence of a protein in a sample suspected of containing the protein  
CC described above; (15) methods of diagnosing the presence of a tumour in a



CC mammal; (16) a method for treating or preventing a cell proliferative  
CC disorder associated with increased expression or activity of the above  
CC protein; and (17) a method of binding an antibody, oligopeptide or  
CC organic molecule to a cell that expresses the protein described above.  
CC The TAT sequences have cytostatic activities, and can be used in gene  
CC therapy. The composition and methods are useful for diagnosing,  
CC preventing or treating cancer. The composition is also used for preparing  
CC a medicament for the therapeutic treatment or diagnostic detection of a  
CC cell proliferative disorder or cancer. The present sequence represents a  
CC human TAT cDNA sequence from the present invention.

XX  
SQ Sequence 2250 BP; 629 A; 469 C; 456 G; 696 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 2,32e-64 Length: 2250  
Score: 621.50 Matches: 113  
Percent Similarity: 80.95% Conservatives: 40  
Best Local Similarity: 59.79% Mismatches: 35  
Query Match: 67.19% Indels: 1  
DB: 12 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADQ84465 (1-2250)

QY 2 ValValAspLeuLeuTyrTrpArgAspLeuLysThrGlyValValPheGlyAlaSer 21  
DB 1 GTGCACGATCTGATTCTTCGGAGAGATGTGAAGAAGACTGGGTTGTCTTTGGCACACG 60  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 61 CTGATCATGCTGCTTTCCTGGCAGCTTTCAGTGTGCATCAGTGGTGTCTTACCTATC 120  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 121 CTGGCTCTCTCTCTGTCACATCAGCTTCAGATCTACAGTCCGTCTATCCAGCTGTA 180  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 181 CAGAAAGTCAGAAAGAGGCCATCCATTCAAAGCTACCTGGAGCTAGACATTACTGTGCC 240  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 241 TCAGAAAGCTTTCATTAATACATGATGCTGCATGCTGCATCAACAGGGCCCTGAAA 300  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 301 CTCATTATTCGCTCTCTTCGTGAGAGATCTGGTTGACTCTTGAAGCTGGCTGCTTC 360  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
DB 361 ATGTGGCTGATGACCTATGTTGGTGTCTGTTTAAACGGAATCACCTTCTAATCTTGTCT 420  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 421 GAACCTGCTCATTTTCAGTGTCCGATGCTGATGAGAAATGACACACCCAGGATGATCAC 480  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 481 TATGTTGGATGCTCCCGAGATCAGACCAAGTCAATTGTTGAAGATCCAGCAAACTC 540  
QY 182 ProGlyLeu---LysArgLysAlaAsp 189  
DB 541 CCTGGAATCGCCAAAAGGAGGACAG 567

## RESULT 93

ADQ86409

ID ADQ86409 standard; cDNA; 2250 BP.

XX AC ADQ86409;

XX DT 07-OCT-2004 (first entry)

XX DE Human tumour-associated antigenic target (TAT) cDNA sequence #3281.

KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;  
XX cancer; cell proliferative disorder; gene; ss.

OS Homo sapiens.

PN WO2004060270-A2.

XX 22-JUL-2004.

PF 15-OCT-2003; 2003WO-US029126.

PR 18-OCT-2002; 2002US-0418988P.

PA (GETH ) GENENTECH INC.

PA (WUTD/) WU T D.

XX (ZHOU/) ZHOU Y.

PI Wu TD, Zhou Y;

DR WPI; 2004-534300/51.

XX New nucleic acid molecule and encoded polypeptide, for diagnosing,  
PT preventing or treating cell proliferative disorders such as cancer.

PS Claim 1; SEQ ID NO 3281; 5504pp; English.

XX The present invention describes an isolated tumour-associated antigenic  
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide  
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of  
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%  
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-  
CC (c). Also described: (1) an expression vector comprising the above  
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)  
CC a process for producing a polypeptide; (4) an isolated polypeptide  
CC comprising: (a) an amino acid sequence encoded by any of the above  
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-  
CC length coding region of the above nucleotide sequences; or (c) a sequence  
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide  
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)  
CC an isolated antibody that binds to the above polypeptide; (7) a process  
CC for producing the antibody; (8) an isolated oligopeptide that binds to  
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)  
CC binding organic molecule that binds to the above polypeptide; (10) a  
CC composition of matter comprising the above (chimeric) polypeptide,  
CC antibody, oligopeptide or TAT binding organic molecule, in combination  
CC with a carrier; (11) an article of manufacture comprising a container and  
CC the composition of matter contained within the container; (12) methods of  
CC inhibiting the growth of a cell that expresses the above protein, where  
CC the growth of the cell is at least in part dependent upon a growth  
CC potentiating effect of the above protein; (13) a method of  
CC therapeutically treating a mammal having a cancerous tumour comprising  
CC cells that express the above protein; (14) a method of determining the  
CC presence of a protein in a sample suspected of containing the protein  
CC described above; (15) methods of diagnosing the presence of a tumour in a  
CC mammal; (16) a method for treating or preventing a cell proliferative  
CC disorder associated with increased expression or activity of the above  
CC protein; and (17) a method of binding an antibody, oligopeptide or  
CC organic molecule to a cell that expresses the protein described above.  
CC The TAT sequences have cytostatic activities, and can be used in gene  
CC therapy. The composition and methods are useful for diagnosing,  
CC preventing or treating cancer. The composition is also used for preparing  
CC a medicament for the therapeutic treatment or diagnostic detection of a  
CC cell proliferative disorder or cancer. The present sequence represents a  
CC human TAT cDNA sequence from the present invention.

SQ Sequence 2250 BP; 629 A; 469 C; 456 G; 696 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 2,32e-64 Length: 2250  
Score: 621.50 Matches: 113  
Percent Similarity: 80.95% Conservatives: 40  
Best Local Similarity: 59.79% Mismatches: 35  
Query Match: 67.19% Indels: 1

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DB: 12 Gaps: 1
US-09-830-972-2_COPY_975_1163 (1-189) x ADQ86409 (1-2250)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
DB 1 GTGCAGATCTGATTTCTGGAGAGATGTGAGAGACTGGTGTCTTTGGCACCAG 60
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 61 CTGATCATGCTGTTTCCCTGAGCAGCTTTTCAGTGTCTCATCAGTGTGTTCTTACCTCATC 120
QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 121 CTGGCTCTTCTCTCTCACCATCAGCTTCAAGATCTACAGTCCGTCTACCAAGCTGTA 180
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerValAlaIleSer 81
DB 181 CAGAAGTCAGAGAGAGCCATCATTTCAAGCTTACTGGAGCTAGACATTACTCTGTCC 240
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
DB 241 TCAGAAGCTTTCATTAATACATGAATGCTGCATGCTGCATCAACAGGGCCCTGAAA 300
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 301 CTCATTATTGCTCTCTTCTGGTAGAAGATCTGGTTGACTCTTGAAGCTGGCTGTCTTC 360
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
DB 361 ATGTGCTGATGACCTATGTTGGTGTCTGTTTAAAGGATCACTCTTCTAATCTTGCT 420
QY 142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
DB 421 GAACTGCTCATTTTCAGTGTCCGATGTCTATGAGAGTGAACAAGCCAGATTCATCAC 480
QY 162 TyrLeuGluLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
DB 481 TAGTTGGATGCTCCCGAGATCAGACCAAGTCAATTTGTTGAAAAGATCCAGCAAAATC 540
QY 182 ProGlyLeu---LysArgLysAlaAsp 189
DB 541 CCTGGATCCCAAAAAGGAGAA 567
RESULT 94
ID ADQ85262
XX ADQ85262 standard; cDNA; 2250 BP.
AC ADQ85262;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2076.
XX
KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW cancer; cell proliferative disorder; gene; ss.
XX
OS Homo sapiens.
XX
XX WO2004060270-A2.
XX
PD 22-JUL-2004.
XX
XX 15-OCT-2003; 2003WO-US029126.
XX
XX 18-OCT-2002; 2002US-0418988P.
XX
XX (GETH ) GENENTECH INC.
XX
XX (WUTD/) WU T D.
XX
XX (ZHOU/) ZHOU Y.
XX
XX Wu TD, Zhou Y;
XX
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DR WPI; 2004-534300/51.
XX
PT New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT preventing or treating cell proliferative disorders such as cancer.
XX
XX Claim 1; SEQ ID NO 2076; 5504pp; English.
XX
CC The present invention describes an isolated tumour-associated antigenic
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC (c). Also described: (1) an expression vector comprising the above
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC a process for producing a polypeptide; (4) an isolated polypeptide
CC comprising: (a) an amino acid sequence encoded by any of the above
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC length coding region of the above nucleotide sequences; or (c) a sequence
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide;
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC an isolated antibody that binds to the above polypeptide; (7) a process
CC for producing the antibody; (8) an isolated oligopeptide that binds to
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC binding organic molecule that binds to the above polypeptide; (10) a
CC composition of matter comprising the above (chimeric) polypeptide,
CC antibody, oligopeptide or TAT binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the composition of matter contained within the container; (12) methods of
CC inhibiting the growth of a cell that expresses the above protein, where
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising
CC cells that express the above protein; (14) a method of determining the
CC presence of a protein in a sample suspected of containing the protein
CC described above; (15) methods of diagnosing the presence of a tumour in a
CC mammal; (16) a method for treating or preventing a cell proliferative
CC disorder associated with increased expression or activity of the above
CC protein; and (17) a method of binding an antibody, oligopeptide or
CC organic molecule to a cell that expresses the protein described above.
CC The TAT sequences have cytostatic activities, and can be used in gene
CC therapy. The composition and methods are useful for diagnosing,
CC preventing or treating cancer. The composition is also used for preparing
CC a medicament for the therapeutic treatment or diagnostic detection of a
CC cell proliferative disorder or cancer. The present sequence represents a
CC human TAT cDNA sequence from the present invention.
XX
SQ Sequence 2250 BP; 629 A; 469 C; 456 G; 696 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.: 2,328-64 Length: 2250
Score: 621.50 Matches: 113
Percent Similarity: 80.95% Conservative: 40
Best Local Similarity: 59.79% Mismatches: 35
Query Match: 67.19% Indels: 1
DB: 13 Gaps: 1
US-09-830-972-2_COPY_975_1163 (1-189) x ADQ85262 (1-2250)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
DB 1 GTGCAGATCTGATTTCTGGAGAGATGTGAGAGACTGGTGTCTTTGGCACCAG 60
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 61 CTGATCATGCTGCTTCTCCCTGAGCTTTCAGTGTCTCATCAGTGTGTTCTTACCTCATC 120
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 121 CTGGCTCTTCTCTCTCACCATCAGCTTCAAGATCTACAGTCCGTCTACCAAGCTGTA 180
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 181 CAGAAGTCAGAGAGAGCCATCATTTCAAGCTTACTGGAGCTAGACATTACTCTGTCC 240
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481 TATGTTGGCATCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAGCAAAATCTC 540

182 ProglyLeu---LysArglyAlaAsp 189  
 541 CCTGGAATCGCCCAAAAAAAGGCAGAA 567

# RESULT 96

ADM36175  
 ID ADM36175 standard; DNA; 3231 BP.

AC ADM36175;

DT 03-JUN-2004 (first entry)

DE Human RTN3 isoform V coding sequence, SEQ ID 58.

KW Neuroprotective; Myotrophic; neuromuscular disease; RTN3; reticulon 3;  
 KW amyotrophic lateral sclerosis; ALS; myopathy; human; gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FT CDS 124..2154  
 FT /tag= a  
 FT /product= "RTN3 isoform V"

XX WO2004001069-A2.

XX 31-DEC-2003.

XX 20-JUN-2003; 2003WO-FR001910.

XX 25-JUN-2002; 2002FR-00007846.

XX (UYPA-) UNIV PASTEUR LOUIS.

XX Dupuis L, Di Scala F, De Tapia M, Larnet Y, Loeffler J;

XX Gonzalez De Aguilar J, Boutillier AL, Gaiddon C, Rene F;

XX WPI; 2004-071743/07.

XX P-PSDB; ADM36176.

PT Diagnosing, prognosing and monitoring neuromuscular disease, particularly  
 PT amyotrophic lateral sclerosis, comprises detecting modulation of the  
 PT reticulon 3 gene.

XX Claim 35; SEQ ID NO 58; 116pp; French.

CC The present invention relates to a method for diagnosing, or evaluating  
 CC progression of, a neuromuscular disease. The method comprises detecting  
 CC modulation of the expression of a product (I) of the RTN (reticulon)3  
 CC gene. Differential expression of RTN3 is a specific marker of  
 CC neuromuscular disease, allowing early diagnosis from readily available  
 CC muscle biopsies. The method is also useful for determining the efficacy  
 CC of treatment. The method is used to diagnose (also to evaluate  
 CC progression or therapy of) neuromuscular disorders, specifically  
 CC amyotrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies  
 CC specific for isoforms of RTN3 or oligonucleotides (antisense sequences or  
 CC small interfering RNA) that can block/reduce expression of these isoforms  
 CC are useful for treating neuromuscular diseases and (ii) cells that  
 CC express RTN3 are useful in screening for therapeutic agents. The present  
 CC sequence is a RTN3 DNA sequence used to illustrate the invention.

XX SQ Sequence 3231 BP; 947 A; 717 C; 690 G; 877 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 3 85e-64 Length: 3231  
 Score: 621.50 Matches: 113  
 Percent Similarity: 80.95% Conservative: 40  
 Best Local Similarity: 59.79% Mismatches: 35  
 Query Match: 67.19% Indels: 1  
 DB: 12 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADM36175 (1-3231)

QY 2 ValValAspLeuLeuTyrTriArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 1585 GTGCACGATCTGATTTTCTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCACCACG 1644

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 1645 CTGATCATGCTGCTTTCCCTGCGACGTTTCACTGTCATCAGTGTGGTTCTTTACCTCATC 1704

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 1705 CTGGCTCTTCTCTCTGTCCATCATCAGCTTCAGANTCTACAAGTCGTCATCCAGCTGTA 1764

QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 1765 CAGAAGTCAGAAGAAGGCCATCCATTTCAAGGCCCTACCTGGACGTAGACATTACTCTGTCC 1824

QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 1825 TCAGAAAGCTTTCCATAATATACATGCTGCCATGTCATCAACAGGGCCCTGAAA 1884

QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 1885 CTCATTATTCGTCTCTTCTGGTAGAAGATCTGGTTGACTCCTTGAAGCTGGCTGTCTTC 1944

QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
 1945 ATGTGGCTGATGACCTATGTTGCTGCTTTTAAACGGAATCACCCCTTCTTAATCTTGT 2004

QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 2005 GAACTGCTCATTTTTCAGTGTCCGATGCTATGAGAAGTACCAAGCCAGATTGATCAC 2064

QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 2065 TATGTTGGCATCGCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAGCAAAATCTC 2124

QY 182 ProGlyLeu---LysArgLysAlaAsp 189  
 2125 CCTGGAATCGCCCAAAAAAAGGCAGAA 2151

RESULT 97  
 ADM36169  
 ID ADM36169 standard; DNA; 3288 BP.

XX AC ADM36169;

XX DT 03-JUN-2004 (first entry)

XX DE Human RTN3 isoform II coding sequence, SEQ ID 52.

XX KW Neuroprotective; Myotrophic; neuromuscular disease; RTN3; reticulon 3;  
 XX amyotrophic lateral sclerosis; ALS; myopathy; human; gene; ds.

XX Homo sapiens.

XX OS  
 XX Key Location/Qualifiers  
 FT CDS 124..2211  
 FT /tag= a  
 FT /product= "RTN3 isoform II"

XX WO2004001069-A2.

XX 31-DEC-2003.

XX 20-JUN-2003; 2003WO-FR001910.

XX 25-JUN-2002; 2002FR-00007846.

XX (UYPA-) UNIV PASTEUR LOUIS.

XX Dupuis L, Di Scala F, De Tapia M, Larnet Y, Loeffler J;

PI Gonzales De Aguilar J, Boutillier AL, Gaidon C, Rene F;  
XX WPI; 2004-071743/07.  
DR P-PSDB; ADM36170.  
XX  
PT Diagnosing, prognosing and monitoring neuromuscular disease, particularly  
PT amyotrophic lateral sclerosis, comprises detecting modulation of the  
PT reticulon 3 gene.  
XX  
PS Claim 35; SEQ ID NO 52; 116pp; French.  
XX  
CC The present invention relates to a method for diagnosing, or evaluating  
CC progression of, a neuromuscular disease. The method comprises detecting  
CC modulation of the expression of a product (i) of the RTN (reticulon)3  
CC gene. Differential expression of RTN3 is a specific marker of  
CC neuromuscular disease, allowing early diagnosis from readily available  
CC muscle biopsies. The method is also useful for determining the efficacy  
CC of treatment. The method is used to diagnose (also to evaluate  
CC progression or therapy of) neuromuscular disorders, specifically  
CC amyotrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies  
CC specific for isoforms of RTN3 or oligonucleotides (antisense sequences or  
CC small interfering RNA) that can block/reduce expression of these isoforms  
CC are useful for treating neuromuscular diseases and (ii) cells that  
CC express RTN3 are useful in screening for therapeutic agents. The present  
CC sequence is a RTN3 DNA sequence used to illustrate the invention.  
XX  
SQ Sequence 3288 BP; 955 A; 736 C; 695 G; 902 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 3.95e-64 Length: 3288  
Score: 621.50 Matches: 113  
Percent Similarity: 80.95% Conservative: 40  
Best Local Similarity: 59.79% Mismatches: 35  
Query Match: 67.19% Indels: 1  
DB: 12 Gaps: 1  
  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADM36169 (1-3288)  
  
QY 2 ValValAspLeuLeuTyrTTPArgAspIleValSerThrGlyValValPheGlyAlaSer 21  
DB 1642 GTGCAGATCTGATTTCTGGAGAGATGTGAAGAGACTGGTTTGTCTTTGGACACAG 1701  
  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaIleAla 41  
DB 1702 CTGATCATGCTGCTTCTCCCTGCAGCTTTTCAGTGTCTCATGCTGTTCTTACCTCATC 1761  
  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 1762 CTGGCTCTCTCTCTGCACCATCATGCTTCAGGATCTCAAGTCCGTCTCAAGCTGTA 1821  
  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 1822 CAGAAGTCAGAAAGAGCCATCCATCAAGGCTTACCTGGAGCTAGATCTACTCTGTGCC 1881  
  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 1882 TCAGAAGCTCTCCATAATATCATGATGCTGCCATGGTGACATCAACAGGGCCCTGAA 1941  
  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 1942 CTCATTATTCTGCTCTCTTCTGTAGAGATCTGGTTGACTCTCTTGAAGCTGGCTGCTTC 2001  
  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheGlnGlyLeuThrLeuLeuIleAla 141  
DB 2002 ATGCGCTGATGACCTATGTGGTGCTGTTTTTAACGGAATCACCCCTTCTAATCTTGCT 2061  
  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 2062 GAACGTCTCTATTTTCAGTGTCCGATGCTCTATGAGAAGTACAGACCCAGATGATCAC 2121  
  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 2122 TATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTTGTAAGATCAAGCAAGCAAACT 2181

QY 182 ProGlyLeu---LysArgLysAlaAsp 189  
DB 2182 CCTGGATCGCCAAAGAAAGGAGCA 2208  
  
RESULT 98  
ADM36179  
ID ADM36179 standard; DNA; 4092 BP.  
XX AC ADM36179;  
XX DT 03-JUN-2004 (first entry)  
XX DE Human RTN3 isoform VII coding sequence, SEQ ID 62.  
XX KW Neuroprotective; Myotropic; neuromuscular disease; RTN3; reticulon 3;  
XX amyotrophic lateral sclerosis; ALS; myopathy; human; gene; ds.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX CDS 163..3015  
XX FT /\*tag= a  
XX FT /product= "RTN3 isoform VII"  
XX PN WO2004001069-A2.  
XX PD 31-DEC-2003.  
XX PF 20-JUN-2003; 2003WO-FR001910.  
XX PR 25-JUN-2002; 2002FR-00007846..  
XX PA (UYPA-) UNIV PASTEUR LOUIS.  
XX PI Dupuis L, Di Scala F, De Tapia M, Larmet Y, Loeffler J;  
XX PI Gonzales De Aguilar J, Boutillier AL, Gaidon C, Rene F;  
XX WPI; 2004-071743/07.  
XX P-PSDB; ADM36180.  
  
Diagnosing, prognosing and monitoring neuromuscular disease, particularly  
reticulon 3 gene.  
  
Claim 35; SEQ ID NO 62; 116pp; French.  
  
The present invention relates to a method for diagnosing, or evaluating  
progression of, a neuromuscular disease. The method comprises detecting  
modulation of the expression of a product (i) of the RTN (reticulon)3  
gene. Differential expression of RTN3 is a specific marker of  
neuromuscular disease, allowing early diagnosis from readily available  
muscle biopsies. The method is also useful for determining the efficacy  
of treatment. The method is used to diagnose (also to evaluate  
progression or therapy of) neuromuscular disorders, specifically  
amyotrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies  
specific for isoforms of RTN3 or oligonucleotides (antisense sequences or  
small interfering RNA) that can block/reduce expression of these isoforms  
are useful for treating neuromuscular diseases and (ii) cells that  
express RTN3 are useful in screening for therapeutic agents. The present  
sequence is a RTN3 DNA sequence used to illustrate the invention.  
  
Sequence 4092 BP; 1286 A; 834 C; 836 G; 1136 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 5.37e-64 Length: 4092  
Score: 621.50 Matches: 113  
Percent Similarity: 80.95% Conservative: 40  
Best Local Similarity: 59.79% Mismatches: 35  
Query Match: 67.19% Indels: 1  
DB: 12 Gaps: 1  
  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADM36179 (1-4092)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLeuLysThrGlyValValPheGlyAlaSer 21  
 Db GTGCAGCATCTGATTTCTGGAGAGATGTGAAGAGACTGGGTTGTCTTTGGCACCACG 2505  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db GTGATCATGCTGCTTCCCTGGCAGCTTTCAAGTGTATCAGTGTGGTGTCTTACCTCATFC 2565  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db GTGGCTCTTCTCTGTACCATCAGCTTCAGAGCTACAGTCCGTATCCAGCTGTA 2625  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db CAGAAGTCAGAAGAGGCCCATCCATTCAAGGCCCTACCTGAGCGTAGACATTACTCTGTCC 2685  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db TCAGAAGCTTTCCATAATTACATGAATGCTGCATGGTCACATCAACAGGCCCTGAAA 2745  
 QY 102 GluLeuArgAlaLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db CTCATTATTCGTCCTCTTCTGGTAGAGATCTGGTTGACTCTTGAAGCTGCTGCTTC 2805  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuAla 141  
 Db ATGTGGCTGATGACCTATGTTGGTGTGTTTTTAACGGAATCACCCCTTCAATTCTTGT 2865  
 QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db GAACGTCTCATTTTCAAGTGTCCGATGTCTATGAGAGATCAAGACCCAGATTGATCAC 2925  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db TATGTGGCATGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAGCAAAATC 2985  
 QY 182 ProGlyLeu---LysArgLysAlaLeu 189  
 Db CCTGGAATCGCCAAAAGGAGGAGAA 3012  
 RESULT 99  
 ADM36173  
 ID ADM36173 standard; DNA; 4239 BP.  
 AC ADM36173;  
 AC ADM36173;  
 DT 03-JUN-2004 (first entry)  
 XX Human RTN3 isoform IV coding sequence, SEQ ID 56.  
 DE Neuroprotective; Myotrophic; neuromuscular disease; RTN3; reticulon 3;  
 KW amytrophic lateral sclerosis; ALS; myopathy; human; gene; ds.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FH 124..3162  
 CDS /\*tag= a  
 FT /product= "RTN3 isoform IV"  
 FT  
 XX WO2004001069-A2.  
 XX 31-DEC-2003.  
 XX 20-JUN-2003; 2003WO-FR001910.  
 XX 25-JUN-2002; 2002FR-00007846.  
 XX (UYPA-) UNIV PASTEUR LOUIS.  
 PA Dupuis L, Di Scala F, De Tapia M, Larmet Y, Loeffler J;  
 PI Gonzales De Aguilar J, Bouillier AL, Gaidon C, Rene F;

XX WPI; 2004-071743/07.  
 DR P-PSDB; ADM36174.  
 XX Diagnosing, prognosing and monitoring neuromuscular disease, particularly  
 PT amytrophic lateral sclerosis, comprises detecting modulation of the  
 PT reticulon 3 gene.  
 XX Claim 35; SEQ ID NO 56; 116pp; French.  
 PS The present invention relates to a method for diagnosing, or evaluating  
 CC progression of, a neuromuscular disease. The method comprises detecting  
 CC modulation of the expression of a product (I) of the RTN (reticulon)3  
 CC gene. Differential expression of RTN3 is a specific marker of  
 CC neuromuscular disease, allowing early diagnosis for determining the efficacy  
 CC of treatment. The method is also useful for determining the efficacy  
 CC of treatment. The method is used to diagnose (also to evaluate  
 CC progression or therapy of) neuromuscular disorders, specifically  
 CC amytrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies  
 CC specific for isoforms of RTN3 or oligonucleotides (antisense sequences or  
 CC small interfering RNA) that can block/reduce expression of these isoforms  
 CC are useful for treating neuromuscular diseases and (ii) cells that  
 CC express RTN3 are useful in screening for therapeutic agents. The present  
 CC sequence is a RTN3 DNA sequence used to illustrate the invention.  
 XX SQ Sequence 4239 BP; 1282 A; 925 C; 890 G; 1142 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 5,64e-64 Length: 4239  
 Score: 621.50 Matches: 113  
 Percent Similarity: 80.9% Conservative: 40  
 Best Local Similarity: 59.79% Mismatches: 35  
 Query Match: 67.19% Indels: 1  
 DB: 12 Gaps: 1  
 US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADM36173 (1-4239)  
 QY 2 ValValAspLeuLeuTyrTrpArgAspIleLeuLysThrGlyValValPheGlyAlaSer 21  
 Db GTGCAGCATCTGATTTCTGGAGAGATGTGAAGAGACTGGGTTGTCTTTGGCACCACG 2652  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db GTGATCATGCTGCTTCCCTGGCAGCTTTCAAGTGTATCAGTGTGGTGTCTTACCTCATC 2712  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db GTGGCTCTTCTCTGTACCATCAGCTTCAGAGCTACAGTCCGTATCCAGCTGTA 2772  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db CAGAAGTCAGAAGAGGCCCATCCATTCAAGGCCCTACCTGAGCGTAGACATTACTCTGTCC 2832  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db TCAGAAGCTTTCCATAATTACATGAATGCTGCATGGTCACATCAACAGGCCCTGAAA 2892  
 QY 102 GluLeuArgAlaLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db CTCATTATTCGTCCTCTTCTGGTAGAGATCTGGTTGACTCTTGAAGCTGCTGCTTC 2952  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuAla 141  
 Db ATGTGGCTGATGACCTATGTTGGTGTGTTTTTAACGGAATCACCCCTTCAATTCTTGT 3012  
 QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db GAACGTCTCATTTTCAAGTGTCCGATGTCTATGAGAGATCAAGACCCAGATTGATCAC 3072  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db TATGTGGCATGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAGCAAAATC 3132

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QY 182 ProGlyLeu---LysArgLysAlaLeu 189
Db 3133 CCTGGAATCGCCCAAAAAAAGGCAGAA 3159

RESULT 100
ADM36167
ID ADM36167 standard; DNA; 4296 BP.
XX
AC ADM36167;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human RTN3 isoform I coding sequence, SEQ ID 50.
XX
KW Neuroprotective; Myotropic; neuromuscular disease; RTN3; reticulon 3;
KW amyotrophic lateral sclerosis; ALS; myopathy; human; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 124..3219
FT FT /*tag= a
FT ET /product= "RTN3 isoform I"
XX
PN WO2004001069-A2.
XX
PD 31-DEC-2003.
XX
PF 20-JUN-2003; 2003WO-FR001910.
XX
PR 25-JUN-2002; 2002FR-00007846.
XX
PA (UYPA-) UNIV PASTEUR LOUIS.
XX
PI Dupuis L, Di Scala F, De Tapia M, Larnet Y, Loeffler J;
PI Gonzales de Aguilar J, Bouillier AL, Gaidon C, Rene F;
XX
DR WPI; 2004-071743/07.
DR P-PSDB; ADM36168.
XX
PT Diagnosing, prognosing and monitoring neuromuscular disease, particularly
PT amyotrophic lateral sclerosis, comprises detecting modulation of the
PT reticulon 3 gene.
XX
PS Claim 35; SEQ ID NO 50; 116pp; French.
XX
CC The present invention relates to a method for diagnosing, or evaluating
CC progression of, a neuromuscular disease. The method comprises detecting
CC modulation of the expression of a product (i) of the RTN (reticulon)3
CC gene. Differential expression of RTN3 is a specific marker of
CC neuromuscular disease, allowing early diagnosis from readily available
CC muscle biopsies. The method is also useful for determining the efficacy
CC of treatment. The method is used to diagnose (also to evaluate
CC progression or therapy of) neuromuscular disorders, specifically
CC amyotrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies
CC specific for isoforms of RTN3 or oligonucleotides (antisense sequences or
CC small interfering RNA) that can block/reduce expression of these isoforms
CC are useful for treating neuromuscular diseases and (ii) cells that
CC express RTN3 are useful in screening for therapeutic agents. The present
CC sequence is a RTN3 DNA sequence used to illustrate the invention.
XX
SQ Sequence 4296 BP; 1290 A; 944 C; 895 G; 1167 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5,75e-64 Length: 4296
Score: 621.50 Matches: 113
Percent Similarity: 80.95% Conservative: 40
Best Local Similarity: 59.79% Mismatches: 35
Query Match: 67.19% Indels: 1
DB: 12 Gaps: 1

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US-09-830-972-2\_COPY\_975\_1163 (1-189) x ADM36167 (1-4296)

Search completed: June 19, 2005, 07:20:15  
Job time : 417 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 18, 2005, 20:51:35 ; Search time 125.5 Seconds  
(without alignments)

2464.194 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163

Perfect score: 925

Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRRAD 189

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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	904	97.7	799	2	US-08-700-607-2
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5	679	73.4	2069	4	US-09-949-016-3309
6	679	73.4	3202	4	US-09-949-016-1127
7	625.5	67.6	2262	4	US-09-949-016-2988
8	622.5	67.3	1766	3	US-09-149-476-254
9	622.5	67.3	2664	3	US-09-149-476-255
10	541	58.5	3517	4	US-09-799-451-111
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17	341	36.9	42075	4	US-09-949-016-14995	Sequence 14995, A
18	286	30.9	443	4	US-09-513-999C-3784	Sequence 3784, Ap
19	282.5	30.5	135667	4	US-09-949-016-15051	Sequence 15051, A
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25	248	26.8	15661	4	US-09-949-016-13161	Sequence 13161, A
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c 27	146	15.8	601	4	US-09-949-016-40170	Sequence 40170, A
c 28	146	15.8	601	4	US-09-949-016-119336	Sequence 119336,
29	142	15.4	1125	4	US-09-248-796A-1905	Sequence 1905, Ap
c 30	114	12.3	601	4	US-09-949-016-117609	Sequence 117609,
31	109	11.8	266	4	US-09-313-294A-703	Sequence 703, App
c 32	102	11.0	601	4	US-09-949-016-48087	Sequence 48087, A
33	100	10.8	425	3	US-08-905-223-178	Sequence 178, App
34	95	10.3	1828	3	US-08-487-596-7	Sequence 7, Appli
35	95	10.3	1828	4	US-08-660-451A-7	Sequence 7, Appli
c 36	94	10.2	1273	4	US-09-949-016-5725	Sequence 5725, Ap
c 37	94	10.2	1722	4	US-08-956-171E-407	Sequence 407, App
c 38	94	10.2	1722	4	US-08-781-986A-407	Sequence 407, App
39	92.5	10.0	12566	3	US-08-961-527-149	Sequence 149, App
40	88.5	9.6	4550	3	US-09-462-136-1	Sequence 1, Appli
41	88.5	9.6	4661	4	US-09-949-016-4281	Sequence 4281, Ap
42	88.5	9.6	4673	4	US-09-814-915A-100	Sequence 100, App
43	86.5	9.4	296	4	US-09-313-294A-81	Sequence 81, Appl
44	86.5	9.4	1779	4	US-09-134-000C-2072	Sequence 2072, Ap
45	86	9.3	1302	4	US-08-956-171E-322	Sequence 322, App

ALIGNMENTS

RESULT 1

US-09-484-970B-106  
; Sequence 106, Application US/09484970B  
; Patent No. 6426186  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Karen A.  
; APPLICANT: Volkmut, Wayne  
; TITLE OF INVENTION: BONE REMODELING GENES  
; FILE REFERENCE: PB-0014 US  
; CURRENT APPLICATION NUMBER: US/09/484,970B  
; CURRENT FILING DATE: 2000-01-18  
; NUMBER OF SEQ ID NOS: 172  
; SOFTWARE: PERL Program  
; SEQ ID NO 106  
; LENGTH: 4822  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 6426186 444857.15CB1  
; NAME/KEY: unsure  
; LOCATION: 33, 51, 79, 211, 369, 483-484, 731, 748, 4803, 4805-4806, 4808-4809,  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-484-970B-106

Alignment Scores:  
Pred. No.: 3.32e-116 Length: 4822  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 3 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-484-970B-106 (1-4822)

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QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
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|
|
Db 3265 TCAGTTGTTGACCTCTGCTACTGCGAGACATTAAGAACACTGGAGTGGTGTGGTGC 3324
|
|
|
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
|
|
|
Db 3325 AGCCTATTCTGCTGCTTTCATGACAGATTACAGATTGTGAGCGTAACACGCTACATT 3384
|
|
|
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
|
|
|
Db 3385 GCCTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGCTGTGATCCAAGCT 3444
|
|
|
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
|
|
|
Db 3445 ATCCAGAAATCAGATGAAGCCACCCATTTCAGGCGCATATCTGGAATCTGAAGTTGCTATA 3504
|
|
|
QY 81 SerGluGluLeuValGlnLysValSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
|
|
|
Db 3505 TCTGAGGAGTTGGTTTCTGAGAGTACAGTAATTTCTGCTTTGGTCATGTGAAGTGCAGATA 3564
|
|
|
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
|
|
|
Db 3565 AAGGAATCAGGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTGGAAGTTTGCAGTG 3624
|
|
|
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
|
|
|
Db 3625 TTGATGTGGGTATTTACCTATGTTGGTGCCTTTGTTTAATGGTCTGCACACTACTGATTTTG 3684
|
|
|
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
|
|
|
Db 3685 GCTCTCATTTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 3744
|
|
|
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
|
|
|
Db 3745 CATTATCTAGGACTTGCAATAAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAA 3804
|
|
|
QY 181 IleProGlyLeuLysArgLysAlaAsp 189
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|
Db 3805 ATCCCTGGATTGAAGCGCAAGCTGAA 3831

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## RESULT 2

```

US-08-700-607-2
; Sequence 2, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166

```

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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 799 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
; US-08-700-607-2

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Alignment Scores:
Pred. No.: 6.66e-117 Length: 799
Score: 504.00 Matches: 183
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.73% Indels: 0
Db: 2 Gaps: 0

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US-09-830-972-2_COPY_975_1163 (1-189) x US-08-700-607-2 (1-799)

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QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
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|
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Db 108 GTTGTGTGACCTCTGCTACTGCGAGACATTAAGAACACTGGAGTGGTGTGGTGC 167
|
|
|
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
|
|
|
Db 168 CTATTCTCTGCTCTTTCATTGACAGTATTACAGCAATGTGAGCGTAACAGCCTACATTGCC 227
|
|
|
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
|
|
|
Db 228 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTTGATCCAAGCTATC 287
|
|
|
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
|
|
|
Db 288 CAGAAATCAGATGAAGGCCACCCATTTCAGGCGCATATCTGGAATCTGAAGTTGCTATATCT 347
|
|
|
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
|
|
|
Db 348 GAGGAGTTGGTTTCTGAGAGTACAGTAATTTCTGCTTTGGTTCATGTGAACTGCACGATAAAG 407
|
|
|
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
|
|
|
Db 408 GAACTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTCAGTGTG 467
|
|
|
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
|
|
|
Db 468 ATGTGGGTATTTACCTATGTTGGTGCCTTGTATTATGGTCTGACACTACTGATTTTGGCT 527
|
|
|
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
|
|
|
Db 528 CTCAATTCACCTCTTCAGTGTCTCTGTTATTTATGAACGCGCATCAGGCACAGATAGATCAT 587
|
|
|
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaValIle 181
|
|
|
Db 588 TATCTAGGACTTGCAATAAAGATGTTAAAGATGCTATGGCTAAATATCCAGCAAAATATC 647
|
|
|
QY 182 ProGlyLeuLysArgLysAlaAsp 189
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|
|
Db 648 CTGGATTGAAGCGCAAGCTGAA 671

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## RESULT 3

```

US-09-949-016-3253
; Sequence 3253, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14

```

;; PRIOR APPLICATION NUMBER: 60/241,755  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/237,768  
;; PRIOR FILING DATE: 2000-10-03  
;; PRIOR APPLICATION NUMBER: 60/231,498  
;; PRIOR FILING DATE: 2000-09-08  
;; NUMBER OF SEQ ID NOS: 207012  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 3253  
;; LENGTH: 1669  
;; TYPE: DNA  
;; ORGANISM: Human  
US-09-949-016-3253

Alignment Scores:  
Pred. No.: 2,18e-116 Length: 1669  
Score: 504.00 Matches: 183  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-949-016-3253 (1-1669)

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Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db GTGTGTGACCTCTGCTACTGGAGACATTAAGAAGACTGGAGTGGTGTGGTCCAGC 307
Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 308 CTATTCTCTGCTCTTTCATTCAGCATTTAGCATTTGTGAGCGTAACAGCCTACATTGCC 367
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 368 TTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAGGGGTGATCCAGCTATC 427
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 428 CAGAAATCAGATGAGGCCACCCATTCAGGCGCATATCTGGAATCTGGAAGTTGCTATATCT 487
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 488 GAGGAGTTGGTTTCAGAGTACAGTAATTTCTGCTCTTGGTTCATGTGAACTGCACGATAAG 547
Qy 102 GluLeuArgArgLeuPheLeuValAspPheLeuValAspSerLeuLysPheAlaValLeu 121
Db 548 GAACTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTGCAGTGTG 607
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 608 ATGTGGGTATTTACTATGTTGGTGCCTTGTATTAATGCTGTGACACTACTGATTTGGCT 667
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 668 CTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATGATCAT 727
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaIle 181
Db 728 TATCTAGACTTGCATAATTAAGATGTTAAAGATGCTATGGTAAATCCAAAGCAAAATC 787
Qy 182 ProGlyLeuLysArgLysAlaAsp 189
Db 788 CTGTGATGAAGCGCAAGCTGAA 811
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## RESULT 4

US-09-023-655-382  
; Sequence 382, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

;; TITLE OF INVENTION: EXPRESSION  
;; NUMBER OF SEQUENCES: 1508  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
;; STREET: 3174 PORTER DRIVE  
;; CITY: PALO ALTO  
;; STATE: CALIFORNIA  
;; COUNTRY: USA  
;; ZIP: 94304  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/023,655  
;; FILING DATE: HEREWITH  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; CLASSIFICATION:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Zeller, Karen J.  
;; REGISTRATION NUMBER: 37,071  
;; REFERENCE/DOCKET NUMBER: PA-0001 US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (650) 855-0555  
;; TELEFAX: (650) 845-4166  
;; INFORMATION FOR SEQ ID NO: 382:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 2610 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; IMMEDIATE SOURCE:  
;; LIBRARY: LUNGN0T14  
;; CLONE: 1508778  
US-09-023-655-382

Alignment Scores:  
Pred. No.: 3e-114 Length: 2610  
Score: 891.00 Matches: 183  
Percent Similarity: 98.41% Conservative: 3  
Best Local Similarity: 96.83% Mismatches: 2  
Query Match: 96.32% Indels: 1  
DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-023-655-382 (1-2610)

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Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 1311 GTTGTTCACCTCTGCTACTGGAGACATTAAGAAGACTGGAGTGGTGTGGTCCAGC 1370
Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr-IleAl 41
Db 1371 CTATTCCTGCTGCTTTTCATTCAGCATTTAGCATTTGAGCGTAACAGCCTACAAATGC 1430
Qy 41 aLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 1431 CTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTAT 1490
Qy 61 eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 81
Db 1491 CCAGAAATCAGATGAAGGCCACCCATTCAGGCCATATCTGGAATCTGAAGTTGCTATATC 1550
Qy 81 rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 1551 TGAGGAGTTGGTTCAGAGTACAGTAATTCCTGCTCTTGGTTCATGTGAACTGCACGATAA 1610
Qy 101 sGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLe 121
Db 1611 GGAACCTCAGGCGCCTCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGT 1670
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QY      121  uMetTrrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAl 141
Db      1671  GATGTGGGTATTAACTATATGTGGTGCTTGTATTAAUGTCTGACACTACTGATTTTGGC 1730

QY      141  aLeuLseLeuPheSerLleProValIleTyrGluArgHisGlnValGlnIleAspHi 161
Db      1731  TCTCATTTCACTCTTCAGTGTCTCTGTATTATTAAGACGGCATCAGGCACAGATAGATCA 1790

QY      161  sTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIl 181
Db      1791  TTATCTAGGACTTGCAATAGAATGTAAAGATGCTATGGCTAAATCCAAGCAAAAT 1850

QY      181  eProGlyLeuLysArgLysAlaAsp 189
Db      1851  CCCTGGGTTGAGCCGCAAGCTGAA 1875

RESULT 5
US-09-949-016-3309
; Sequence 3309, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3309
; LENGTH: 2069
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-3309

Alignment Scores:
Pred. No.:      1,17e-84      Length:      2069
Score:          679.00      Matches:      127
Percent Similarity: 84.49%      Conservative: 31
Best Local Similarity: 67.91%      Mismatches: 29
Query Match:      73.41%      Indels:      0
DB:              4          Gaps:      0

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-949-016-3309 (1-2069)

QY      3  ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22.
Db      757  ATTCACTCTGTTGTTATGGCGGACATCAAGCAGACGGGCATCGTGTGGAGTTTCCTG 816

QY      23  PheLeuLeuLeuSerLeuThrValPheSerLleValSerValThrAlaTyrLleAlaLeu 42
Db      817  CTGTGCTCTTCTCCCTGACCCAGTTCAGCGTGTGGTGGCGTGTGGCTTACCTGGCCCTG 876

QY      43  AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62
Db      877  GCCGACTCTCAGCCACCATCAGTTTCCGCATCTCAAGTCTGTTTTACAGCAGTGCAG 936

QY      63  LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
Db      937  AAAACCGAGGAAGGCCACCTTTCAAGCCCTACTTTGGAGCTTGAGATCACCTTTCTCAG 996

QY      83  GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102
Db      997  GAGCAGATTTCAGAGTAGTACACGGACTGCTGCTGAGTTCTACGTGAACAGCACACTTAAAGAA 1056

QY      103  LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet 122

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Db      1057 CTGAGGAGGCTTCCCTGTTCACGAGCCTGGTGATTCCTAAATAATTGCAGTCCCTCATG 1116
Qy      123 TtpValPheThrTyrrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu 142
Db      1117 TGGCTCTGACCTACCGTTGGCGCTCTCTCAATGGCGCTGACCCTGCTGCCTCATGGCTGTG 1176
Qy      143 IleSerLeuPheSerIleProValIleTyrrGluArgHisGlnValGlnIleAspHisIleTy 162
Db      1177 GTTTCATGTTACTCTACCTGTAGTGTATGTTAAGCACCCAGGCACAGATTGACCAATAT 1236
Qy      163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlalysIleGlnAlaLysIlePro 182
Db      1237 CTGGGACTTGTGAGGACTCACATAAATGCTGTGTGGCAAAGATTCAAGGCTAAAATCCCCA 1296
Qy      183 GlyLeuLysArgLysAlaAsp 189
Db      1297 GGCCTAAGAGCGCAGCTGAG 1317

RESULT 6
US-09-949-016-1127
; Sequence 1127, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1127
; LENGTH: 3202
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1127

Alignment Scores:
Pred. No.:          2,37e-84          Length:          3202
Score:              679.00           Matches:          127
Percent Similarity: 84.49%           Conservative:     31
Best Local Similarity: 67.91%        Mismatches:      29
Query Match:       73.41%            Indels:           0
DB:                4                 Gaps:             0

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-949-016-1127 (1-3202)
Qy      3 ValAspLeuLeuTyrrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22
Db      1990 ATTGACCTGTGTATTCGGCGGACATCAAGCAGACGGGCATCGTGTGTTGGAGTTTCCTG 1949
Qy      23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrrIleAlaLeu 42
Db      1950 CTGCTGTCTTCTCCCTGACCCAGTTCAGCGTGGTGAGCGTCTGCTGGCTACCTGGGCCCTG 2009
Qy      43 AlaLeuLeuSerValThrIleSerPheArgIleTyrrLysGlyValIleGlnAlaIleGln 62
Db      2010 GCCGCATCTTCAGCCACCATCAGTTTCGGCATCTACAAGTCTGTTTACAGCAGTGCAG 2069
Qy      63 LysSerAspGluGlyHisProPheArgAlaTyrrLeuGluSerGluValAlaIleSerGlu 82
Db      2070 AAAACCCAGNAGGCCACCCCTTTCAGGCCCTACTTGGAGCTTGAGATCACCCCTTTCAG 2129
Qy      83 GluLeuValGlnLysTyrrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102
Db      2130 GAGCAGATTACAGAAGTACACGGATCGCTCGACGTTCTACCGTAGAACGACACACTTAAGGAA 2189

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QY 103 LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
DB 2190 CTGAGGAGCTCTCTCTGTCAGGACCTGCTGGATTCCTAAATTTGCAGTCTGATG 2249  
QY 123 TrpValPheThrTyValGlyAlaLeuPheLeuGlyLeuThrLeuLeuAlaLeu 142  
DB 2250 TGGCTCCTGACCTACGTTGGGCTCTCTCAATGGCCTGACCTGCTCATGGCTGTG 2309  
QY 143 IleSerLeuPheSerIleProValIleTyGluArgHisGlnValGlnIleAspHisTy 162  
DB 2310 GTTTCATGTTTACTCTACCTGTAGTGTATGTAAGCACCGACGACATGACCAATAT 2369  
QY 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
DB 2370 CTGGGACTTGTGAGGACTCACATAATGCTGTGTGGCAAGATTCAGGCTAAATCCCA 2429  
QY 183 GlyLeuLysArgLysAlaAsp 189  
DB 2430 GCGCGTAAGAGGACGCTGAG 2450  
RESULT 7  
US-09-949-016-2988  
; Sequence 2988, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 2988  
; LENGTH: 2262  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-2988  
Alignment Scores:  
Pred. No.: 4,36e-77 Length: 2262  
Score: 625.50 Matches: 114  
Percent Similarity: 81.0% Conservative: 40  
Best Local Similarity: 60.0% Mismatches: 35  
Query Match: 67.6% Indels: 1  
DB: 4 Gaps: 1  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-949-016-2988 (1-2262)  
QY 1 SerValValAspLeuLeuTyTrpArgAspIleLysValThrGlyValPheGlyAla 20  
DB 7 TCAGTGCAGATCTGATTTCTGGAGAGATGGAAGAGACTGGGTTGTTCTTTGGCACC 66  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyIle 40  
DB 67 ACGCTGATCATGCTCTTCCCTGGCAGCTTTCAGTGTTCATCAGTGTGTTCTTACCTC 126  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyLysGlyValIleGlnAla 60  
DB 127 ATCTGGCTCTCTCTGTCCACCATCAGCTTCAGGATCTACAGTCCGTCATCCAGCT 186  
QY 61 IleGlnLysSerAspGlyHisProPheArgAlaTyLeuLeuGluSerGluValAlaIle 80  
DB 187 GTACAGAAGTCAGAAGAGGCCATCCATTCAAAGCTTACCTGGACGTAGACATTAATCTG 246  
QY 81 SerGluGluLeuValGlnLysTySerAsnSerAlaLeuGlyHisValAsnSerThrIle 100

DB 247 TCCTCAGAAGCTTTCATATAATTCATGAATGCTGCCATGTCATCAACAGGCGCCCTG 306  
QY 101 LysGluLeuArgGlyLeuPheLeuValAspPheLeuValAspSerLeuLysPheAlaVal 120  
DB 307 AAATCATTATTTCGTCTCTTTCTGGTAGAAGATCTGGTTGACTCTCTTGAAGCTGGCTGT 366  
QY 121 LeuMetTrpValPheThrTyValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
DB 367 TTCAATGGCTGATGACCTATGTTGGTCTGTTTAAACGGAATCACCTTCTAATCTT 426  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyGluArgHisGlnValGlnIleAsp 160  
DB 427 GCTCAACTGCTCAATTTTCAGTGTCCGATTCCTATGAGAAGTACAGACCCAGATTCAT 486  
QY 161 HisTyLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
DB 487 CACTATGTTGGCATCGCCCGAGATCAGACCAAGTCATTTGTAAGATCCACAGCAAA 546  
QY 181 IleProGlyLeu--LysArgLysAlaAsp 189  
DB 547 CTCCTGGAATCGCCAAAAAAGGCAGAA 576  
RESULT 8  
US-09-149-476-254  
; Sequence 254, Application US/09149476  
; Patent No. 6420526  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P1  
; CURRENT APPLICATION NUMBER: US/09/149,476  
; CURRENT FILING DATE: 1998-09-08  
; EARLIER APPLICATION NUMBER: PCT/US98/04493  
; EARLIER FILING DATE: 1998-03-06  
; EARLIER APPLICATION NUMBER: 60/040,162  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,333  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/038,621  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,626  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,334  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,336  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,163  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/047,600  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,615  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,597  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,502  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,633  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,583  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,617  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,618  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,503  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,592  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,581  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,584  
; EARLIER FILING DATE: 1997-05-23

[illegible]

EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

## Alignment Scores:

Pred. No.: 7,72e-77 Length: 1766  
Score: 622.50 Matches: 113  
Percent Similarity: 81.0% Conservative: 41  
Best Local Similarity: 59.4% Mismatches: 35  
Query Match: 67.30% Indels: 1  
DB: 3 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-149-476-254 (1-1766)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
DB 287 GCGGTGCAGATCTGATTTCTGGAGAGATGTGAAGAGACTGGGTTGTCTTTGGCACC 346  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 347 AGCGTGATCATGCTGCTTCCCTGGCAGCTTTTCAGTGTTCATCAGTGTGTTTCTTACCTC 406  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
DB 407 ATCTGGCTCTCTCTCTGCACCATCAGCTTCAGAGTCACTAAGTCGTCATCCAGCT 466  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
DB 467 GTACAGAAGTCAGAAGAGGCCCATTCATCAAGGCTTACCTGAGCTAGACATTACTCTG 526  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
DB 527 TCTTCAGAAGCTTTCATTAATACATGATGCTGCTGTCATCAACAGGCCCTG 586  
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
DB 587 AAATCATATTATTCGCTCTCTCTGAGAGATCTGGTGTACTCTTGAAGCTGCTGTC 646  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
DB 647 TTCATGTGCTGATGACCTATGTTGGTGTGTTTAAACGGAATCACCTTCTAATCTT 706  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
DB 707 GCTGAAGTCTCATTTTCAGTGTCCCGATTGTCTATGAGAGTCAACAGCCAGATTGAT 766  
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
DB 767 CACTATGTGGATGCCCGAGATCAGACCAGTCAATTGTTGAAGAAGATCCAGCAAA 826  
QY 181 IleProGlyLeu--LysArgLysAlaAsp 189  
DB 827 CTCCTCGAATGCCCAAAAAAGGCAGAA 856

## RESULT 9

US-09-149-476-255  
Sequence 255, Application US/09149476  
Patent No. 6420526  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: PZ002PI  
CURRENT APPLICATION NUMBER: US/09/149,476  
CURRENT FILING DATE: 1998-09-08  
EARLIER APPLICATION NUMBER: PCT/US98/04493  
EARLIER FILING DATE: 1998-03-06  
EARLIER APPLICATION NUMBER: 60/040,162  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,333  
EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/038,621  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,626  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,334  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,336  
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EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/047,600  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,615  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,597  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,502  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,633  
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EARLIER APPLICATION NUMBER: 60/047,617  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,618  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,503  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,592  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,581  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,584  
EARLIER FILING DATE: 1997-05-23  
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EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,587  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,492  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,598  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,613  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,582  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,596  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,612  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,632  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,601  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,580  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,568  
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EARLIER APPLICATION NUMBER: 60/043,314  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,569  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,311  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,671  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,674  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,669  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,312  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,313

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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
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; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
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; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
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; EARLIER APPLICATION NUMBER: 60/056,872
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; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02
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## Alignment Scores:

Pred. No.:	1,5e-76	Length:	2664
Score:	622.50	Matches:	113
Percent Similarity:	81.05%	Conservative:	41
Best Local Similarity:	59.47%	Mismatches:	35
Query Match:	67.30%	Indels:	1
DB:	3	Gaps:	1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-149-476-255 (1-2664)

Qy	1	SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla	20
Db	262	GGGTGACGATCTGATTTCTGGAGAGATGTGAAGAGACTGGGTTCTCTTTGGCACC	321
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	322	ACGCTGATCATGCTGCTTTCCCTGGCAGCTTTTCAGTGTCTCAGTGTGTTTCTTACCTC	381
Qy	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
Db	382	ATCCTGGCTCTTCTCTGTCCACCATCAGTTCCAGATCTACAGTCCGCTCATCCAGCT	441
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
Db	442	GTACAGAGTCAAGAGAGGCCATCCATTCAAAGCTACCTGACGACGTAGACATTACTCTG	501
Qy	81	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle	100
Db	502	TCCTCAGAGCTTTCATTAATTACATGAATGTGCATGTGTCATCAACAGGCGCCCTG	561
Qy	101	LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal	120





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; LENGTH: 1095 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: THPINOB01
; CLONE: 31870
US-08-700-607-4

Alignment Scores:
Pred. No.: 2,036-63 Length: 1095
Score: 524.50 Matches: 102
Percent Similarity: 72.77% Conservative: 37
Best Local Similarity: 53.40% Mismatches: 30
Query Match: 56.70% Indels: 22
DB: 2 Gaps: 2

US-09-830-972-2_COPY_975_1163 (1-189) x US-08-700-607-4 (1-1095)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
   ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 329 GCGGTGCAGATCTGATTTTGGAGAGATGTGAAGACTGGGTTGCTTTGGCACC 388
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
   ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 389 ACGCTGATCATGCTGCTTCCCTGGCAGCTTTTCAGTGTCTCAGTGTGGTCTTACCTC 448
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
   ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 449 ATCTGGCTCTCTCTCTGTCACCATCAGCTTCAGATCTACAGTCCGCTCATCCAGCT 508
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
   ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 509 GTACAGAAGTCAGAAAGGCCATCCATTCAAAGCTTACCTGGACGTACAGCTTACTCTG 568
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
   ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 569 TCTCAGAAAGCTTCCATTAATTACATGAATGTGCGCATCAACAGGCGCCCTG 628
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
   ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 629 AAATCATTAATTCGCTCTCTCTGAGAGATCTGTTGACTCTCTGAAGCTGGCTGTC 688
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
   ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 689 TTCATGTGCTGATGACCTATGTTGTGCTGTTTAAACGGAATCACCCTTCTAATTCCT 748
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
   ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 749 GCTGAACCTGCTCATTTTNAAGTGTCCCGATTGTTNATNAGAAGTAC----- 793
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
   ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 794 -----AAGTTCCAGCAAA 808

QY 180 sIleProGlyLeu---LysArgLysAlaAsp 189
   ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 809 ACTCCCTGGAATCGCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 839

RESULT 12
US-09-270-767-13561
; Sequence 13561, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13561

; LENGTH: 2014
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13561

Alignment Scores:
Pred. No.: 4,436-62 Length: 2014
Score: 518.00 Matches: 93
Percent Similarity: 75.28% Conservative: 41
Best Local Similarity: 52.25% Mismatches: 44
Query Match: 56.00% Indels: 0
DB: 4 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-270-767-13561 (1-2014)
QY 5 LeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPheLeu 24
   ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 164 CTTATCTACTGGCGGATGTGAAGAAATCCGGCATTTGCTTCGGCGCTGGCTGATCACA 223
QY 25 LeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu 44
   ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 224 CTGGCGGCATCTCCAGCTTCTCGGTGATCAGCGTGTTCGCTACTTGTGCTCTCAACC 283
QY 45 LeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSer 64
   ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 284 CTCCTCGGCACCGTCGCTTCAGAAATCTACAAATCTGTGACACACGCGCTGCNAAAGACA 343
QY 65 AspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeu 84
   ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 344 AACGAGGCTCACCCCTTTAAGGATTACCTGGAGCTGGATCTGACGCTGTGCACGAAAG 403
QY 85 ValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArg 104
   ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 404 GTACAGAAACATTTGCCGGCTGCTGTGCACATATCAATGGCTTCATCTCCGAGCTGAGG 463
QY 105 ArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrpVal 124
   ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 464 CCTCTGTTCTTGTGTGAGATATCATCGATTTCGATTCGATTCGCGGTCTATCTGTGGTTC 523
QY 125 PheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuLeuLeuLeuLeu 144
   ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 524 TTCACCTACGTTGGTGGCTGGTTCAATGGCATGACTCTGGTTCATCTTGGCCCTTTGTCTCG 583
QY 145 LeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGly 164
   ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 584 CTGTTTACCTTGGCCCAAGCTCTACGAGAACACAAAGCAATCGATCGACACTCACTTGGAT 643
QY 165 LeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
   ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 644 CTGGTGGCAGCAAAATTGACAGAAATCACCAGCAAGATCCGAGTGGCCATCCCC 697

RESULT 13
US-09-149-476-102
; Sequence 102, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
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[illegible]

EARLIER APPLICATION NUMBER: 60/047,501  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,670  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/056,632  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,664  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,876  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,881  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,909  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,875  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,862  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Alignment Scores:  
Pred. No.: 1,546-61  
Score: 509.50  
Percent Similarity: 76.37%  
Best Local Similarity: 55.49%  
Query Match: 55.08%  
DB: 3  
Indels: 3  
Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-149-476-102 (1-794)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 254 GCGGTGCAGCATCTGATTTCTGGAGAGATGTGAAGAGACTGGGTTTGTCTTTGGAC-- 311  
QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerVal-ThrAlaTyrIle 40  
Db 312 ACCTGATCATGCTGCTTTCCCTGGCAGCTTTTCAGTGTTCATCATGTGGGTTTCTTAMCT 371  
QY 40 eAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAl 60  
Db 372 CATCTCGGCTCTTCTCTGTACCATCATCTTCAGATCTACAGTCCGTATCCAGC 431  
QY 60 alleGlnLysSerAspGluGlyHisProPhe-ArgAlaTyrLeuGluSerGluValAlaI 80  
Db 432 TGTWCAAGARTCAGAAAGGCCATCCATCCAAAGCCCTACCTGGAGCTAGACATTACTC 491  
QY 80 leSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrI 100  
Db 492 TGTCTCTCAGAAAGCTTTCCCAATATACATGAATGCTGCCATGTGGTCACATCAACAGGCC 551  
QY 100 leLysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 552 TGAATCATATTCTCTCTTCTGTGTAGAAATCTGGTGTACTCTCTTGAAGCTGGCTG 611  
QY 120 allLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIle 140  
Db 612 TCTTCATGTGGCTGATGACCATATGTTGGTCTGTTTTTAACGGAATCACCCCTCTAATTC 671

QY 140 euAlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleA 160  
Db 672 TTGCTGAACCTGCTCATTTTCAGTCCCGATTGTCTATGAGAAGTACAGACCCAGATTG 731  
QY 160 spHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAla 180  
Db 732 ATCACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAGATCCCAAGCA 791  
QY 180 Ys 180  
Db 792 AA 793

## RESULT 14

US-09-949-016-1419  
Sequence 1419, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE OF INVENTION: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
PRIOR FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1419  
LENGTH: 2181  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-1419

Alignment Scores:  
Pred. No.: 5,466-56  
Score: 475.00  
Percent Similarity: 70.33%  
Best Local Similarity: 50.55%  
Query Match: 51.35%  
DB: 4  
Indels: 0  
Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-949-016-1419 (1-2181)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 1162 GTGGCGGACCTGCTGTACTGTGAAGACACGAGGACGTGAGGAGTGGTCTTCAGGCCCTG 1221  
QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 1222 ATGGTCTCCCTCTCTGCTGCTGCTAGCATCGTTCGCTGGCCGCGACTTGGCT 1281  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 1282 CTGTTGCTGCTCTGGCGGACCATCTCTCTCAGGGTTTACCGAAAGTGTCTGAGGCCGCTG 1341  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 1342 CACCGGGGGGATGGAGCCCAACCTTTCAGGCTTACCTGGATGTGGACCTCACCTGACT 1401  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
Db 1402 CGGAGACAGACGGAACGTTGTCCACCATGATCACCTCCGCGGTGCTCTCGCGGCCACG 1461  
QY 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 1462 CAGCTGCGGACATCTTCTCTGTGTAGAGACCTCTGAGATTCCTCAAGCTGGCCCTCCTC 1521  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141

```
Db 1522 TTCTACATCTTGACCTTCTGGTGGCCATCTTCAATGGTTTGACCTCTCTCATCTTGGGA 1581
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 1582 GTGATTGGTCTATTACCATCCCTCTGTGTAACCGGAGCACCAGCTCAGATCGACCA 1641
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValIleTyrGluArgHisGlnValGlnIleAspHis 181
Db 1642 TATGTGGGGTGTGGTACCAATCAGTTGAGCCACATCAAAGCTAAGATCGAGCTAAATC 1701
Qy 182 ProGly 183
Db 1702 CCAGGG 1707
RESULT 15
US-09-949-016-117588/c
; Sequence 117588, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 117588
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-117588
Alignment Scores:
Pred. No.: 4,38e-38 Length: 601
Score: 341.00 Matches: 70
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 36.86% Indels: 0
DB: 4 Gaps: 0
US-09-830-972-2_COPY_975_1163 (1-189) x US-09-949-016-117588 (1-601)
Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 518 GTTGTGACCTCTGTACTGGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGGCCAGC 459
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 458 CTATTCCTGCTGCTTTCATTGACAGTATTGACGATTGAGCGTAACAGCCTACATTGCC 399
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 398 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 339
Qy 62 GlnLysSerAspGluGlyHisPropheArg 71
Db 338 CAGAAATCAGATGAAGGCCACCCATTCCAGG 309
RESULT 17
US-09-949-016-14995
; Sequence 14995, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14995
; LENGTH: 42075
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14995
Alignment Scores:
Pred. No.: 4.13e-35 Length: 42075
Score: 341.00 Matches: 70
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
```

```
Db 1522 TTCTACATCTTGACCTTCTGGTGGCCATCTTCAATGGTTTGACCTCTCTCATCTTGGGA 1581
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 1582 GTGATTGGTCTATTACCATCCCTCTGTGTAACCGGAGCACCAGCTCAGATCGACCA 1641
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValIleTyrGluArgHisGlnValGlnIleAspHis 181
Db 1642 TATGTGGGGTGTGGTACCAATCAGTTGAGCCACATCAAAGCTAAGATCGAGCTAAATC 1701
Qy 182 ProGly 183
Db 1702 CCAGGG 1707
RESULT 15
US-09-949-016-117588/c
; Sequence 117588, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 117588
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-117588
Alignment Scores:
Pred. No.: 4,38e-38 Length: 601
Score: 341.00 Matches: 70
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 36.86% Indels: 0
DB: 4 Gaps: 0
US-09-830-972-2_COPY_975_1163 (1-189) x US-09-949-016-117588 (1-601)
Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 224 GTTGTGACCTCTGTACTGGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGGCCAGC 165
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 164 CTATTCCTGCTGCTTTCATTGACAGTATTGACGATTGAGCGTAACAGCCTACATTGCC 105
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 104 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 45
Qy 62 GlnLysSerAspGluGlyHisPropheArg 71
Db 44 CAGAAATCAGATGAAGGCCACCCATTCCAGG 15
RESULT 16
US-09-949-016-117589/c
; Sequence 117589, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
```

```
Query Match: 36.86% Indels: 0
DB: 4 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-949-016-14995 (1-42075)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
DB 24648 GTTGTGACCTCTGTACTGGAGACATTAGAGACTGGAGTGGTGTGTTGGTCCAGC 24707
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 24708 CTATTCTGCTGCTTTCATTGACAGTATTGAGCATTTGAGCGTAACAGCCATACATTGCC 24767
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 61
DB 24768 TTGGCCCTCTCTCTGTGACCATCATGCTTTTAGGATATACAAAGGTGTGTATCAAGCTATC 24827
QY 62 GlnLysSerAspGluGlyHisProPheArg 71
DB 24828 CAGAAATCAGATGAGAGCCACCATTCAGG 24857

RESULT 18
US-09-513-999C-3784
; Sequence 3784, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 6783961
; CURRENT APPLICATION NUMBER: US/09/513,999C
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 3784
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 96..437
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 96..239
; OTHER INFORMATION: score 4.6
; OTHER INFORMATION: seq VFGSFLILLFSLT/QF
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 305
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 323
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 335
; OTHER INFORMATION: s=g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 360
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 22
; OTHER INFORMATION: Xaa=Phe or Leu
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 41
```

```
; OTHER INFORMATION: Xaa= * or Gly or Arg
US-09-513-999C-3784
```

## Alignment Scores:

```
Pred. No.: 1.4e-30 Length: 443
Score: 286.00 Matches: 59
Percent Similarity: 80.00% Conservative: 17
Best Local Similarity: 62.11% Mismatches: 19
Query Match: 30.92% Indels: 1
DB: 4 Gaps: 0
```

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-513-999C-3784 (1-443)

```
QY 3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22
DB 159 ATTGACCTGTTGTATTGGCGGACATCAAGCAGACGGCATCGTGTGTTGGGAGTTTCCCTG 218
QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
DB 219 CTGCTGCTCTCTCTCCCTGACCATTCAGCTTCAGCTGGTGAGCTGCTGCCTACTGCGCCCTG 278
QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62
DB 279 GCGGCACCTCTCAGCCACCATCAGTTTTCGTCATCTACAAGTCTGTGTTTACAGCAGTSCAG 338
QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
DB 339 ATACCCGACGAGGCCACCG-TNGAAGGCTACTTTGGAGCTTGAGATCACCTTTTCTCAG 397
QY 83 GlnLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsn 97
DB 398 GAGCAGATTACAGATACAGGACTGCTGCTGAGTTCTACGTGAC 442
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## RESULT 19

```
US-09-949-016-15051
; Sequence 15051, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15051
; LENGTH: 135667
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-15051
```

## Alignment Scores:

```
Pred. No.: 4.43e-26 Length: 135667
Score: 282.50 Matches: 73
Percent Similarity: 50.52% Conservative: 24
Best Local Similarity: 38.02% Mismatches: 51
Query Match: 30.54% Indels: 4
DB: 4 Gaps: 4
```

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-949-016-15051 (1-135667)

```
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
DB 122176 GCAGCTATTGACCTGTGTATTGGCGGACATCAAGCAGACGGCATCGTGTGTTGGAGT 122235
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
```

```
Db 122236 TTCTGCTGCTGCTCTCTCTCCCTGACCCAGTTACGGTGGTGGAGCTGCTGGCTTACCTG 122295
Qy 41 AlalaLeuLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 122296 GCCCTGGCGGCAGCTCTTCAGCCACCATCATAGTTTCGCCATCTACAAGTCTGTTTACAAGCA 122355
Qy 61 IleGlnLysSerAspGluGlyHisProPheArg----- 71
Db 122356 GTGCAGAAACCGACGAGGCCACCTTTCAAGTGAGTGCCTCAGCTGAGGAGCCCTCAC 122415
Qy 72 -----AlaTyrLeuGluSerGluValAlaIleSerGlu 82
Db 122416 CCACTGACGAGGGCTTTTACCTCCTGATTTTTCAGTCTCAGATGCATCTGAGTCAT 122475
Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThr----- 99
Db 122476 -----GTTTCTCTGAGACCCACAGACCTCTTAGAGTCTCCCTTAACACCCCTGCTTTG 122529
Qy 100 -----IleLysGluLeuArgLeuPheLeuValAspAspLeu 112
Db 122530 AATATCTAACATTTCTGCTGTAATTTCTGAAACAACACTCGATTTCTTTTCCATATCTT 122589
Qy 113 ValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPhe 132
Db 122590 ATTGCTTTGTTGAGTTTTCATATGTAT----- 122616
Qy 133 AsnGlyLeuThrLeuLeuLeuLeuLeuSerLeuPheSer-IleProValIleTy 152
Db 122617 -----TTACTATTAAACAGTAATCATATAATCAACAATTAATCTCTCAGCAATATC 122670
Qy 152 rGluArgHisGlnValGlnIleAspHisTyrLeu 163
Db 122671 AGAAGGCACAGCAGGCATTTTGTCCCTATTATA 122704
```

## RESULT 20

```
US-09-949-016-12869
; Sequence 12869, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12869
; LENGTH: 152486
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12869
```

```
Alignment Scores:
Pred. No.: 5,35e-26 Length: 152486
Score: 282.50 Matches: 73
Percent Similarity: 50.52% Conservative: 24
Best Local Similarity: 38.02% Mismatches: 51
Query Match: 30.54% Indels: 44
DB: 4 Gaps: 4
```

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-949-016-12869 (1-152486)

```
Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 90995 GCAGCTATTGACCTGTTGTTGGCGGACATCAAGCAGCGGATCGTGTGTTGGAGT 91054
```

```
Qy 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 91055 TTCTGCTGCTGCTCTCTCTCCCTGACCCAGTTACGGTGGTGGAGCTGCTGGCTTACCTG 91114
Qy 41 AlalaLeuLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 91115 GCCCTGGCGGCAGCTCTTCAGCCACCATCATAGTTTCGCCATCTACAAGTCTGTTTACAAGCA 91174
Qy 61 IleGlnLysSerAspGluGlyHisProPheArg----- 71
Db 91175 GTGCAGAAACCGACGAGGCCACCTTTCAAGTGAGTGCCTCAGCTGAGGAGCCCTCAC 91234
Qy 72 -----AlaTyrLeuGluSerGluValAlaIleSerGlu 82
Db 91235 CCACTGACGAGGGCTTTTACCTCCTGATTTTTCAGTCTCAGATGCATCTGAGTCAT 91294
Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThr----- 99
Db 91295 -----GTTTCTCTGAGACCCACAGACCTCTTAGAGTCTCCCTTAACACCCCTGCTTTG 91348
Qy 100 -----IleLysGluLeuArgLeuPheLeuValAspAspLeu 112
Db 91349 AATATCTAACATTTCTGCTGTAATTTCTGAAACAACACTCGATTTCTTTTCCATATCTT 91408
Qy 113 ValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPhe 132
Db 91409 ATTGCTTTGTTGAGTTTTCATATGTAT----- 91435
Qy 133 AsnGlyLeuThrLeuLeuLeuLeuLeuSerLeuPheSer-IleProValIleTy 152
Db 91436 -----TTACTATTAAACAGTAATCATATAATCAACAATTAATCTCTCAGCAATATC 91489
Qy 152 rGluArgHisGlnValGlnIleAspHisTyrLeu 163
Db 91490 AGAAGGCACAGCAGGCATTTTGTCCCTATTATA 91523
```

## RESULT 21

```
US-09-949-016-40169/c
; Sequence 40169, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40169
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-40169
```

```
Alignment Scores:
Pred. No.: 2.59e-29 Length: 601
Score: 278.50 Matches: 72
Percent Similarity: 50.00% Conservative: 24
Best Local Similarity: 37.50% Mismatches: 52
Query Match: 30.11% Indels: 44
DB: 4 Gaps: 4
```

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-949-016-40169 (1-601)

```
Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
```

```
Db      580 GCAGCTATTGACCTGTTGATGGCGGACATCAAGCAGCGGCATCGTTGGAGT 521
Qy      21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db      520 TTCCTGCTGCTCTCTCTCCCTGACCCAGTTCAGCGTGTGAGCGTCTGGCCTACCTG 461
Qy      41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db      460 GGCCTGGCGCACTCTCAGCCACCATCAGTTCCGCATCTACAAGTCTGTTTACAAGCA 401
Qy      61 IleGlnLysSerAspGluGlyHisProPheArg----- 71
Db      400 GTGCAGAAAACCGAAGGCCACCCCTTTCAAGTGAGTGCCTCAGCTGAGGAGCCCTCAC 341
Qy      72 -----AlaTyrLeuGluSerGluValAlaIleSerGlu 82
Db      340 CCACTGACAGGGGCTTTTACCTCACCTGATTTTCAGCYCACAGATGCACTTGATCAT 281
Qy      83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThr----- 99
Db      280 -----GTTTCTCTGAGACCCCAACAGACCTCTTAGAGTCTCCCTAACACCTGTCTTTG 227
Qy      100 -----IleLysGluLeuArgLeuPheLeuValAspLeu 112
Db      226 AATATCTAACATTCTGTGTGAATTTCTGAAACAAACTCGATTATTCTTATCCAAATATT 167
Qy      113 ValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPhe 132
Db      166 ATTGCTTTGAGTTTCATATGAT----- 140
Qy      133 AsnGlyLeuThrLeuLeuIleAlaLeuLeuSerLeuPheSer-IleProValIleTyr 152
Db      139 -----TTACTATTACAGTAATATAATCCAACTTACTTAATCTCTCAGCAATATC 86
Qy      152 rGluArgHisGlnValGlnIleAspHisTyrLeu 163
Db      85 AGAAAGGCACAGCAGGCACTTTTGTCCCTATTATTA 52
```

## RESULT 22

```
US-09-949-016-119335/c
; Sequence 119335, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119335
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-119335
```

```
Alignment Scores:
Pred. No.: 2,59e-29 Length: 601
Score: 278.50 Matches: 72
Percent Similarity: 50.00% Conservative: 24
Best Local Similarity: 37.50% Mismatches: 52
Query Match: 30.11% Indels: 4
DB: 4 Gaps: 4
```

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-949-016-119335 (1-601)

```
Qy      1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
Db      580 GCAGCTATTGACCTGTTGATGGCGGACATCAAGCAGCGGCATCGTTGGAGT 521
Qy      21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db      520 TTCCTGCTGCTCTCTCTCCCTGACCCAGTTCAGCGTGTGAGCGTCTGGCCTACCTG 461
Qy      41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db      460 GGCCTGGCGCACTCTCAGCCACCATCAGTTCCGCATCTACAAGTCTGTTTACAAGCA 401
Qy      61 IleGlnLysSerAspGluGlyHisProPheArg----- 71
Db      400 GTGCAGAAAACCGAAGGCCACCCCTTTCAAGTGAGTGCCTCAGCTGAGGAGCCCTCAC 341
Qy      72 -----AlaTyrLeuGluSerGluValAlaIleSerGlu 82
Db      340 CCACTGACAGGGGCTTTTACCTCACCTGATTTTCAGCYCACAGATGCACTTGATCAT 281
Qy      83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThr----- 99
Db      280 -----GTTTCTCTGAGACCCCAACAGACCTCTTAGAGTCTCCCTAACACCTGTCTTTG 227
Qy      100 -----IleLysGluLeuArgLeuPheLeuValAspLeu 112
Db      226 AATATCTAACATTCTGTGTGAATTTCTGAAACAAACTCGATTATTCTTATCCAAATATT 167
Qy      113 ValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPhe 132
Db      166 ATTGCTTTGAGTTTCATATGAT----- 140
Qy      133 AsnGlyLeuThrLeuLeuIleAlaLeuLeuSerLeuPheSer-IleProValIleTyr 152
Db      139 -----TTACTATTACAGTAATATAATCCAACTTACTTAATCTCTCAGCAATATC 86
Qy      152 rGluArgHisGlnValGlnIleAspHisTyrLeu 163
Db      85 AGAAAGGCACAGCAGGCACTTTTGTCCCTATTATTA 52

RESULT 23
US-08-700-607-9
; Sequence 9, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
```



TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 261 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; IMMEDIATE SOURCE:

; LIBRARY: SPLNET01

; CLONE: 28742

US-08-700-607-9

## Alignment Scores:

Pred. No.:	1,51e-29	Length:	261
Score:	276.00	Matches:	59
Percent Similarity:	89.71%	Conservative:	2
Best Local Similarity:	86.76%	Mismatches:	7
Query Match:	29.84%	Indels:	0
DB:	2	Gaps:	0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-08-700-607-9 (1-261)

Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

Db 2 CTATNCCNGCTGCTTTCATTGACAGTATTCAGCATTTGAGCGTAACAGCCTACATTGCC 61

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

Db 62 TTNGCCCTGCGNCTCTGTGACCATCAGCTNTAGGCTATACAAAGGGGTGATCCAGCTATC 121

Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81

Db 122 CAGAAATCAGATGAGGNCACCCATTCAGGCGATATCTGGANTCTGAAGTTGCTATATCT 181

Qy 82 GluGluLeuValGlnLysTyrSer 89

Db 182 GAGGAGTTGNTTCAGAGTACACG 205

RESULT 24

US-09-949-016-14730

; Sequence 14730, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR FILING DATE: 2000-04-14

; PRIOR FILING DATE: 2000-10-20

; PRIOR FILING DATE: 2000-10-20

; PRIOR FILING DATE: 2000-10-03

; PRIOR FILING DATE: 2000-10-03

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14730

; LENGTH: 13906

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-14730

## Alignment Scores:

Pred. No.:	4.63e-26	Length:	13906
Score:	271.00	Matches:	50
Percent Similarity:	87.32%	Conservative:	12
Best Local Similarity:	70.42%	Mismatches:	9
Query Match:	29.30%	Indels:	0
DB:	4	Gaps:	0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-949-016-14730 (1-13906)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20

Db 2007 TCAGTGCACGATCTGATTTCTGGAGATGTGAGAGAGACTGGGTGTCTTTGGCACC 2066

Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40

Db 2067 ACGTGTATCATGCTGCTTTCCCTGCGAGCTTTCAGTGTTCATCAGTGTGTTCTTACCTC 2126

Qy 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60

Db 2127 ATCCTGGCTCTCTCTGTGACCATCAGCTTCAGGATCTCAAGTCCGTCATCCAGCT 2186

Qy 61 IleGlnLysSerAspGluGlyHisProPheArg 71

Db 2187 GTACAGAGTCAGAGAGAGGCGCATCCATTCAG 2219

RESULT 25

US-09-949-016-13161

; Sequence 13161, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR FILING DATE: 2000-04-14

; PRIOR FILING DATE: 2000-10-20

; PRIOR FILING DATE: 2000-10-20

; PRIOR FILING DATE: 2000-10-03

; PRIOR FILING DATE: 2000-10-03

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13161

; LENGTH: 15661

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-13161

Alignment Scores:

Pred. No.:	9.48e-23	Length:	15661
Score:	248.00	Matches:	86
Percent Similarity:	30.69%	Conservative:	34
Best Local Similarity:	21.99%	Mismatches:	53
Query Match:	26.81%	Indels:	220
DB:	4	Gaps:	4

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-949-016-13161 (1-15661)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20

Db 9398 ACAGTGGCGGACCTGCTGTACTGGAAGACACGAGGAGCTCAGGAGTGTCTTCACAGGC 9457

Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40

Db 9458 CTGATGGTCTCCCTCTGCTCTGCTGCTTATGACATTCGTCGTCGCGCGGCACTTG 9517

Qy 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60

Db 9518 GCTCTGTTGCTGCTCTGCGGACCATCTCTCTCAGGGTTTACCGCAAGTGTCTGACGCC 9577

Qy 61 IleGlnLysSerAspGluGlyHisProPhe 70

Db 9578 GTGCACCGGGGGATGG-AGCCAAACCTTTCCAGTGAGAACCCCGGCCCTGACCTGAG 9636

Qy 70 ----- 70

Db 9637 CCCCTGTCTGACCCCTAAAGCATGACCCACGACTCAATCAGGACCGGACTCCACCCG 9696

Qy 70 ----- 70

```
Db 9697 GACCCGACTCATCTTGATCATTTTTCATCCGATCCCTAACCTACCCCTTCAATCCTAA 9756
Qy 70 ----- 70
Db 9757 TCTCTGATCCTAACTGGTACCTTTCATCTCGATCCCTTCCCTGACCTGACCTGAC 9816
Qy 70 ----- 70
Db 9817 CCCAGCCCTTACATGTGATTCCTCTGAGCTGCCCTCAGTCTAACTCTGTCTTCTCC 9876
Qy 70 ----- 70
Db 9877 CACCCGCAATTCCTCTCCCTTGTTCAGCTGCCCTGCACCACTGTGACCTGGTCAACCA 9936
Qy 71 ----- 80
Db 9937 CTGAGTCGCCACACACTCTTTGTCCCGCAGGGCTACCTGGATGTGGACCTCACCCCTG 9996
Qy 81 SerGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 9997 ACTCGGAGCAGACGGAACGTTGTCTCCACCAAGATCACCTCCCGCGTGGTCTCGGGGCC 10056
Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLys----- 117
Db 10057 ACGAGCTCGGCACCTTCTCTCTGTGTAGAAGACCTCGTGATTCCTCAAGGTGGCTGG 10116
Qy 117 ----- 117
Db 10117 AGCTCTCAGCCCTCCTCGGTTCCCCCAATTCACCTCTGCATGGCTAGGGGGTGGAGGCG 10176
Qy 117 ----- 117
Db 10177 GACTGTGGTAAATTCACAGATGAGAGGAATTCCTCGGTGGCTCTCTGACCCCTGAC 10236
Qy 118 -----PheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsn 133
Db 10237 CTTACCCCCAGTGGCCCTCTCTCTACATCTTGACCTTCTGGGTGCCATCTTCAT 10296
Qy 134 GlyLeuThrLeuLeuLeuAla----- 141
Db 10297 GGTGTGACTCTTCTCATTCTGGG-TGAGCTGGAGGCGGTAAAGGGCAATGGGACTT 10355
Qy 141 ----- 141
Db 10356 GGAGTCTGTGGGGGACAGGGCTCCAGATGGAACCTGTTCACTCTTTGGGAAACCCCTGAC 10415
Qy 142 -----LeuIleSerLeuPheSerIleProValIleTyrGlu 153
Db 10416 GCCCCCATCTCTGATCCACAGAGTGTGGTCTATTACCATCCCTGCTGTACCGG 10475
Qy 154 ArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAla 173
Db 10476 CAGCACCGGTG-----AGTGTGACCCCTCA 10502
Qy 174 MetAlaLysIleGlnAlaLysIleProGlyLeu 184
Db 10503 GTTGTGACGACCCCACTGATAACATGGGGTCTG 10535

RESULT 26
US-09-513-999C-11198
; Sequence 11198, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J. B.
; APPLICANT: Duclert, A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487

; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 11198
; LENGTH: 200
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-11198

Alignment Scores:
Pred. No.: 4.22e-25 Length: 200
Score: 243.00 Matches: 48
Percent Similarity: 98.08% Conservative: 3
Best Local Similarity: 92.31% Mismatches: 1
Query Match: 26.21% Indels: 0
DB: 4 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-513-999C-11198 (1-200)

Qy 138 LeuIleLeuAlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnVal 157
Db 2 CTGATTTTGGGCTCTCATTTCACTCTTCAGTGTCTCTGTTATTATGAACGGCATCAGCA 61
Qy 158 GlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIle 177
Db 62 CAGATAGATCATATCTAGGACTTCGAAATGAAGATGTTAAAGATGCTATGGCTAAATC 121
Qy 178 GlnAlaLysIleProGlyLeuLysArgLysAlaAsp 189
Db 122 CAAGCAAAATCCCTGGATTGAAGCGCAAGCTGAA 157

RESULT 27
US-09-949-016-40170/c
; Sequence 40170, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40170
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-40170

Alignment Scores:
Pred. No.: 1.02e-10 Length: 601
Score: 146.00 Matches: 29
Percent Similarity: 82.22% Conservative: 8
Best Local Similarity: 64.44% Mismatches: 8
Query Match: 15.78% Indels: 0
DB: 4 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-949-016-40170 (1-601)

Qy 71 ArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsn 90
Db 136 AGGGCTACTTGGAGCTTGAGATCACCTTCTCAGGACGATTCAGAGTACAGGAC 77
Qy 91 SerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAsp 110
Db 76 TGCCTGCAGTTCTACGTGAACAGCACACTTAAGGAACCTGAGGAGGCTCTTCTTGTCCAG 17
```

QY 111 AspLeuValAspSer 115  
Db 16 GACCTGGTGGATTCC 2

RESULT 28  
US-09-949-016-119336/c  
; Sequence 119336, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 119336  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-119336

Alignment Scores:  
Pred. No.: 1,02e-10 Length: 601  
Score: 146.00 Matches: 29  
Percent Similarity: 82.22% Conservative: 8  
Best Local Similarity: 64.44% Mismatches: 8  
Query Match: 15.78% Indels: 0  
Gaps: 4

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-949-016-119336 (1-601)

QY 71 ArgAlaThrLeuGluSerGluValAlaLeuSerGluLeuValGlnLysTyrSerAsn 90  
Db 136 AGGCGCTACTTGGAGCTTGGATCACCCTTCTCAGGAGCAGATTTCAGAACTACACGGAC 77

QY 91 SerAlaLeuGlyHisValAspSerThrIleLysGluLeuArgCysLeuPheLeuValAsp 110  
Db 76 TGCCTGCAGTCTCTACGTGAACAGCACACTTAAGGAACCTGAGAGGCTCTCTCTGTCCAG 17

QY 111 AspLeuValAspSer 115  
Db 16 GACCTGGTGGATTCC 2

RESULT 29  
US-09-248-796A-1905  
; Sequence 1905, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 1905  
; LENGTH: 1125  
; TYPE: DNA  
; ORGANISM: Candida albicans  
US-09-248-796A-1905

Alignment Scores:  
Pred. No.: 1,02e-09 Length: 1125  
Score: 142.00 Matches: 50  
Percent Similarity: 48.40% Conservative: 41  
Best Local Similarity: 26.60% Mismatches: 75  
Query Match: 15.35% Indels: 22  
Gaps: 4

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-248-796A-1905 (1-1125)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
Db 187 TCAACCACTGATTTTTCACCTTGAAGAACCAATCAAACTGGTAAAGTTTTTGGTTCC 246

QY 21 SerLeuPhe-----LeuLeuLeuSerLeuThrValPheSerIleValSerValThr 37  
Db 247 CTGTGTTTGGTTTGAATGCTCTGAAACTGTCAATTTATTCAATATCTTTTCCATTTA 306

QY 38 AlaTyrIleAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyVal 57  
Db 307 GCTTACATTGGTTTA---TTGATCTCTGCTGCTGCTGAA-----TATTCCCGT--- 351

QY 58 IleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGlu 77  
Db 352 -----AAATTGATTACTGCTAAAGGGTTCTTGTCTAATTTCAACCA--- 393

QY 78 ValAlaIleSerGluLeuValGlnLysTyrSerAsnSer-----AlaLeu 93  
Db 394 -----ACTGGTAAATTTGACGCTAAAGATTCAATGATGAAGTATTGCCAGAAITG 444

QY 94 GlyHisValAsnSerThrIleLysGlu---LeuArgArgLeuPheLeuValAspLeu 112  
Db 445 CCCAACTTAAATGTCATTTCGAAAGAAAGTTTAAATAAATTTCTATTACATGACATT 504

QY 113 ValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPhe 132  
Db 505 GAAACCACTTTGAAAGCTGCTGTTTCTTATATATATATATAAATTCATGCTGTTT 564

QY 133 AsnGlyLeuThrLeuLeuLeuAlaLeuLeuSerLeuPheSerIleProValIleTyr 152  
Db 565 TCATTGTACACTTTGATTTTTCATTTCGTTGTTGATTTCACCGTTTCTGTCATTTC 624

QY 153 GluArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerValLysAsp 172  
Db 625 AAAACTTCAAGAAAGAAATTTGATGCTGCTGTTGCCGATATTACCAAGACCATTAAC 684

QY 173 AlaMetAlaLysIleGlnAlaLys 180  
Db 685 AAGTCTGCTGAATTTACTGAAAG 708

RESULT 30  
US-09-949-016-117609/c  
; Sequence 117609, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 117609  
; LENGTH: 601  
; TYPE: DNA

```
; ORGANISM: Human
US-09-949-016-117609

Alignment Scores:
Pred. No.: 3,17e-06 Length: 601
Score: 114.00 Matches: 36
Percent Similarity: 35.19% Conservative: 2
Best Local Similarity: 33.33% Mismatches: 3
Query Match: 12.32% Indels: 67
DB: 4 Gaps: 1

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-949-016-117609 (1-601)

QY 141 AlaLeuileSerLeuPheSerIleProValIleTyrGluArgHisGlnVal----- 157
Db 505 GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGCATCAGGTAATTTCCCTAA 446
QY 157 ----- 157
Db 445 CTAAGTGTGACTTCAGAAATAGAGCACTCACTTATACATGGGATTTACGGATGTATTA 386
QY 157 ----- 157
Db 385 GTGCCAATTTCAATGCTCTTACAAAATGAGAGTGTGATGTTCTTAAAGCCTTTAGCT 326
QY 157 ----- 157
Db 325 TGACACATAGTAGTGGTTAATAAGMTTCTTTAGCAACGGTAATAATTCCTTTATACCTCT 266
QY 158 -----GlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerValIlyAspAlaMe 174
Db 265 CTTTCAGGCACAGATAGATCATATCTAGGACTTGCAAAATAGAATGTTTAAAGATGCTAT 206
QY 174 tAlaLysIleGlnAlaLysIle 181
Db 205 GGCTAAGTAAGTATTAAATC 184

RESULT 31
US-09-313-294A-703
; Sequence 703, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 703
; LENGTH: 266
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700549677H1
US-09-313-294A-703

Alignment Scores:
Pred. No.: 4,29e-06 Length: 266
Score: 109.00 Matches: 21
Percent Similarity: 65.08% Conservative: 20
Best Local Similarity: 33.33% Mismatches: 20
Query Match: 11.78% Indels: 2
DB: 4 Gaps: 1

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-313-294A-703 (1-266)

QY 106 LeuPheLeuValAspLeuValAspSerLeu-----LysPheAlaValLeuMetTrp 123
Db 71 CTTCTAATTAATGATGCTCTTATCCCTGTTCTTGGTGCAAAAGGTGATATGATTTGTGG 130

QY 124 ValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuLeuLeuLeu 143
Db 131 GTGGTTTCATTCATTTGAATGCTCTTCAATTTTCTAGCTTATTTACATTTGGTGTAAAG 190
QY 144 SerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyrLeu 163
Db 191 CTTTCTCTGTTGGTTCCCACTCTATGAGAAAGTAGTACCAGGACCAAGGTTGATGAGAAG 250
QY 164 GlyLeuAla 166
Db 251 GGTGTAGCG 259

RESULT 32
US-09-949-016-48087/c
; Sequence 48087, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48087
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-48087

Alignment Scores:
Pred. No.: 0.000153 Length: 601
Score: 102.00 Matches: 21
Percent Similarity: 70.00% Conservative: 7
Best Local Similarity: 52.50% Mismatches: 12
Query Match: 11.03% Indels: 0
DB: 4 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-949-016-48087 (1-601)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 120 ACAGTGGCGGACCTGCTGCTACTGGAAGGACACGAGGACGCTGAGGAGTGTCTTCACAGGC 61
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 60 CTGATGGTCTCCCTCTCTGCTCTGACATTAGCATGCTGCTCCGTGGCGGCACTTG 1

RESULT 33
US-08-905-223-178
; Sequence 178, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duclert, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
```

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Win95  
SOFTWARE: Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/905,223  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Israelsen, Ned A.  
REGISTRATION NUMBER: 29,655  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 235-8550  
TELEFAX: (619) 235-0176  
INFORMATION FOR SEQ ID NO: 178:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 425 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: DOUBLE  
TOPOLOGY: LINEAR  
MOLECULE TYPE: CDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo Sapiens  
TISSUE TYPE: Brain  
FEATURE:  
NAME/KEY: other  
LOCATION: 73..317  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 97  
OTHER INFORMATION: region 1..245  
OTHER INFORMATION: id HUM506F10B  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 314..376  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 98  
OTHER INFORMATION: region 243..305  
OTHER INFORMATION: id HUM506F10B  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 63..193  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 99  
OTHER INFORMATION: region 1..131  
OTHER INFORMATION: id AA056148  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 314..401  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 95  
OTHER INFORMATION: region 254..341  
OTHER INFORMATION: id AA056148  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 277..317  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 97  
OTHER INFORMATION: region 216..256  
OTHER INFORMATION: id AA056148  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 397..426  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 96  
OTHER INFORMATION: region 338..367  
OTHER INFORMATION: id AA056148

OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 88..189  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 98  
OTHER INFORMATION: region 1..102  
OTHER INFORMATION: id HSC1FF051  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 314..401  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 96  
OTHER INFORMATION: region 230..317  
OTHER INFORMATION: id HSC1FF051  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 187..271  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 95  
OTHER INFORMATION: region 101..185  
OTHER INFORMATION: id HSC1FF051  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 269..317  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 93  
OTHER INFORMATION: region 184..232  
OTHER INFORMATION: id HSC1FF051  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 397..426  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 96  
OTHER INFORMATION: region 314..343  
OTHER INFORMATION: id HSC1FF051  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 87..200  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 92  
OTHER INFORMATION: region 1..114  
OTHER INFORMATION: id HSC16E081  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 314..401  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 96  
OTHER INFORMATION: region 231..318  
OTHER INFORMATION: id HSC16E081  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 199..275  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 94  
OTHER INFORMATION: region 114..190  
OTHER INFORMATION: id HSC16E081  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 269..317  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 91  
OTHER INFORMATION: region 185..233  
OTHER INFORMATION: id HSC16E081  
OTHER INFORMATION: est





```
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5725
; LENGTH: 1273
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-5725

Alignment Scores:
Pred. No.: 0.00681 Length: 1273
Score: 94.00 Matches: 41
Percent Similarity: 38.22% Conservative: 32
Best Local Similarity: 21.47% Mismatches: 62
Query Match: 10.16% Indels: 56
DB: 4 Gaps: 7

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-949-016-5725 (1-1273)

QY 24 LeuLeuLeuSerLeuThrValPheSerIleVal----- 34
Db 605 GTACTGTGCTTGTGACTGCTCTCTCTGTTATTGAAGAGATCATACCATCTTCA 664
QY 35 -----SerValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSer 50
Db 665 AAGTCATACCTCTAATTGGAGATCTGGTATTACCATGATTTTGTGACACTGTCA 724
QY 51 PheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisPro--- 69
Db 725 ATTATGGTAACGCTCTCTCGCTATCATCATTCATCGTCTCTCTCAACACATAATGCC 784
QY 70 -----PheArg 71
Db 785 ATGGCGCCTTTGTGTCGCAAGATATTTCTTCACACGCTTCCCAAACTGCTTTCATGAGA 844
QY 72 AlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGln-----Lys 87
Db 845 AGTCATGTAGACAGGTACTCTCTCAGAAAGAGAACTGAGAGTGGTAGTGACCAAAA 904
QY 88 TyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArgLeuPhe 107
Db 905 TCTTCTAGAAACACATTTGGAAGTCGCGCTCGATTCTTCTTACATTACAGACATC 964
QY 108 Leu-----ValAspLeuValAspSerLeuLysPhe----- 118
Db 965 ATGAAGGAAATCATGCTCGTGGTGTGGAAGATTGGAATTCATAGCCAGGTCTT 1024
QY 119 ---AlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeu 137
Db 1025 GATCGGATGTTCTGTGGACTTCTTCTTCTGTTCA----- 1060
QY 138 LeuIleAlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnVal 157
Db 1061 ---ATTGTTGGATCTCTGCGCTTTT---GTTCTGTTATTATATAATGGGCAATATA 1114
QY 158 GlnIleAspHisTyrLeuGlyLeuAlaAsnLys 168
Db 1115 TTAATACCATGTTTCATATTGGAATGCAATAAG 1147

RESULT 37
US-08-956-171E-407/C
; Sequence 407, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon

;
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 407:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1722 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 407:
US-08-956-171E-407

Alignment Scores:
Pred. No.: 0.0111 Length: 1722
Score: 94.00 Matches: 36
Percent Similarity: 48.87% Conservative: 29
Best Local Similarity: 27.07% Mismatches: 42
Query Match: 10.16% Indels: 26
DB: 4 Gaps: 6

US-09-830-972-2_COPY_975_1163 (1-189) x US-08-956-171E-407 (1-1722)

QY 26 LeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle----- 40
Db 1067 TTGAGTTAATTGTATATATAATCTTATCTATTGTTAAGTATGTCACGGGTTTGTCTTT 1008
QY 41 -----AlaLeuAlaLeuSerValThr-----IleSerPhe 51
Db 1007 AACTCTGCAGCTGTGAAGCGCCGATGATCAATAAATAATATGACAGATATTATCGTTCTTTA 948
QY 52 ArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArg 71
Db 947 GCTGTTATTATTGGATTGAAATTCATTAATTAACCTGCCGATCGAAATCATCTTAT--- 891
QY 72 AlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSer 91
Db 890 GGCCATTGAAGTCTGAAATAATTTCTTCA-----TTATTGTTGTCATTGTCATTATG 837
QY 92 AlaLeuGlyHisValAsnSerThrIleLysGluLeuArgLeuPheLeuValAspAsp 111
Db 836 TTTGTAGGT---ATCCAAGTAGTATTCAAAATGCAACCTCGTTGTTTCAAGAAGATGAC 780
QY 112 LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeu 131
```



Db 779 GTTGACCTAAC-----GCAATAACAATTATCGTCAGCTTA 744  
Qy 132 PheAnGlyLeuThrLeuLeuLeuLeuAlaLeuLeuSer 144  
Db 743 ATCAGTGGTCTTGTAATGTTGATTGTTATTTGTCAGTCAAT 705  
RESULT 38  
US-08-781-986A-407/c  
; Sequence 407, Application US/08781986A  
; Patent No. 6737248  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 5255  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/781,986A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Benson, Bob  
; REGISTRATION NUMBER: 30,446  
; REFERENCE/DOCKET NUMBER: PB248PP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 407:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1722 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
US-08-781-986A-407  
Alignment Scores:  
Pred. No.: 0.0111 Length: 1722  
Score: 94.00 Matches: 36  
Percent Similarity: 48.87% Conservative: 29  
Best Local Similarity: 27.07% Mismatches: 42  
Query Match: 10.16% Indels: 26  
DB: 4 Gaps: 6  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-08-781-986A-407 (1-1722)  
Qy 26 LeuSerLeuThrValPheSerileValSerValThrAlaTyrlle----- 40  
Db 1067 TTGAGTTTAAATGTTATATAATCTTATCTATTGTTAAGTATGTCACGGGTTTGTCTTT 1008  
Qy 41 -----AlaLeuAlaLeuSerValThr-----IleSerPhe 51  
Db 1007 AACTCTGCAGCTGTAAGACCGCATTAACAATATGACAGATATTATCGTTCTTTA 948  
Qy 52 ArgIleTyLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPhearg 71  
Db 947 GCTGTATTATGTAATGAAATTTCAATTAACCTGCCGATCGAATCATCCTTAT--- 891  
Qy 72 AlaTyLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTySerAsnSer 91  
Db -----

Db 830 GGCCATTGAAGTCTGAAATAATATTCTTCA-----TTATTGGTGTCTATTTGTCATTATG 837  
Qy 92 AlaLeuGlyHisValAsnSerThrIleLysGluLeuArgLeuPheLeuValAspAsp 111  
Db 836 TTTGTAGGT---ATCCAAGTAGTATTATCAAAATGACCTCGTTTGTTCAAAGNAGATGAC 780  
Qy 112 LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTy-ValGlyAlaLeu 131  
Db 779 GTTGACCTAAC-----GCAATAACAATTATCGTCAGCTTA 744  
Qy 132 PheAnGlyLeuThrLeuLeuLeuLeuAlaLeuLeuSer 144  
Db 743 ATCAGTGGTCTTGTAATGTTGATTGTTATTTGTCAGTCAAT 705  
RESULT 39  
US-08-961-527-149  
; Sequence 149, Application US/08961527  
; Patent No. 6420135  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 391  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/961,527  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PB340P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 149:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12566 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
US-08-961-527-149  
Alignment Scores:  
Pred. No.: 0.444 Length: 12566  
Score: 92.50 Matches: 41  
Percent Similarity: 46.99% Conservative: 37  
Best Local Similarity: 24.70% Mismatches: 57  
Query Match: 10.00% Indels: 31  
DB: 3 Gaps: 8  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-08-961-527-149 (1-12566)  
Qy 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerileValSerValThrAlaTyrlle 40  
Db 344 TCGATAGTCTTACTATTATGCGCCACCCCTATGCTGCTAGTCTAGTATTATTTCTG 403  
Qy 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyLysGlyValIleGlnAla 60  
Db 404 ---CTGACCTTTATGAGTCTGACCCCTGATTTATCGGATC---AAATCCCTTCGTCAGGCA 457

```
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyLeuGluSerGluValAlaIle 80
Db 458 GGGATTGGCTTAATAGCTGGT-----CAGAGCTTGTGTTGAGATT 496
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 497 GCT-----CTCAGACAGTGTTA 514
QY 101 LysGluLeuArgGluPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 515 GAAGATGTGACAGCTT---ATCTGCTCAGTCTGTTATCCAGTCTTTTGGGATTGGGG 571
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db 572 ATTTCTCG-----TATCAAGGTGCTTGTTTATGGCAACGGTGAACCTGGTCAATC 622
QY 141 AlaLeuLysSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 623 ATTGCTCTTCTTACTTATGATTGACCTTGGCAGGGGATTCTTACCTTACTTAAGTGTGCTG 682
QY 161 HisTyLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 683 TATCTACTTGGTTTACAGGAATACTCTGGTGGATCTA-----TTGAAGGGAAA 733
QY 181 IleProGlyLeuLysArg 186
Db 734 CTCCTCT---CTCAACAGT 748

RESULT 40
US-09-462-136-1
; Sequence 1, Application US/09462136
; Patent No. 6426198
; GENERAL INFORMATION:
; APPLICANT: Carlsce, et al.
; TITLE OF INVENTION: Genes for Niemann-Pick Type C Disease
; FILE REFERENCE: 4239-53894
; CURRENT APPLICATION NUMBER: US/09/462,136
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/US98/13862
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/051,682
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4550
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3837)
US-09-462-136-1

Alignment Scores:
Pred. No.: 0.314 Length: 4550
Score: 88.50 Matches: 39
Percent Similarity: 42.11% Conservative: 25
Best Local Similarity: 25.66% Mismatches: 51
Query Match: 9.57% Indels: 37
DB: 3 Gaps: 7

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-462-136-1 (1-4550)
QY 46 SerValThrIleSerPheArgIleTyLysGlyValIleGlnAlaIleGlnLysSerAsp 65
Db 1792 AATCTGACCATTTCTTCTACTGCTGAACGAGTATTGAAGTAACTAAATCGTGAAGT 1851
QY 66 GluGlyHisProPheArgAlaTyLeuGluSerGluValAlaIleSerGluLeuVal 85
Db 1852 GACAGTGATGCTCTTC-----ACCGTTGTAATTAGCTATGCAATCATG 1893
QY 86 GlnLysTySerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArg 105

US-09-949-016-4281
; Sequence 4281, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4281
; LENGTH: 4661
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4281

Alignment Scores:
Pred. No.: 0.327 Length: 4661
Score: 88.50 Matches: 39
Percent Similarity: 42.11% Conservative: 25
Best Local Similarity: 25.66% Mismatches: 51
Query Match: 9.57% Indels: 37
DB: 4 Gaps: 7

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-949-016-4281 (1-4661)
QY 46 SerValThrIleSerPheArgIleTyLysGlyValIleGlnAlaIleGlnLysSerAsp 65
Db 1913 AATCTGACCATTTCTTCTACTGCTGAACGAGTATTGAAGTAACTAAATCGTGAAGT 1972
QY 66 GluGlyHisProPheArgAlaTyLeuGluSerGluValAlaIleSerGluLeuVal 85
Db 1973 GACAGTGATGCTCTTC-----ACCGTTGTAATTAGCTATGCAATCATG 2014
QY 86 GlnLysTySerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArg 105
Db 2015 TTTCTATATATTCTTCCATGCTTGGGGCAC-----ATCAAAAGCTGTCGAGC 2062
QY 106 LeuPheLeuValAspAsp-----LeuValAspSerLeu 116
Db 2063 CTT---CTGGTGGATTGCAAGGTCTCACTAGGCATCGGGCATCTTGATCGTGTGAGC 2119
```

QY 117 LysPheAlaValLeuMetTrpValPheThrValGlyAlaLeuPheAsnGlyLeuThr 136  
Db 2120 TCGGTGGCTTGTCTCTGGGTGCTTCAGCTACATGGGTG-----CCCTTGACC 2170  
QY 137 LeuLeuLeuLeuAlaLeuLeu-----SerLeuPhe 146  
Db 2171 CTCATTGTGATTGAAGTCATCCGCTCTCTGGTGTCTGGCTGTGGAGTGGACACATCTTC 2230  
QY 147 SerLeuProValIleTyrGluArgHisGln-----ValGlnIleAspHisTyr 162  
Db 2231 ATTCTGGTGCAGGCTTACAGAGATGAACGTCTTCAAGGGGAACCTCGATCAGCAG 2290  
QY 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMet 174  
Db 2291 CTGGCAGGGTCTTAGGAGAAGTGGCTCCAGTATG 2326  
RESULT 42  
US-09-814-915A-100  
; Sequence 100, Application US/09814915A  
; Patent No. 6750015  
; GENERAL INFORMATION:  
; APPLICANT: Horwitz, Kathryn  
; APPLICANT: Richer, Jennifer  
; TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Relat  
; FILE REFERENCE: 2848-39  
; CURRENT APPLICATION NUMBER: US/09/814,915A  
; PRIOR FILING DATE: 2002-03-21  
; PRIOR FILING DATE: 2000-06-28  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 100  
; LENGTH: 4673  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-814-915A-100  
Alignment Scores:  
Pred. No.: 0.328 Length: 4673  
Score: 88.50 Matches: 39  
Percent Similarity: 42.11% Conservative: 25  
Best Local Similarity: 25.66% Mismatches: 51  
Query Match: 9.57% Indels: 37  
DB: 4 Gaps: 7  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-814-915A-100 (1-4673)  
QY 46 SerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAsp 65  
Db 1915 AATCTGACCATTTCTTCACTGCTGAACGAGTATTGAAGATGAAGTAAATCGTGAAGT 1974  
QY 66 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluLeuVal 85  
Db 1975 GACAGTGTATGCTTC-----ACCGTTGTAATAGCTATGCTATGCTCATG 2016  
QY 86 GlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArg 105  
Db 2017 TTCTATATATTTCTCCTAGCTTGGGGCAC-----ATCAAAAGCTGTGGCAGG 2064  
QY 106 LeuPheLeuValAspAsp-----LeuValAspSerLeu 116  
Db 2065 CTT---CTGTGGATTGGAAGTCTCAGTGGCATCGGGGCATCTTGATCGTGTGAGC 2121  
QY 117 LysPheAlaValLeuMetTrpValPheThrValGlyAlaLeuPheAsnGlyLeuThr 136  
Db 2122 TCGGTGGCTTGTCTCTGGGTGCTTCAGCTACATGGGTG-----CCCTTGACC 2172  
QY 137 LeuLeuLeuLeuAlaLeuLeu-----SerLeuPhe 146  
Db 2173 CTCATTGTGATTGAAGTCATCCGCTCTCTGGTGTCTGGCTGTGGAGTGGACACATCTTC 2232

QY 147 SerLeuProValIleTyrGluArgHisGln-----ValGlnIleAspHisTyr 162  
Db 2233 ATTCTGGTGCAGGCTTACAGAGATGAACGTCTTCAAGGGGAACCTCGATCAGCAG 2292  
QY 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMet 174  
Db 2293 CTGGCAGGGTCTTAGGAGAAGTGGCTCCAGTATG 2328  
RESULT 43  
US-09-313-294A-81  
; Sequence 81, Application US/09313294A  
; Patent No. 6476212  
; GENERAL INFORMATION:  
; APPLICANT: Lalquidi, Raghunath V.  
; APPLICANT: Ito, Laura Y.  
; APPLICANT: Sherman, Bradley K.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR  
; FILE REFERENCE: PL-0017 US  
; CURRENT APPLICATION NUMBER: US/09/313,294A  
; CURRENT FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 7600  
; SOFTWARE: PERL Program  
; SEQ ID NO 81  
; LENGTH: 296  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No. 6476212 700548479H1  
; NAME/KEY: unsure  
; LOCATION: 109  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-313-294A-81  
Alignment Scores:  
Pred. No.: 0.00732 Length: 296  
Score: 86.50 Matches: 30  
Percent Similarity: 52.58% Conservative: 21  
Best Local Similarity: 30.93% Mismatches: 41  
Query Match: 9.35% Indels: 6  
DB: 4 Gaps: 2  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-313-294A-81 (1-296)  
QY 96 ValAsnSerThrIleLysGluLeuArgLeuPheLeuValAspLeuValAspSer 115  
Db 3 ATCAACAGGGGCTTGTACCTTGAGGGAGATTGGACATGGACATGCTAAAGAAATTC 62  
QY 116 LeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeu 135  
Db 63 CTAATTGTTATCGCAGGCTCTCGCTCTCTTTCAGTTCTTGGGAGCCNTGC-AACTTCCTG 121  
QY 136 ThrLeuLeuLeuLeuAlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHis 155  
Db 122 ACACGTGTTCTATATTGCTTGTGGCAGCTGTACACTATACCTGTCTCTGTATGAGAAATAT 181  
QY 156 GlnValGlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAla 175  
Db 182 GAGGACAAAGGTGTGATGCTTTTGGTGAGAGCTATGATCGAACTGAAGAGTATTATGCC 241  
QY 176 -----LysIleGlnAlaLysIlePro---GlyLeuLysArgLys 187  
Db 242 ATCTTCGATGAGAAGTGCCTATCGAGATTCGAAAGGCGCTCAAGGATAAG 292  
RESULT 44  
US-09-134-000C-2072  
; Sequence 2072, Application US/09134000C  
; Patent No. 6617156  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; FILE REFERENCE: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 032796-032

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; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2072
; LENGTH: 1779
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-2072

Alignment Scores:
Pred. No.: 0.132 Length: 1779
Score: 86.50 Matches: 49
Percent Similarity: 38.46% Conservative: 41
Best Local Similarity: 20.94% Mismatches: 61
Query Match: 9.35% Indels: 83
DB: 4 Gaps: 12

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-134-000C-2072 (1-1779)

QY 7 TyrTrpArgAspIleuValSerLeuPheGlyValValPheGlyAlaSerLeuPheLeuLeu 26
DB 133 TTCTGGAACAGTGAAAGCT-----TTATTTCGATACATG 168

QY 27 SerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuSer 46
DB 169 TCTAAACGAATGCTGCAATTATTGCTGTC-----TTAGTATTAGCAATTGCGAGC 219

QY 47 ValThrIleSerPheArg-----IleTyrIys 55
DB 220 GTCTGTTTCCAAATTCACACCAAAAGTATTAGGACAGGCAACACTGAATTTTAA 279

QY 56 GlyValIleGlnAlaIleGlnIysSerAspGluGlyHisProPheArgAla----- 72
DB 280 GCGTCATGAAGGCGCTGCTGAATGAACAGGCTTAAATAATACATCTTTTCCAATT 339

QY 73 -----TyrLeuGluSerGlu 77
DB 340 GATTTTGACAAAATTGGTCAAATTTTATTAAATTGTTATTGTCATGATCTTATTCTGCT 399

QY 78 Val-----Ala 79
DB 400 GTCTTTAAATTTCTTGACGAAGTAATATTGACACGCTGTTTACAGCGAAGCTTTATGAA 459

QY 80 IleSerGluGluLeuValGlnIysTyrSerAsnSerAlaLeuGly-----His 95
DB 460 TTACGTCAGAAATTAGAACGGAATAATGAACAAAGTTCCAAATTCCTATTATGATATTCAT 519

QY 96 ValAsnSerThrIleIysGluLeuArgArgLeuPheLeuValAspLeuValAspSer 115
DB 520 AGTAATGGGACATTATGTC---CGGGCAATTACGACATGATAAATTGCGAGTACT 576

QY 116 LeuIys-----PheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPhe 132
DB 577 TTACACCAAAACTTAACCCAAATTAATTACAGTATCGTCACATTTGTGGGTGACTTTGG 636

QY 133 AsnGlyLeuThr-----LeuLeuIleLeuAlaLeu-----IleSer 144
DB 637 ATGATGCTGACCAATTAGCTGGCGNGTTACACTAAATTTGCCTTAGCAACAGTGCATTAAGT 696

QY 145 LeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr----- 162
DB 697 TTAATTGTTGATGTTGTGGCGCTCGCTCGCAA-----AAACATTTTGGCGCT 747

QY 163 -----LeuGlyLeuAlaAsnIysSerValIysAsp 172
DB 748 CAACAAAAAGCTTAGGATTATTGTAATAACCAAGTCGAAGAA 789

RESULT 45
US-09-830-972-2_COPY_975_1163 (1-189) x US-09-956-171E-322 (1-1302)
; Sequence 322, Application US/08956171E

; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 322:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1302 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 322:
US-08-956-171E-322

Alignment Scores:
Pred. No.: 0.0937 Length: 1302
Score: 86.00 Matches: 42
Percent Similarity: 41.80% Conservative: 37
Best Local Similarity: 22.22% Mismatches: 78
Query Match: 9.30% Indels: 32
DB: 4 Gaps: 7

US-09-830-972-2_COPY_975_1163 (1-189) x US-08-956-171E-322 (1-1302)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleIysLysThrGlyVal---ValPheGlyAla 20
DB 68 ATAGTTATTTCCTGCTGTTTAAAGAAACATTCGTACGACGCAATTCCTATTATATCGATT 127

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 128 CGGTTATCATCTCTTATGCGCTTATGCTCTGAAATTGAGTGATGTTTCATTGTAATA 187

QY 41 ---AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGln 59
DB 188 CTAACGTTAGTGCTTACATACGATCGATTGGA---CGTGTGATAGACCGATTCGATTGTA 244

QY 60 AlaIleGlnIysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAla 79
DB 245 GTTGTGTTGAA-----AATATTATTCGACGCTTAACACAGATTTCAGAAAGCAAA 289
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;; PRIOR APPLICATION NUMBER: US 60/024,428  
;; PRIOR FILING DATE: 1996-08-22  
;; NUMBER OF SEQ ID NOS: 3  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 1 1664976  
;; LENGTH: 1664976  
;; TYPE: DNA  
;; ORGANISM: Methanococcus jannaschii  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (28222)..(28222)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (28257)..(28258)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (84773)..(84773)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (84808)..(84808)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (84812)..(84812)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (98120)..(98120)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (98159)..(98159)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (98239)..(98239)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (98266)..(98266)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (98343)..(98343)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (103998)..(103998)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (148948)..(148948)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (163385)..(163385)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (191989)..(191989)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (191995)..(191995)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (231980)..(231980)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (234187)..(234187)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (234220)..(234220)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (234814)..(234814)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (309398)..(309398)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (309418)..(309418)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (312837)..(312837)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (312993)..(312993)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (319226)..(319226)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (559167)..(559167)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (559241)..(559241)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (600992)..(600992)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (622708)..(622708)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (657081)..(657081)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (657203)..(657203)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (674435)..(674435)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (682442)..(682442)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (713652)..(713652)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (741684)..(741684)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (779455)..(779455)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (779676)..(779676)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (855539)..(855539)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (871619)..(871619)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (1084830)..(1084830)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (1096846)..(1096846)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (1119881)..(1119881)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (1130881)..(1130881)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (1310988)..(1310988)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (1313224)..(1313224)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (1349473)..(1349473)  
;; OTHER INFORMATION: n equals a, t, c, or g  
;; NAME/KEY: misc feature  
;; LOCATION: (1349491)..(1349491)

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; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1470091)..(1470091)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1569020)..(1569020)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1602912)..(1602912)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1603734)..(1603734)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1637998)..(1637998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1664854)..(1664855)
; OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1
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## Alignment Scores:

Pred. No.:	1.32e+04	Length:	1664976
Score:	85.00	Matches:	46
Percent Similarity:	42.54%	Conservative:	25
Best Local Similarity:	27.54%	Mismatches:	56
Query Match:	9.19%	Indels:	40
DB:	4	Gaps:	8

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-08-916-421B-1 (1-1664976)

```
QY 6 LeuTyrTrpArgAspIle-----LysLysThrGlyValValPhe 18
Db 771873 CTATATAAAGAACATAAAAGGAATATTATACCTCTTTAAAAAACTTCGTAAGGATTTT 771932
QY 19 GlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIle---ValSerValThr 37
Db 771933 GACGAAAAAAGTTTATATTATTTGTTAAATATAGTCGCGATACCTCTCTTAATATCA 771992
QY 38 AlaTyrIleAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyVal 57
Db 771993 TATTATTACACTTAACCTTAAGAGTAGATTATATTGTTAGTTATATACCTGGGAGCT 772052
QY 58 Ile-----GlnAlaIleGlnLysSerAspGluGlyHis 68
Db 772053 GCATTGTTCCATCCATCTATTTTATATGAAAAATAAATAAGAACTCTTGAGATAACATT 772112
QY 69 ProPheArgAlaTyr-----LeuGluSerGluValAlaIleSerGluGlu 83
Db 772113 CCACAGCTCTTTATATTATGATATTAGCCCTCGAATCTGGAGGTCCTAATACCGAAGCA 772172
QY 84 LeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeu 103
Db 772173 TTACTTGAAGTT-----GTTAAAGTAATATAAAGGAAGTT 772208
QY 104 -----ArgArgIlePheLeuValAspLeuValAspSerLeuLysPhe 118
Db 772209 AGCGATATATTTAGAAAAGTTTATACCTTAATAGGAAAC-----CAAAAATTAAGTTT 772262
QY 119 AlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeu 138
Db 772263 GAAGAGTCTATG-----ACAATTGATCAATTTATATGATTCCTAAAGTATTAAAGG 772313
QY 139 IleLeuAlaLeuIleSerLeu 145
Db 772314 ATGTTAGCAAGAATTATGATT 772334
```

## RESULT 50

```
US-09-692-570-1
; Sequence 1, Application US/09692570
; Patent No. 6797466
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
```

```
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco-
; Patent No. 6797466
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275C1
; CURRENT APPLICATION NUMBER: US/09/692,570
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; PRIOR APPLICATION NUMBER: US 08/916,421
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28222)..(28222)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28257)..(28258)
; OTHER INFORMATION: n equals a, t, c, or g
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; LOCATION: (84808)..(84808)
; OTHER INFORMATION: n equals a, t, c, or g
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; NAME/KEY: misc feature
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; NAME/KEY: misc feature
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; NAME/KEY: misc feature
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; NAME/KEY: misc feature
; LOCATION: (148948)..(148948)
; OTHER INFORMATION: n equals a, t, c, or g
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; NAME/KEY: misc feature
; LOCATION: (163385)..(163385)
; OTHER INFORMATION: n equals a, t, c, or g
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; NAME/KEY: misc feature
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; FEATURE:
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; LOCATION: (191995)..(191995)
; OTHER INFORMATION: n equals a, t, c, or g
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; NAME/KEY: misc feature
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; NAME/KEY: misc feature
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; LOCATION: (234220)..(234220)
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; NAME/KEY: misc feature
; LOCATION: (234814)..(234814)
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; LOCATION: (309398)..(309398)
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; LOCATION: (657203)..(657203)
; OTHER INFORMATION: n equals a, t, c, or g
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; NAME/KEY: misc feature
; LOCATION: (674435)..(674435)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (682442)..(682442)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
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; LOCATION: (713652)..(713652)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (741684)..(741684)
; OTHER INFORMATION: n equals a, t, c, or g
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; NAME/KEY: misc feature
; LOCATION: (779455)..(779455)
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; NAME/KEY: misc feature
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; LOCATION: (871619)..(871619)
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; NAME/KEY: misc feature
; LOCATION: (1084830)..(1084830)
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; LOCATION: (1096846)..(1096846)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1119881)..(1119881)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1130881)..(1130881)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1310988)..(1310988)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1313224)..(1313224)
; OTHER INFORMATION: n equals a, t, c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1349473)..(1349473)
; OTHER INFORMATION: n equals a, t, c, or g
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Alignment Scores:
Pred. No.: 1.32e+04 Length: 1664976
Score: 85.00 Matches: 46
Percent Similarity: 42.51% Conservative: 25
Best Local Similarity: 27.54% Mismatches: 56
Query Match: 9.19% Indels: 40
DB: 4 Gaps: 8
```

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-692-570-1 (1-1664976)

```
Oy 6 LeuTyrTrpArgAspIle-----LysLysThrGlyValValPhe 18
|||||
Db 771873 CTATATAAGACAAATATAATATATATCTTTAAAGAACTGGTAAGGATTTT 771932

Oy 19 GlyAlaSerLeuPheLeuLeuLeuSerValThrValPheSerIle---ValSerValThr 37
|||||
Db 771933 GACGAAAAAAGTTTATATTATTCTTAATTAATTAAGTGGATACCTCTCTTAATATCA 771992

Oy 38 AlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrGlyVal 57
|||||
Db 771993 TATTATTACACTTAACCCCTAAAAAGTATGATTATTTTGTAGTTATATACGTGGAGCT 772052
```

QY 58 Ile-----GlnAlaIleGlnLysSerAspGluGlyHis 68  
Db 772053 GCATTGTTCCATCTATTTTATATAGAAATAAATAAGAACTCTTCGAGAAATACATT 772112  
QY 69 ProPheArgAlaTyr-----LeuGluSerGluValAlaIleSerGluGlu 83  
Db 772113 CCACAGCTCTTTATATATATATATAGCCCTCGAATCTCGAAGGTCCATAACGAGCA 772172  
QY 84 LeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeu 103  
Db 772173 TTACTTGAAGTT-----GTTAAAGTAATATAAAGGAAGTT 772208  
QY 104 -----ArgArgLeuPheLeuValAspLeuValAspSerLeuLysPhe 118  
Db 772209 AGCGATATATTTAGAAAGCTTTTATATCTTAATGGAAAC-----CAAAATTAAGTTTT 772262  
QY 119 AlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeu 138  
Db 772263 GAAGAGTCTATG-----ACNATTGTATCAATTTATATATGATCTTAAGTATTAGG 772313  
QY 139 IleLeuAlaLeuIleSerLeu 145  
Db 772314 ATGTTAGCAAGAATTATGATT 772334

## RESULT 51

US-09-543-681A-2003  
; Sequence 2003, Application US/09543681A  
; Patent No. 6605709

## GENERAL INFORMATION:

; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; PRIOR FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 2003

LENGTH: 843

TYPE: DNA

ORGANISM: Proteus mirabilis

US-09-543-681A-2003

## Alignment Scores:

Pred. No.: 0.0755 Length: 843  
Score: 84.50 Matches: 38  
Percent Similarity: 39.25% Conservative: 35  
Best Local Similarity: 20.43% Mismatches: 67  
Query Match: 9.14% Indels: 46  
DB: 4 Gaps: 6

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-543-681A-2003 (1-843)

QY 2 ValValAspLeuLeuTyr---TrpArgAspIleLysLysThr----- 14  
Db 58 GTGGTAGGATCATTTATGATGAG-----ATAAACGCTCTCTACCCCTAAACAGGT 111  
QY 15 -----GlyValValPheGlyAlaSerLeuPheLeuLeuSerLeu 28  
Db 112 ATCAATATATCTCGGGAGGAGTAAATAGTAGAATACTACTCTCTATTCTTTAGCTCT 171  
QY 29 ThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuSerValThr 48  
Db 172 AGCAATTATGGGTATTTAGTCTCTTAGAAGATATCTGGCAATCTCTGTTATGGTTATG 231  
QY 49 IleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln---LysSerAspGluGly 67  
Db 232 ATGGAATCATTCCTCGCTCTTAAATTTGTTGATGATGATGATGATGATGATGATGATG 291  
QY 68 HisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluLeuValGlnLys 87  
Db 292 AAATCACTAAAGCCAATATCGAAAC-----GAAATTGACACAAAAA 333

QY 88 TyrSerAsnSerAlaLeu----- 93  
Db 334 ACGCAACAACAAGTGTCTGGGGGATTTTACTGATCATCGCATTCGCCATTCGAGAGAA 393  
QY 94 -----GlyHisValAsnSerThrIleLysGluLeuArg 104  
Db 394 GCGCGGAGGTGGTGTCTTCTATCAAGCCATATTTATGGCTCTCACAGCACAAACCGCG 453  
QY 105 ArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrpVal 124  
Db 454 TTGTCTTCTTCTGATTGAAGTATTCTATTCGCTTATGATAGCGGACTAATCTATGTTA 513  
QY 125 PheThrTyrValGlyAlaLeu-PheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIle 144  
Db 514 TTTTGTCAACATCAAAAATGATTTCTTGGCGTAAATTTCTTTGTTATTATACCGGATTTT 573  
QY 144 rLeuPheSerIlePro 149  
Db 574 CTGCTTTTCTCGCGC 589

## RESULT 52

US-09-328-352-740

; Sequence 740, Application US/09328352

; Patent No. 6562958

## GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 740

LENGTH: 1782

TYPE: DNA

ORGANISM: Acinetobacter baumannii

US-09-328-352-740

## Alignment Scores:

Pred. No.: 0.252 Length: 1782  
Score: 84.50 Matches: 35  
Percent Similarity: 44.06% Conservative: 28  
Best Local Similarity: 24.48% Mismatches: 48  
Query Match: 9.14% Indels: 33  
DB: 4 Gaps: 6

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-328-352-740 (1-1782)

QY 8 TrpArgAspIleLysLysThr-----GlyValValPheGlyAlaSerLeuPheLeuLeu 25  
Db 772 TGGCGTGGTGTAAAGAACTTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 831  
QY 26 LeuSerLeuThrValPheSerIleVal-----SerValThrAlaTyrIle 40  
Db 832 GCCCAGTATCTCACCTTAACCTTTATTTGCCCCCTGAGTTACACAGACATTACCGCAAT 891  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 892 GCT---TCATTGGTCAGCTGACGTTGTTATTCGCTGTTTGGAAA----- 933  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 934 -----CCAAACATATTTCCCTTTTGAACCTGACCGGCTCAGACTTTG 978  
QY 81 SerGluGlu-----LeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSer 98  
Db 979 GCTCAGCAACCTTCAACAGTTTCAACGTTATAGCATTTGGGAAAATTCGAAAGGCTGCT 1038  
QY 99 -----ThrIleLysGluLeuArgLeu 106  
Db 1039 CCATTTGCTATTTTAAACGTAATGTCAGATTTCGAGCGTTTAAGCCATTAAAGCATTA 1098

Qy 107 PheLeuValAspAspLeuValAspSerLeuTyrPheAlaValLeuMetTrpValPheThr 126  
Db 1099 TTTGCAAAAGATGGTCTTGAACACTGGATTTTAAACTTGAAGTGC-GTATTTACA 1157  
Qy 127 TyrValGly 129  
Db 1158 CAATTTGTT 1166

## RESULT 53

US-09-602-787A-301  
; Sequence 301, Application US/09602787A  
; Patent No. 6696561  
; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Mark  
; APPLICANT: Krüger, Burkhard  
; APPLICANT: Schöder, Hartwig  
; APPLICANT: Zeider, Oskar  
; APPLICANT: Haberhauer, Gregor  
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE  
; TITLE OF INVENTION: TRANSPORT  
; FILE REFERENCE: BGI-125CP  
; CURRENT APPLICATION NUMBER: US/09/602,787A  
; CURRENT FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: USN 60/141031  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: DE 19931454.3  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931478.0  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931563.9  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19932122.1  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932124.8  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932125.6  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932128.0  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932180.9  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932182.5  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932190.6  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932191.4  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932209.0  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932212.0  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932227.9  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932228.7  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932229.5  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932230.9  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932927.3  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19933005.0  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19933006.9  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19940764.9  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: DE 19940765.7  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: DE 19940766.5  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: DE 19940830.0

; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: DE 19940831.9  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: DE 19940832.7  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: DE 19940833.5  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: DE 19941378.9  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: DE 19941379.7  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: DE 19941395.9  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: DE 19942077.7  
; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: DE 19942078.5  
; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: DE 19942079.3  
; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: DE 19942088.2  
; PRIOR FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 678  
; SEQ ID NO 301  
; LENGTH: 1500  
; TYPE: DNA  
; ORGANISM: Corynebacterium glutamicum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (101)..(1477)  
; OTHER INFORMATION: RXN00456  
US-09-602-787A-301

## Alignment Scores:

Pred. No.:	0.264	Length:	1500
Score:	83.50	Matches:	41
Percent Similarity:	40.38%	Conservative:	22
Best Local Similarity:	26.28%	Mismatches:	50
Query Match:	9.03%	Indels:	43
DB:	4	Gaps:	6

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-602-787A-301 (1-1500)

Qy	8	TrpArgAspIleLeuLys-----ThrGlyVal-----ValPheGlyAla 20
Db	53	TGGCGTCTCGTCGCAGACITTTGCTCATTCGCCCTAGGTGTTACTTGGTGTCTGCAGGCA 112
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db	113	CTGCTGGCGATCATGTGTCTTGAGCGTAGCCCATCTTGAGGGAAACCGAGCACTT 172
Qy	41	AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db	173	GTTGGATTGCTGCTTGTTACCATCGTTGGGTTTG-----GGGGTGGCGCAGTGG 220
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db	221	ATTCAAAA-----GTAGTG 235
Qy	81	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db	236	GCAGAAGATCTAGGCCAGCATAT-----GTGCATGAGGTGCGT 274
Qy	101	LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPhe----- 118
Db	275	CGTGAATTGGTGGTGTGCTGCTCGCTCGAATAACGGCCTCGTTGGCGGTGACTGTC 334
Qy	119	-----AlaValLeuMetTrpValPheThrTyrValGlyAla 130
Db	335	ACCCGAGCCAGCATGATCTCACCGCGTGGCGCAATTGGGTGGCTTTGGGCATTGTTCCG 394
Qy	131	LeuPheAsnGlyLeuThrLeuLeuAlaLeuIleSerLeuPhe 146
Db	395	ATGGTCACCGGCTGCGGCTTGATTGCGATTGTGCTGGTGGCGGTTGTTT 442

## RESULT 54

US-09-583-110-1302  
; Sequence 1302, Application US/09583110  
; Patent No. 6699703  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al.  
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus  
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics  
; FILE REFERENCE: PATH00-07A  
; CURRENT APPLICATION NUMBER: US/09/583,110  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/107,433  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/085,131  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: US 60/051,553  
; PRIOR FILING DATE: 1997-07-02  
; NUMBER OF SEQ ID NOS: 5322  
; SEQ ID NO 1302  
; LENGTH: 1233  
; TYPE: DNA  
; ORGANISM: Streptococcus pneumoniae  
US-09-583-110-1302

Alignment Scores:  
Pred. No.: 0.266 Length: 1233  
Score: 82.50 Matches: 38  
Percent Similarity: 47.40% Conservative: 35  
Best Local Similarity: 24.68% Mismatches: 50  
Query Match: 8.92% Indels: 31  
DB: 4 Gaps: 7

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-583-110-1302 (1-1233)

QY 11 IleLysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrVal 30  
Db 235 ATTGCCAAATCAAAATCTGCTACGCTATTTTGACAGATTTCTGCTGTGCGCC 294  
QY 31 PheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSer 50  
Db 295 TTTTCATTAGTTTCAGTCATTATGATGTCATCATCAACCTCATCTCTGACACCTTGAC 354  
QY 51 PheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPhe 70  
Db 355 TAC-----CTG 360  
QY 71 ArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAen 90  
Db 361 TGTGCTCATCATGATGACGCCCTCTACATCAGT-----GTAATTAGACGACCTGCAT 414  
QY 91 SerAlaLeuGlyHisValAenSerThrIleLysGluLeuArgArgLeuPheLeuValAsp 110  
Db 415 GATGCCATGGGTTTCAGGAGTCTCTGATGAGGGTTGTCGGT-----CTG 456  
QY 111 AspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThr---TyrValGly 129  
Db 457 ---ATTGTGCCAAATCTGCTGCGCATTCCTTATCAATGTTTATAGTATTCAAACTATT 513  
QY 130 AlaLeuPheAsnGlyThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 148  
Db 514 TCCCTTATCAACTCTGACT---TTTGTCAATGCTCTTTTGGCCCTGATGTTATTCTGA 570  
QY 149 ProValIleTyrGlu---ArgHisGlnValGlnIleAspHis 161  
Db 571 CATACCTTGTATGAGGTTGAAAGAAATGAAATGTCACAT 612

## RESULT 55

US-09-107-433-2599  
; Sequence 2599, Application US/09107433  
; Patent No. 6800744  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-107-433-2599 (1-1275)  
QY 11 IleLysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrVal 30  
Db 277 ATTGCCAAATCAAAATCTGCTACGCTATTTTGACAGATTTCTGCTGTGCGCC 336  
QY 31 PheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSer 50  
Db 337 TTTTCATTAGTTTCAGTCATTATGATGTCATCATCAACCTCATCTCTGACACCTTGAC 396  
QY 51 PheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPhe 70  
Db 397 TAC-----CTG 402  
QY 71 ArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAen 90  
Db 403 TCTGCTCATCATGATGACGCCCTCTACATCAGT-----GTAATTAGACGACCTGCAT 456

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID  
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGN  
THERAPEUTICS  
NUMBER OF SEQUENCES: 5206  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: <Unknown>  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: <Unknown>  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,433  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/ 085131  
FILING DATE: May 12, 1998  
APPLICATION NUMBER: 60/051553  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Arinello, Pamela Deneka  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-011  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 2599:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1275 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus pneumoniae  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (B) LOCATION 1...1275  
SEQUENCE DESCRIPTION: SEQ ID NO: 2599:  
US-09-107-433-2599  
Alignment Scores:  
Pred. No.: 0.281 Length: 1275  
Score: 82.50 Matches: 38  
Percent Similarity: 47.40% Conservative: 35  
Best Local Similarity: 24.68% Mismatches: 50  
Query Match: 8.92% Indels: 31  
DB: 4 Gaps: 7

```

Qy 91 SerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAsp 110
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
457 GATGCCATGGGTTTCAGGCAGTCTCTGATGAGGTTGTCGGT----- 498

Qy 111 AspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThr---TyrValGly 129
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
499 ---ATTGTGCGCAATCTGGCTGGCGCATTCCTTATCAATGTTATTAAGTATTCAAACTATT 555

Qy 130 AlaLeuPheAnGlyLeuThrLeuLeuLeuAlaLeuLeuSerLeuPheSerIle--- 148
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
556 TCCCTTATCAACTCTGACT---TTTGTCAATGCTTTTGGGCTGTATGTTATTTCGA 612

Qy 149 ProValIleTyrGlu---ArgHisGlnValGlnIleAspHis 161
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
613 CATACCTTGTATGAGTTGAAAAAGAAATGAAATGTCACAT 654

RESULT 56
US-08-961-527-146
; Sequence 146, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 146:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1187 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-146

Alignment Scores:
Pred. No.: 10.3 Length: 1187
Score: 82.50 Matches: 38
Percent Similarity: 47.40% Conservative: 35
Best Local Similarity: 24.68% Mismatches: 50
Query Match: 8.92% Indels: 31
DB: 3 Gaps: 7

US-09-830-972-2_COPY_975_1163 (1-189) x US-08-961-527-146 (1-11887)

Qy 11 IleLysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrVal 30
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
9678 ATTGCCAAATCAAAATCCTGCTACGCTATTTCGACAGTATTTCGCTCTGTCGCC 9737

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Qy 31 PheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSer 50
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
9738 TTTTCATTAGTTTCAGTCATTATGATTCATCAACCTCATCTCTGACACCTTGAGC 9797

Qy 51 PheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPhe 70
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
9798 TAC-----CTG 9803

Qy 71 ArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAen 90
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
9804 TCTGCTACATGATGAAGCCCTCTACATCAGT-----GTAATTAGACGACCTGTCAT 9857

Qy 91 SerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAsp 110
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
9858 GATGCCATGGGTTTCAGGCAGTCTCTGATGAGGTTGTCGGT----- 9899

Qy 111 AspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThr---TyrValGly 129
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
9900 ---ATTGTGCGCAATCTGGCTGGCGCATTCCTTATCAATGTTATTAAGTATTCAAACTATT 9956

Qy 130 AlaLeuPheAnGlyLeuThrLeuLeuLeuAlaLeuLeuSerLeuPheSerIle--- 148
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
9957 TCCCTTATCAACTCTGACT---TTTGTCAATGCTTTTGGGCTGTATGTTATTTCGA 10013

Qy 149 ProValIleTyrGlu---ArgHisGlnValGlnIleAspHis 161
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
10014 CATACCTTGTATGAGTTGAAAAAGAAATGAAATGTCACAT 10055

RESULT 57
US-09-540-236-938
; Sequence 938, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 938
; LENGTH: 1845
; TYPE: DNA
; ORGANISM: M.catarrhalis
US-09-540-236-938

Alignment Scores:
Pred. No.: 0.599 Length: 1845
Score: 82.00 Matches: 35
Percent Similarity: 45.28% Conservative: 37
Best Local Similarity: 22.01% Mismatches: 59
Query Match: 8.86% Indels: 28
DB: 4 Gaps: 7

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-540-236-938 (1-1845)

Qy 33 IleValSerValThrAlaTyrIleAlaLeuAlaLeuLeu---SerValThrIleSerPhe 51
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
265 ATGTGCGAATCAGTCGATTCATTCCTGCTGGTGTGTTTGTGAAACACCATTCACCAT 324

Qy 52 ArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArg 71
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
325 CAGGTGCTACAGGAGTAGTA-----CCAAATGGGT 354

Qy 72 AlaTyrLeuGluSerGluValAlaIleSerGluLeuValGlnLysTyrSerAsnSer 91
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
355 TTACGCTGGATTTTTCATCAGCAAAATCTGGCCAGTCGATGCAATTTTATCAAGATCAA 414

Qy 92 AlaLeuGlyHisValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAsp 111
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
415 TTCTCTGCGCGTGTGTGAGCC-----AAGGTGATGCAAAACCGCTTTAGCGGTGCGTGT 468

Qy 112 LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrVal----- 128

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QY 127 -----TyrValGlyAlaLeuPheAsnGlyLeu----- 135  
Db 111000 TCCCAAGGATGGTGTGTGCAGATAGGTTCCATGTGCCAGGCTCTTGTTCAGTTTA 111059  
QY 136 -----ThrLeuLeuLeuAlaLeuLeuSerLeuPheSerIlePro 149  
Db 111060 GTGTATTATTCTGCCACACTTGTCTTAATTCAGATTGATTGCTTTTATATGAAGATA 111119  
QY 150 ValIleTyrGluArgHis 155  
Db 111120 GTAATATATGGAGGCAT 111137  
RESULT 60  
US-09-949-016-12412  
; Sequence 12412, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12412  
; LENGTH: 476044  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-12412  
Alignment Scores:  
Pred. No.: 4,63e+03 Length: 476044  
Score: 82.00 Matches: 46  
Percent Similarity: 38.71% Conservative: 26  
Best Local Similarity: 24.73% Mismatches: 48  
Query Match: 8.86% Indels: 66  
DB: 4 Gaps: 8  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-949-016-12412 (1-476044)  
QY 24 LeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAla 43  
Db 124072 CTACTTTGTCTAGTATCTAC-----ATTACACCGATTAACTTAATCAGT 124119  
QY 44 LeuLeu-----SerValThrIleSerPheArgIleTyrIlyGly 56  
Db 124120 GTCATGGTCTGCTAACTGATTAATTTGTCTGATTATTCATCCGATCTACAAAATG 124179  
QY 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76  
Db 124180 GTAATAACATA-----GGACATATTTTATAGGGCTATATATGTAAT 124221  
QY 77 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal 96  
Db 124222 -----GTATTAAATGAGAAAATCCTTCGATTATTCCTTAGCAGTGTGCTAGAACATGAA 124275  
QY 97 AsnSer-----ThrIleLysGluLeuArgArgLeuPheLeuValAsp 110  
Db 124276 AACTCTTAATAAGCTTGGCTATTAGTCTTGTCTGTAACCGTAAGACATGTTTCTGTCTTAT 124335  
QY 111 AspLeuValAspSerLeuLysPheAlaValLeuMetTrp----- 123  
Db 124336 CCCTGTGTATCCCACTTCTTTCGACAGAACTTGTGGCAGCAGATTAATCATAGAA 124395  
QY 124 -----ValPheThr----- 126

Db 124396 TTATTGAATAAAATAATAGTCCCACTTTTTCCTAGCTCCACTGTGTGGAAGTCTCAGAT 124455  
QY 127 -----TyrValGlyAlaLeuPheAsnGlyLeu----- 135  
Db 124456 TCCCAAGGATGGTGTGTGCAGATAGGTTCCATGTGCCAGGCTCTTGTTCAGTTTA 124515  
QY 136 -----ThrLeuLeuLeuAlaLeuLeuSerLeuPheSerIlePro 149  
Db 124516 GTGTATTATTCTGCCACACTTGTCTTAATTCAGATTGATTGCTTTTATATGAAGATA 124575  
QY 150 ValIleTyrGluArgHis 155  
Db 124576 GTAATATATGGAGGCAT 124593  
RESULT 61  
US-09-248-796A-730  
; Sequence 730, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA  
; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 730  
; LENGTH: 1152  
; TYPE: DNA  
; ORGANISM: Candida albicans  
US-09-248-796A-730  
Alignment Scores:  
Pred. No.: 0.329 Length: 1152  
Score: 81.50 Matches: 41  
Percent Similarity: 36.16% Conservative: 23  
Best Local Similarity: 23.16% Mismatches: 44  
Query Match: 8.81% Indels: 69  
DB: 4 Gaps: 7  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-248-796A-730 (1-1152)  
QY 13 LysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSer 32  
Db 91 AAAACTTCAATTGAATTCAATCAAAACACTC-----CTGACACTATTATT 135  
QY 33 IleValSerValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerPheArg 52  
Db 136 ATGATTTTCCTTAAGGCGAGTAATCGCACTATTCTTTTACCACCTAAATTTATTATTGT 195  
QY 53 IleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAla 72  
Db 196 TTAATCAAA-----TATCCATTT----- 213  
QY 73 TyrLeuGluSerGluValAlaIleSerGluLeuValGlnLysTyrSerAsnSerAla 92  
Db 213 ----- 213  
QY 93 LeuGlyHisValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeu 112  
Db 214 TTCGGGGGTGAACCCCTATATACAAG-----AATGATTG 249  
QY 113 ValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPhe 132  
Db 250 GTCAATTCCTTGAATTAACCGTT-----TAT 276  
QY 133 AsnGlyLeuThrLeuLeuIleAlaLeuLeuSerLeuPheSerIleProValIleTyr 152  
Db 277 CAAGCATTAATCAATTTCCCACTTGCATGATGATGATTTTTCATTA----- 324







Db 1610 AGAACCCAGCAATAGAGCTGACCATCTGGCTTACCACCTTTGTGTCTCCTCCCTGTTCTCG 1669  
QY 134 GlyLeuThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 153  
Db 1670 GCGTTGGACTAGCGACTGATTACTGCTGTGATCAITTCCTGCTGCTGCTGCTGCTGCTGCTG 1726  
QY 154 ArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAla 173  
Db 1727 -----AGAACCCAGCGAGTCCGAGTACAAGGTCCTGGGCGACGCTCCCTGACACCGCATGA 1780  
QY 174 MetAlaLysIleGlnAla-----LysIleProGlyLeuLys 185  
Db 1781 TACATGACATAGACCATATGAGGAGGTGAAGAAATTCCTGGATATAAA 1831  
RESULT 66  
US-08-545-528D-1  
; Sequence 1, Application US/08545528D  
; Patent No. 6537773  
; GENERAL INFORMATION:  
; APPLICANT: Fraser et al.  
; TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragment  
; FILE REFERENCE: PB193P1  
; CURRENT APPLICATION NUMBER: US/08/545,528D  
; CURRENT FILING DATE: 1995-10-19  
; PRIOR APPLICATION NUMBER: US 08/488,018  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: US 08/473,545  
; PRIOR FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; TYPE: DNA  
; ORGANISM: Mycoplasma genitalium  
US-08-545-528D-1  
Alignment Scores:  
Pred. No.: 8.79e+03 Length: 580073  
Score: 81.00 Matches: 45  
Percent Similarity: 42.42% Conservative: 39  
Best Local Similarity: 22.73% Mismatches: 72  
Query Match: 8.76% Indels: 42  
DB: 4 Gaps: 7  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-08-545-528D-1 (1-580073)  
QY 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22  
Db 17615 GTTGACTCAATATAT-----TCATTAAATTTACCACCAAAATTTA 17653  
QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerIleAlaTyrIleAlaLeu 42  
Db 17654 ATGTATTCAATAGGCTCACA-----ATTGTGAGGTAAGTCTTTTGTAGCTTAT 17704  
QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
Db 17705 GCATTAATCTTTGTTTAAATGTAGCGCAAAACTATGTAGG---ATTAACTTTACCAA 17761  
QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
Db 17762 CAAACATGTGCTACTTTGGTTGGAAGGCGATATTTAAATATGACAGTAGTATGCAACGAC 17821  
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102  
Db 17822 TTTTGTATACGCAAAATATGCTGATCTTATGAGTAGGTTAACTAATGATATGATATAAC 17881  
QY 103 LeuArgArgLeuPhe-----LeuValAspLeuValAspSerLeu 116  
Db 17882 ATTGATAACCTATTCACTCAAGCTGGTGACAGCTATTCAAAGTTTGTGTTAATATTTTA 17941  
QY 117 LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaPheAsnGlyLeuThr 136

Db 17942 ACAACTCAGTATTAATATTTTATTAAGCCAGTATTCACATT-----ATTCA 17992  
QY 137 LeuLeuIleLeuAlaLeuIleSerLeuPheSerIleProValIleTyrGluArg----- 154  
Db 17993 CTTTCAATTTTAGCTACATTAATTACTTTTCTTTTGGCTTTCTTAAGAAATCAAAACT 18052  
QY 155 -----HisGlnValGln----- 158  
Db 18053 TCATATAGTCAAGTACAAAATAATTTGGTGATATGTCGTGTTATATTGAAGAGGTTTTA 18112  
QY 159 -----IleAspHisTyrLeuGlyLeuAlaAsnLysSerValLysAsp 172  
Db 18113 ACTAATCATAGGTTGTTCATGCTCTTGAAGTTGCAAGAGATATGATTAGGAT 18166  
RESULT 67  
US-09-557-884-1  
; Sequence 1, Application US/09557884  
; Patent No. 6506581  
; GENERAL INFORMATION:  
; APPLICANT: Fleischmann et al.  
; TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments  
; Thereof, and Uses Thereof  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3 1/2 inch diskette  
; COMPUTER: Dell Pentium  
; OPERATING SYSTEM: MS DOS v6.22  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/557,884  
; FILING DATE: 25-Apr-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/476,102  
; FILING DATE: JUN-5-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Michelle S. Marks  
; REGISTRATION NUMBER: 41,971  
; REFERENCE/DOCKET NUMBER: PB186P3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-309-8504  
; TELEFAX: 301-309-8439  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1830121 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-557-884-1  
Alignment Scores:  
Pred. No.: 5.54e+04 Length: 1830121  
Score: 81.00 Matches: 61  
Percent Similarity: 33.71% Conservative: 29  
Best Local Similarity: 22.85% Mismatches: 80  
Query Match: 8.76% Indels: 97  
DB: 4 Gaps: 13  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-557-884-1 (1-1830121)  
QY 6 LeuTyrTrp-----ArgAspIleLysTyrThrGlyValValPheGlyAlaSerLeuPhe 23  
Db 37676 CTTATTTGGATTTTACAAACGCTAGCCATCACTCAGTCGCTCTTTAGTTTGGCATTTT 37735

```
Qy 24 LeuLeuLeuSerLeuThr----- 29
|||||:|:|
37736 CTTTGGTGGCGTTTACCAAGTGGGAAAAACAATTTTGGATGTTTGCAGCGGTATCTT 37795
Qy 30 -----ValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu 44
:|:|:|:|:|
37796 TCACCTAAACGATGACATTAACCTATCTTCTTCTGCTTATTTGTCATGACATTA 37855
Qy 45 LeuSerValThrIleSerPhe-----ArgIleTyrLysGlyValIleGlnAlaIle 61
|||||:|:|
37856 CTTAGCGTACGTATCAGCTTGTAAATCTGTAGTGTATATAAATATGTATACCTCATTTG 37915
Db 62 GlnLysSerAspGluGlyHisProPhe----- 70
|||||:|:|
37916 CAAGAATTAATGAA--CATGTATTTGGCAACAATGGGCTTATTCTGGCTCATCGCA 37972
Qy 71 -----ArgAlaTyrLeuGluSerGluValAlaIle----- 80
|||||:|:|
37973 GCAAGTTCTGTTTCAGCAGCATTAAGTATTTATTAGACCAACGTTTCGTATCAAC 38032
Db 81 -----SerGluGluLeuValGlnLys-----Tyr 88
|||||:|:|
38033 TGGATTGAATGCTTAACGACGCTTGTATAAATGATGGGCACATCGCGCCTATTATAC 38092
Qy 89 SerAsnSerAlaLeuGlyHis-----Val 96
|||||:|:|
38093 AAAACACAGTATTATATCAGAAAACTTGTATAACCCCGATCAACGTTATCAACAGATGTG 38152
Qy 97 AsnSerThrIleLysGluLeuArgLeuPhe-----LeuValAspLeuValAsp 114
|||||:|:|
38153 CAATCTTATGAAAAACACGCTTCTTTAAAGCACTGGCGCTCAITGTAGTGGCTCACCTCG 38212
Qy 115 SerLeuLysPheAlaValLeuMetTrp----- 123
|||||:|:|
38213 ATGATCTCTTACACGATTTGTATGATGGGATAGCCGCTCAAGATAGTGTGGTGTA 38272
Qy 124 -----ValPheThrTyrValGlyAlaLeuPheAsnGly 134
|||||:|:|
38273 GAAATTCGCATATGATGATATTTTATAGTGTGGTATGTC-----ATTTTCACACC 38326
Qy 135 LeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerIleProValIleTyrGluArg 154
|||||:|:|
38327 CTCATCGCATCTTGGCTGGTCGC---CCATTAATCTCATTTGAATTTTATTAATGAACGC 38383
Qy 155 HisGlnValGlnIleAspHisTyr-LeuGlyLeuAlaAsnLysSerValLysAspAlaIle 174
|||||:|:|
38384 CTAACGCAAACTAT---CGTTATCTTTAATTCGCATTAAGAATAATGTGGAAGCATT 38440
Qy 174 tAlaLysIleGlnAlaLys 180
:|:|:|:|:|
38441 GCTTTTATGAGGGGAA 38459
```

## RESULT 68

US-09-643-990A-1  
; Sequence 1, Application US/09643990A  
; Patent No. 6528289

## GENERAL INFORMATION:

APPLICANT: Robert D. Fleischmann  
Mark D. Adams  
Owen White  
Hamilton O. Smith  
J. Craig Venter

TITLE OF INVENTION: The Nucleotide sequence of  
the Haemophilus influenzae rd Genome, Fragments  
Thereof, and Uses Thereof

## NUMBER OF SEQUENCES: 1

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville,  
STATE: MD  
COUNTRY: USA

ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3 1/2 inch diskette  
COMPUTER: Dell Pentium  
OPERATING SYSTEM: MS DOS v6.22  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/643,990A  
FILING DATE: 23-Aug-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/487,429  
FILING DATE: 1995-06-07  
APPLICATION NUMBER: 08/426,787  
FILING DATE: 1995-04-21  
ATTORNEY/AGENT INFORMATION:  
NAME: Kenley K. Hoover  
REGISTRATION NUMBER: 40,302  
REFERENCE/DOCKET NUMBER: PB186P1C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-610-5790  
TELEFAX: 310-309-8439  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1830121 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-643-990A-1

## Alignment Scores:

Pred. No.:	5.54e+04	Length:	1830121
Score:	81.00	Matches:	61
Percent Similarity:	33.71%	Conservative:	29
Best Local Similarity:	22.85%	Mismatches:	80
Query Match:	8.76%	Indels:	97
DB:	4	Gaps:	13

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-643-990A-1 (1-1830121)

```
Qy 6 LeuTyrTrp-----ArgAspIleLysThrGlyValValPheGlyAlaSerLeuPhe 23
|||||:|:|
37676 CTTATTTGGATTTTACAAACGCTAGCCATCACCTCAGTCGCTCTTTAGTTTGGCATTTT 37735
Qy 24 LeuLeuLeuSerLeuThr----- 29
|||||:|:|
37736 CTTTGTGGCGTTTATCCCAATGGGAAAAACAATTTTGGATGTTTGCAGCGGTATCTT 37795
Qy 30 -----ValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu 44
:|:|:|:|:|
37796 TCACCTAAACGATGACATTAACCTATCTTATCTTCTGCTTATTTGTCATGACATTA 37855
Qy 45 LeuSerValThrIleSerPhe-----ArgIleTyrLysGlyValIleGlnAlaIle 61
|||||:|:|
37856 CTTAGCGTACGTATCAGCTTGTAAATCTGTAGTGTATATAAATATGTATACCTCATTTG 37915
Qy 62 GlnLysSerAspGluGlyHisProPhe----- 70
|||||:|:|
37916 CAAGAATTAATGAA---CATGTATTTGGCAACAATGGGCTTATTCTGGCTCATCGCA 37972
Qy 71 -----ArgAlaTyrLeuGluSerGluValAlaIle----- 80
|||||:|:|
37973 GCAAGTTCTGTTTCAGCAGCATTAAGTATTTATTAGACCAACGTTTCGTATCAAC 38032
Qy 81 -----SerGluGluLeuValGlnLys-----Tyr 88
|||||:|:|
38033 TGGATTGAATGCTTAACGACGCTTGTATAAATGATGGGCACATCGCGCCTATTATAC 38092
Qy 89 SerAsnSerAlaLeuGlyHis-----Val 96
|||||:|:|
38093 AAAACACAGTATTATATCAGAAAACTTGTATAACCCCGATCAACGTTATCAACAGATGTG 38152
```

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QY 97 AsnSerThrIleLysGluLeuArgLeuPhe-----LeuValAspSerLeuValAsp 114
Db 38153 CAATCTTATGTAACCAACCGCTTTCTTTAAGACACTGGCGTCATTGATCGGTCACTCG 38212
QY 115 SerLeuLysPheAlaValLeuMetTrp----- 123
Db 38213 ATGACTCTTACAGCATTTTGTATGGGATTAAGCGGTCCCAATGATAGTGTGTTGTA 38272
QY 124 -----ValPheThrTyrValGlyAlaLeuPheAsnGly 134
Db 38273 GAAATTCGCATATGATGATATTTTAGTGTGTTGTTATGTC-----ATTTTCAAC 38326
QY 135 LeuThrLeuLeuLeuLeuLeuLeuSerLeuPheSerIleProValIleTyrGluArg 154
Db 38327 CTCATCGCATTCGGCTCGGTGCG-----CCATTAAATCTCAATGAATTTTAATGAACG 38383
QY 155 HisGlnValGlnIleAspHisTyr-LeuGlyLeuAlaAsnLysSerValLysAspAlaMe 174
Db 38384 CTAAACGCAACTAT---CGTTATCTTTTAATTCGCATTAAAGAAATATGCTGAAGCAT 38440
QY 174 talalysIleGlnAlaLys 180
Db 38441 GCTTTTATGCAGGCGAAA 38459

RESULT 69
US-09-583-110-2219
; Sequence 2219, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 2219
; LENGTH: 759
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-2219

Alignment Scores:
Pred. No.: 0.232 Length: 759
Score: 80.50 Matches: 49
Percent Similarity: 38.73% Conservative: 30
Best Local Similarity: 24.02% Mismatches: 62
Query Match: 8.70% Indels: 63
DB: 4 Gaps: 10

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-583-110-2219 (1-759)
QY 1 SerValValAspLeu---LeuTyrTrpArgAspIleLysLysThrGlyValValPheGly 19
Db 157 TCAATAGTATCACTACCTCTATATCTGTGAAAAATAAATAGTATCTATCTGTCTAGCC 216
QY 20 AlaSerLeuPheLeuLeuLeuSerLeuThrValPhe-----Ser 32
Db 217 ATAAATTCGATTCGTGTAATAGTGTTCCTCCATTTTAATCAATAAGTTTTTCCAGAAAGT 276
QY 33 IleValSerValThrAlaTyrIleAlaLeuLeuSerValThrIleSerPheArg 52
Db 277 TTTTGGACATTACCGTATTAATAGTGTTTTATCTAGATTAGCAATCTTCAATTA 336
QY 53 Ile-----TyrLysGlyValIleGlnAlaIle 61
Db 337 ATTGGGAAGATTTTGTCTACTAAATGACTAAAGAAATAAAGAAATAGTCAGTTTGA 396
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QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 397 AGCAAGGTGTCCTCACTCT---CCTTGATAAAATATTTAGAG-----ATTTCT 441
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGly-----HisVal--- 96
Db 442 AGTTTATATACTATATATTTCCATCTATTTCTTTATGGTACAGTTGATAATCATGTACTG 501
QY 97 -----AsnSerThrIleLysGluLeu----- 103
Db 502 ACTCTTATCTTTTTCATAAAAATTTGTCAGATACACAGATAAAATTTTATTCATCAGA 561
QY 104 -----ArgArgLeuPheLeuValAspSerLeuValAsp 114
Db 562 TTATTTGCACACAAGTACTTTAATGAAGAGGAGATATTTTCTT----- 606
QY 115 SerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPhe----- 132
Db 607 -----TTGCAATGATGATGATATAGTTACTTATTTTATAGGATATCTTTTAGTGATT 657
QY 133 -----AsnGlyLeuThrLeuLeuLeuAlaLeuIleSerLeuPheSerIleProVal 150
Db 658 CAAAAAGCAGGCTATTTGTTTCGGTTTTACTTCTTTTCTTAATTTTTCAGTTCATTT 717
QY 151 IleTyrGluArg 154
Db 718 ATCAAGAAAG 729

RESULT 70
US-09-107-433-2215
; Sequence 2215, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; TITLE OF INVENTION: SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 2215:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
```

```
;
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...774
; SEQUENCE DESCRIPTION: SEQ ID NO: 2215:
US-09-107-433-2215

Alignment Scores:
Pred. No.: 0.24 Length: 774
Score: 80.50 Matches: 49
Percent Similarity: 38.73% Conservative: 30
Best Local Similarity: 24.02% Mismatches: 62
Query Match: 8.70% Indels: 63
DB: 4 Gaps: 10

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-107-433-2215 (1-774)
Qy 1 SerValValAspLeu---LeuTyrTrpArgAspIleLysLysThrGlyValValPheGly 19
Db 172 TCATAGATGCTACCTCTATCTCTGTAATAAATAAGTATCTCTGTCTAGCC 231
Qy 20 AlaSerLeuPheLeuLeuSerLeuThrValPhe-----Ser 32
Db 232 ATAAATTCGATTCGTCTAATGAGTTCCCATTTTAAATCAATAAGTTTCCAGAAAGT 291
Qy 33 lleValSerValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerPheArg 52
Db 292 TTTTGGACTTATACCGTATTAATAAGTCTTTTATCCTAGAGTTAGCAATCTTTCATT 351
Qy 53 lle-----TyrLysGlyValIleGlnAlaIle 61
Db 352 ATTCGGGAGAGATTTTGCTACTATAATGACTAAGCAATATAGAAATTAGTCAGTTTGA 411
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 412 AGCAAGGTGCTCAATCT---CCTTGGATAAAATATTAGAG-----ATTCT 456
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGly-----HisVal--- 96
Db 457 AGTTTATATTAATACTATATTTCCATCTATTTCTTATGCTACAGTTTGAATAATCATG 516
Qy 97 -----AenSerThrIleLysGluLeu----- 103
Db 517 ACTCTTATCTTTTGCATAAAATTTGTGCAGATACCCAGCAAAATTTTATTCATCAGA 576
Qy 104 -----ArgArgLeuPheLeuValAspLeuValAsp 114
Db 577 TTATTTGACACAGTACTTTAATGAGAGGAGATAATTTTCTT----- 621
Qy 115 SerLeuLysPheAlaValLeuMetTrpValPheThrValGlyAlaLeuPhe----- 132
Db 622 -----TTGCAATTCGATGTTATAGTTTACTTATTTTAGGATATCTTTTAGTGATT 672
Qy 133 -----AsnGlyLeuThrLeuLeuIleAlaLeuIleSerLeuPheSerIleProVal 150
Db 673 CAAAGAGGAGCTATTGTTTTCGGTTTACTTCTTTTCTTCTTCTTCTTCTTCTTCTTCT 732
Qy 151 IleTyrGluArg 154
Db 733 ATCAAGAAAG 744

RESULT 71
US-08-853-659A-28
; Sequence 28, Application US/08853659A
; Patent No. 5925522
; GENERAL INFORMATION:
; APPLICANT: Wong, K.K.; Safer, J.D.
; TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
; TITLE OF INVENTION: Of A
; TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella

;
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Paul W. Zimmerman
; ADDRESSEE: Intellectual Property Services
; ADDRESSEE: Battelle Memorial Institute
; ADDRESSEE: PNNL P.O. Box 999
; CITY: Richland
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 99352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (WordPerfect 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/853.659A
; FILING DATE: Unknown
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
; FILING DATE: n/a
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1797 bases
; TYPE: nucleotide
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: the coding nucleotides of SEQ ID
; OTHER INFORMATION: NO:28 correspond to nucleotides 22630 through
; OTHER INFORMATION: 24426 of SEQ ID NO:2
US-08-853-659A-28

Alignment Scores:
Pred. No.: 0.932 Length: 1797
Score: 80.50 Matches: 36
Percent Similarity: 41.24% Conservative: 37
Best Local Similarity: 20.34% Mismatches: 71
Query Match: 8.70% Indels: 33
DB: 2 Gaps: 6

US-09-830-972-2_COPY_975_1163 (1-189) x US-08-853-659A-28 (1-1797)
Qy 8 TrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu 26
Db 487 TGGATGAGTTTCAGAAATTTAAACCCGTTTATTAAACTCGATCTTTCAACGTATAGCC 546
Qy 27 SerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu----- 44
Db 547 GATATTCATATTTATATATATTTCTCATCTGTTATATATGTAATTTAGGTCGTGTTGTT 606
Qy 45 -----LeuSerValThrIleSerPheArgIleTyrLysGly 56
Db 607 ATTGTACTATTACCAGTTTATCGTCTCTATTTATTTCCCTCGTTAACCCATTAT 666
Qy 57 ValIleGlnAlaIleGlnLysSerAspGlyHisProPheArgAlaTyrLeuGluSer 76
Db 667 ACTAATGAGTTTAATGAACAAACAAAGAGGACAGAAACACGGAATATTTTATCTCA 726
Qy 77 GluValAlaIleSerGluLeuValGlnLysTyrSerAsnSerAlaLeu----- 93
Db 727 GAAGTTTCTTATCTATTAATATGATCCATACCTTAATAATATCAAGTTTACTTTTGTAT 786
Qy 94 -----GlyHisValAsnSerThrIleLysGluLeuArg 105
Db 787 TGGGTTAATACATCAATGAACAGTCGTATCTTAACCTGAAGATAAGAAATTAATCTT 846
Qy 106 LeuPhe-----LeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 123
Db 847 ATCTATCAATCTATATTGGGAGTATGTCATCTATTACCCAAATAACTATTATTGTAATA 906
```

```
QY 124 ValPheThrTyrVal-----GlyAlaLeuPheAsnGlyLeuThr 136
Db 907 GCCTTTTATGATCAAGGGTGATGTACTACTGGCGCAATTGTTTCATCTGTCA 966
QY 137 Leu-----LeuLeuAlaLeuLeuSerLeuPheSerIleProValIle 151
Db 967 GTCCTGGCGGATATTCGGGATCAITTCGAATTTTCTTACATTAAATC 1017

RESULT 72
US-08-853-659A-6
; Sequence 6, Application US/08853659A
; Patent No. 5925522
; GENERAL INFORMATION:
; APPLICANT: Wong, K.K.; Saffer, J.D.
; TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
; TITLE OF INVENTION: Of A
; TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Paul W. Zimmerman
; ADDRESSEE: Intellectual Property Services
; ADDRESSEE: Battelle Memorial Institute
; ADDRESSEE: PNNL P.O. Box 999
; STREET: Washington Way
; CITY: Richland
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 99352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (WordPerfect 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/853,659A
; FILING DATE: Unknown
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
; FILING DATE: n/a
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8967 bases
; TYPE: nucleotide
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: SEQ ID NO:6 corresponds to
; OTHER INFORMATION: nucleotides 15735 through 24701 of SEQ ID NO:2
US-08-853-659A-6

Alignment Scores:
Pred. No.: 12.4 Length: 8967
Score: 80.50 Matches: 36
Percent Similarity: 41.24% Conservative: 37
Best Local Similarity: 20.34% Mismatches: 71
Query Match: 8.70% Indels: 33
DB: 2 Gaps: 6

US-09-830-972-2_COPY_975_1163 (1-189) x US-08-853-659A-6 (1-8967)
QY 8 TrpArgAspIleIysIysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu 26
Db 7382 TCGAATGAGTTTCAGAAAAATTAACCCGTTTATTAAATCGATCTTTCAACGTATAGCC 7441
QY 27 SerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu----- 44
Db 7442 GATATTCGAATATTATTATATTCTCATGTGTATATGTAATTTAGTCTGGTGTGT 7501
QY 45 -----LeuSerValThrIleSerPheArgIleTyrIysGly 56
Db 7502 ATTGTACCTATTACCAGTGTATTCGTCCTATTATTATTTCCCTCGTGAACCACTTAT 7561
```

```
QY 57 ValIleGlnAlaIleGlnIysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76
Db 7562 ACTAATGAGTTAATGAACAAACAAAGAGACAGACAGAAATATTTTATCTCA 7621
QY 77 GluValAlaIleSerGluGluLeuValGlnIysTyrSerAsnSerAlaLeu----- 93
Db 7622 GAAGTTTCTTATCTATTAAATGATCCATACCTTAAATATCAAGGTTTACTTTTGTAT 7681
QY 94 -----GlyHisValAsnSerThrIleLysGluLeuArg 105
Db 7682 TGGGTTAATACATCAATGAACAGTCGTATCTTAACTGAAGATAAGAAATTAATCTT 7741
QY 106 LeuPhe-----LeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 123
Db 7742 ATCTATCAATCTATATTCGGGAGTATCATCTATTACCCAAATAACTATTATGTAATA 7801
QY 124 ValPheThrTyrVal-----GlyAlaLeuPheAsnGlyLeuThr 136
Db 7802 GCCTTTTATGCGTAATCAAGGTGATGTACTACTGGCGCAATGTTTCATCTGTCA 7861
QY 137 Leu-----LeuIleLeuAlaLeuLeuSerLeuPheSerIleProValIle 151
Db 7862 GTCTCTGGCGGATTTTCGGGATCATTTTCGAATTTTCTTCTACATTAAATC 7912

RESULT 73
US-08-853-659A-9/c
; Sequence 9, Application US/08853659A
; Patent No. 5925522
; GENERAL INFORMATION:
; APPLICANT: Wong, K.K.; Saffer, J.D.
; TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
; TITLE OF INVENTION: Of A
; TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Paul W. Zimmerman
; ADDRESSEE: Intellectual Property Services
; ADDRESSEE: Battelle Memorial Institute
; ADDRESSEE: PNNL P.O. Box 999
; STREET: Washington Way
; CITY: Richland
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 99352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (WordPerfect 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/853,659A
; FILING DATE: Unknown
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
; FILING DATE: n/a
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8967 bases
; TYPE: nucleotide
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; US-08-853-659A-9

Alignment Scores:
Pred. No.: 12.4 Length: 8967
Score: 80.50 Matches: 36
Percent Similarity: 41.24% Conservative: 37
Best Local Similarity: 20.34% Mismatches: 71
Query Match: 8.70% Indels: 33
DB: 2 Gaps: 6

US-09-830-972-2_COPY_975_1163 (1-189) x US-08-853-659A-9 (1-8967)
```

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Qy 8 TrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu 26
Db 1586 TGGATGAGTTTCAGAAATTAACCCGTTTATTAACTCGATCTTCAACGATAGCC 1527
Qy 27 SerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu----- 44
Db 1526 GATATTCGAATATTATTATATTTCTCATTTGTTATATATGTAATAATTTAGGTCGTGTTGTT 1467
Qy 45 -----LeuSerValThrIleSerPheArgIleTyrIysGly 56
Db 1466 ATTGTACTATTACCATGTTTATCGTCTCTATTATTATTTCCCTCGTTAAACCATATTAT 1407
Qy 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76
Db 1406 ACTAATGAGTTTAATGAACACAAACAAAGAGGACAGACAGAGCAAGATATTTTATCTCA 1347
Qy 77 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeu----- 93
Db 1346 GAAGTGTTCCTTATCTATTATAAATGATCATACCTTAAATAATCAAGGTTTACTTTTGTAT 1287
Qy 94 -----GlyHisValAsnSerThrIleLysGluLeuArg 105
Db 1286 TGGGTTAATACATAAATGAACAGTCGTATCTTAACTTGAAGATAAGAAATTAATCTT 1227
Qy 106 LeuPhe-----LeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 123
Db 1226 ATCTATCAATCTATATTCGGGAGTATGTCATCTATTACCCAAATAACTATTATGGTAATA 1167
Qy 124 ValPheThrTyrVal-----GlyAlaLeuPheAsnGlyLeuThr 136
Db 1166 GCCTTTTATGTTAATCAAGGGTGATGTTACTACTGCGCAATTTGTTTCATCTGTCATT 1107
Qy 137 Leu-----LeuLeuLeuAlaLeuIleSerLeuPheSerIleProValIle 151
Db 1106 GTCTCTGCGGTATTTCCGGGATCATTTTCGAATTTTCTTCTACATTAAATC 1056

RESULT 74
US-08-853-659A-64
; Sequence 64, Application US/08853659A
; Patent No. 5925522
; GENERAL INFORMATION:
; APPLICANT: Wong, K.K.; Saffer, J.D.
; TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
; TITLE OF INVENTION: Of A
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Paul W. Zimmerman
; ADDRESSEE: Intellectual Property Services
; ADDRESSEE: Battelle Memorial Institute
; ADDRESSEE: PNNL P.O. Box 999
; STREET: Washington Way
; CITY: Richland
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 99152
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (WordPerfect 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/853.659A
; FILING DATE: Unknown
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
; FILING DATE: n/a
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8967 bases
; TYPE: nucleotide

```

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; STRANDEDNESS: single stranded
; TOPOLOGY: linear
US-08-853-659A-64
Alignment Scores:
Pred. No.: 12.4 Length: 8967
Score: 80.50 Matches: 36
Percent Similarity: 41.24% Conservative: 37
Best Local Similarity: 20.34% Mismatches: 71
Query Match: 8.70% Indels: 33
DB: 6

US-09-830-972-2_COPY_975_1163 (1-189) x US-08-853-659A-64 (1-8967)
Qy 8 TrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu 26
Db 7382 UGGAUGAGUUUCAGAAAUUUAACCCGUUUUUUAUUAACUCGCUUUUUAACGAGUUUAGCC 7441
Qy 27 SerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu----- 44
Db 7442 GAUAUCCAAUUAUUAUUAUUCUCAUUGUAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7501
Qy 45 -----LeuSerValThrIleSerPheArgIleTyrIysGly 56
Db 7502 AUUGUACCUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 7561
Qy 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76
Db 7562 ACUAUAGAGUUUAUGAACAAACAAAGAGGACAGAGAACAGAAUUAUUUUUAUUAUUAUUA 7621
Qy 77 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeu----- 93
Db 7622 GAAGUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7681
Qy 94 -----GlyHisValAsnSerThrIleLysGluLeuArg 105
Db 7682 UGGGUUAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 7741
Qy 106 LeuPhe-----LeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 123
Db 7742 AUCUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 7801
Qy 124 ValPheThrTyrVal-----GlyAlaLeuPheAsnGlyLeuThr 136
Db 7802 GCCUUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7861
Qy 137 Leu-----LeuLeuLeuAlaLeuIleSerLeuPheSerIleProValIle 151
Db 7862 GUCUCUGCGGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7912

RESULT 75
US-08-853-659A-67/c
; Sequence 67, Application US/08853659A
; Patent No. 5925522
; GENERAL INFORMATION:
; APPLICANT: Wong, K.K.; Saffer, J.D.
; TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
; TITLE OF INVENTION: Of A
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Paul W. Zimmerman
; ADDRESSEE: Intellectual Property Services
; ADDRESSEE: Battelle Memorial Institute
; ADDRESSEE: PNNL P.O. Box 999
; STREET: Washington Way
; CITY: Richland
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 99152
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
; COMPUTER: IBM PC/XT/AT

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; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (WordPerfect 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/853,659A
; FILING DATE: Unknown
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
; FILING DATE: n/a
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8967 bases
; TYPE: nucleotide
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; US-08-853-659A-67

Alignment Scores:
Pred. No.: 12.4 Length: 8967
Score: 80.50 Matches: 36
Percent Similarity: 41.24% Conservative: 37
Best Local Similarity: 20.34% Mismatches: 71
Query Match: 8.70% Indels: 33
DB: 2 Gaps: 6

US-09-830-972-2_COPY_975_1163 (1-189) x US-08-853-659A-67 (1-8967)

QY 8 TpaArgAspIleLysThrGlyValPheGlyAlaSerLeuPhe---LeuLeuLeu 26
Db 1586 TGAATGAGTTTCAGAAATAAACCCTTTTATTAACTCGATCTTCAACGTATAGCC 1527
QY 27 SerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu----- 44
Db 1526 GATATTCGAATATTATTATTTCTCATTTGTTATATATGTAATTTAGGTTCTGGTTGTT 1467
QY 45 -----LeuSerValThrIleSerPheArgIleTyrLysGly 56
Db 1466 ATGTGACCTATTACCATGTTTATGCTCTCTATTATTATTTCTCTGCTTAACCACTTAT 1407
QY 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76
Db 1406 ACTAATGAGTTAATGAACAAACAAAGAGGACAGAGAACAGGAATATTTTATCTCA 1347
QY 77 GluValAlaIleSerGluLeuValGlnLysTyrSerAsnSerAlaLeu----- 93
Db 1346 GAAGTTTCTTCTATTAAATGATCCATACCTTAAATTAATCAAGGTTTACTTTTGTAT 1287
QY 94 -----GlyHisValAsnSerThrIleLysGluLeuArgArg 105
Db 1286 TGGGTTAATACATCAATGAACAGTCGTATCTTAACTGAAGATAGGAATTAATCTT 1227
QY 106 LeuPhe-----LeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTyr 123
Db 1226 ATCTATCAATCTATATTGGGAGTATGTCATCTATTACCAAAATAACTATTATGGTAATA 1167
QY 124 ValPheThrTyrVal-----GlyAlaLeuPheAsnGlyLeuThr 136
Db 1166 GCCTTTTGTGTAATCAAGGGTGATGTTACTACTGCGGCAATGTTTCTCATCTGTCATT 1107
QY 137 Leu-----LeuIleLeuAlaLeuIleSerLeuPheSerIleProValIle 151
Db 1106 GTCTCTGGCGGATTTCCGGGATCATTTTCAATTTTCTTCTACATTAATC 1056

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## RESULT 76

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US-08-853-659A-2
; Sequence 2, Application US/08853659A
; Patent No. 5925522
; GENERAL INFORMATION:
; APPLICANT: Wong, K.K.; Saffer, J.D.
; TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
; TITLE OF INVENTION: Of A
; TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
; NUMBER OF SEQUENCES: 67

```

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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Paul W. Zimmerman
; ADDRESSEE: Intellectual Property Services
; ADDRESSEE: Battelle Memorial Institute
; ADDRESSEE: PNNL P.O. Box 999
; STREET: Washington Way
; CITY: Richland
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 99352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (WordPerfect 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/853,659A
; FILING DATE: Unknown
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
; FILING DATE: n/a
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24701 bases
; TYPE: nucleotide
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; US-08-853-659A-2

Alignment Scores:
Pred. No.: 63.7 Length: 24701
Score: 80.50 Matches: 36
Percent Similarity: 41.24% Conservative: 37
Best Local Similarity: 20.34% Mismatches: 71
Query Match: 8.70% Indels: 33
DB: 2 Gaps: 6

US-09-830-972-2_COPY_975_1163 (1-189) x US-08-853-659A-2 (1-24701)

QY 8 TpaArgAspIleLysThrGlyValPheGlyAlaSerLeuPhe---LeuLeuLeu 26
Db 23116 TGAATGAGTTTCAGAAATAAACCCTTTTATTAACTCGATCTTCAACGTATAGCC 23175
QY 27 SerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu----- 44
Db 23176 GATATTCGAATATTATTATTTCTCATTTGTTATATATGTAATTTAGGTTCTGGTTGTT 23235
QY 45 -----LeuSerValThrIleSerPheArgIleTyrLysGly 56
Db 23236 ATGTGACCTATTACCATGTTTATGCTCTCTATTATTATTTCTCTGCTTAACCACTTAT 23295
QY 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76
Db 23296 ACTAATGAGTTAATGAACAAACAAAGAGGACAGAGAACAGGAATATTTTATCTCA 23355
QY 77 GluValAlaIleSerGluLeuValGlnLysTyrSerAsnSerAlaLeu----- 93
Db 23356 GAAGTTTCTTCTATTAAATGATCCATACCTTAAATTAATCAAGGTTTACTTTTGTAT 23415
QY 94 -----GlyHisValAsnSerThrIleLysGluLeuArgArg 105
Db 23416 TGGGTTAATACATCAATGAACAGTCGTATCTTAACTGAAGATAGGAATTAATCTT 23475
QY 106 LeuPhe-----LeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTyr 123
Db 23476 ATCTATCAATCTATATTGGGAGTATGTCATCTATTACCAAAATAACTATTATGGTAATA 23535
QY 124 ValPheThrTyrVal-----GlyAlaLeuPheAsnGlyLeuThr 136
Db 23536 GCCTTTTGTGTAATCAAGGGTGATGTTACTACTGCGGCAATGTTTCTCATCTGTCATT 23595
QY 137 Leu-----LeuIleLeuAlaLeuIleSerLeuPheSerIleProValIle 151

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Qy   94  -----GlyHisValasnSerThrIleLysGluLeuArg 105
Db    1286 TGGGTTAATACATCAAAATGAACAGTCGTATCTTTAAACCTGAAGATAAAGAAATTAAAAATCTT 1227
Qy   106 LeuPhe-----LeuValAspAspLeuAlaSpSerLeuLysPheAlaValLeuMetTrp 123
Db    1226 ATCTATCAATCTATATTTGGGAGTAGTGTCATCTATTACCCTAACATAACTATTATGGTAATA 1167
Qy   124 ValPheThrTyrrVal-----GlyAlaLeuPheAsnGlyLeuThr 136
Db    1166 GCCTTTTTTATGTAATCAAGGGTGATGTTACTACTGGCGCAATTGTTTCATCTGTGCATT 1107
Qy   137 Leu-----LeuIleLeuAlaLeuIleSerLeuPheSerIleProValIle 151
Db    1106 GTCTCTGCCGTATTTCCGGGATCATTTCCGAATTTTCTTCTACATTAATC 1056

RESULT 78
US-08-853-659A-60
; Sequence 60, Application US/08853659A
; Patent No. 5925522
; GENERAL INFORMATION:
; APPLICANT: Wong, K.K.; Saffer, J.D.
; TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
; TITLE OF INVENTION: Of A
; TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Paul W. Zimmerman
; ADDRESSEE: Intellectual Property Services
; ADDRESSEE: Battelle Memorial Institute
; ADDRESSEE: PNNL P.O. Box 999
; STREET: Washington Way
; CITY: Richland
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 99352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (WordPerfect 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/853,659A
; FILING DATE: Unknown
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
; FILING DATE: n/a
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24701 bases
; TYPE: nucleotide
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
US-08-853-659A-60

Alignment Scores:
Pred. No.:      63.7      Length:      24701
Score:          80.50     Matches:       36
Percent Similarity: 41.24% Conservative: 37
Best Local Similarity: 20.34% Mismatches: 71
Query Match:     8.70% Indels: 33
DB:              Gaps: 6

US-09-830-972-2_COPY_975_1163 (1-189) x US-08-853-659A-60 (1-24701)

Qy   8 TrpArgAspIleLysThrGlyValAlaPheGlyAlaSerLeuPhe---LeuLeuLeu 26
Db    23116 UGGAUUGAGUUUCAGAAAUAUUAACCGUUUUUAUUAACCUCAUCAUUCACGUAGGCC 23175
Qy   27 SerLeuThrValPheSerIleValSerValThrAlaTyrlleAlaLeuAlaLeu----- 44
Db    23176 GAUUAUCCAUAUAUAUAUAUAUUUCAUUGUUAUAUAUGUAAAUUAUUGAGUCUGUGUUUU 23235

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QY 45 -----LeuSerValThrIleSerPheArgIleTyrIysGly 56
DB 23236 AUUGUACCUUAUACCAUGUUUAUUGCUCUUAUUUCCUGCUUAACCAUUAU 23295
QY 57 ValIleGlnAlaIleGlnIysSerAspGluGlyHisProPheArgAlaTyrIleGluSer 76
DB 23296 ACUAUGAGUUUAUGAACCAACAAAGAAAGGACAGAAACAGGAAUUAUUUUAUCUCA 23355
QY 77 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeu----- 93
DB 23356 GAAGUUUUUAUCUAUUUAUAAUGAACCAUUAUUAUUAUUAUUAUUAUUAUUAU 23415
QY 94 -----GlyHisValAsnSerThrIleLysGluLeuArgArg 105
DB 23416 UGGUUUAUUAUCAACAAAGAACAGUGCUUAUUAUUAUUAUUAUUAUUAUUAUUAU 23475
QY 106 LeuPhe-----LeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTTP 123
DB 23476 AUCUAUCAUUAUUAUUGGGAGUAUGUAUCUAUUAUUAUUAUUAUUAUUAUUAUUAU 23535
QY 124 ValPheThrTyrVal-----GlyAlaLeuPheAsnGlyLeuThr 136
DB 23536 GCCUUUUUAUGUAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 23595
QY 137 Leu-----LeuIleLeuAlaLeuIleSerLeuPheSerIleProValIle 151
DB 23596 GUCUCUGCGUAUUUCCGCGUAUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 23646

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## RESULT 79

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US-08-853-659A-61/c
; Sequence 61, Application US/08853659A
; Patent No. 5925522
; GENERAL INFORMATION:
; APPLICANT: Wong, K.K.; Saffer, J.D.
; TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
; TITLE OF INVENTION: Of A
; TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Paul W. Zimmerman
; ADDRESSEE: Intellectual Property Services
; ADDRESSEE: Battelle Memorial Institute
; ADDRESSEE: PNNL P.O. Box 999
; STREET: Washington Way
; CITY: Richland
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 99352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (WordPerfect 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/853,659A
; FILING DATE: Unknown
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
; FILING DATE: n/a
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24701 bases
; TYPE: nucleotide
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
US-08-853-659A-61

```

```

Alignment Scores:
Pred. No.: 63.7 Length: 24701
Score: 80.50 Matches: 36
Percent Similarity: 41.24% Conservative: 37

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```

Best Local Similarity: 20.34% Mismatches: 71
Query Match: 8.70% Indels: 33
DB: 2 Gaps: 6
US-09-830-972-2_COPY_975_1163 (1-189) x US-08-853-659A-61 (1-24701)
QY 8 TrpArgAspIleLysIysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu 26
DB 1586 TGGAAATGATTTTCAGAAAATTAACCCGTTTATTAAATCGATCTTTCAACGTATAGCC 1527
QY 27 SerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu----- 44
DB 1526 GATATTCCAATATTTATTATTTCTCATTTATATATATATATATATATATATATATAT 1467
QY 45 -----LeuSerValThrIleSerPheArgIleTyrIysGly 56
DB 1466 ATTGTACCTATTACCATTGTTTATCGTCTCTATTATTATTTCCCTCGTTAACCACTAT 1407
QY 57 ValIleGlnAlaIleGlnIysSerAspGluGlyHisProPheArgAlaTyrIleGluSer 76
DB 1406 ACTAATGATGTTAATGAACAAACAAAGAGGACAGAAAGCAAGAAATATTTTATCTCA 1347
QY 77 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeu----- 93
DB 1346 GAAGTTTCTTATCTATTAAATGATCCATACCTTAATATATCAAGTTTACTTTTGTAT 1287
QY 94 -----GlyHisValAsnSerThrIleLysGluLeuArgArg 105
DB 1286 TGGGTTAATACATCAATGAACAGTCGTATCTTAACCTGAAGATAAGGAAATTAATCTT 1227
QY 106 LeuPhe-----LeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTTP 123
DB 1226 ATCTATCAATCTATATTGGGGAGTATGTCATCTATTACCAATATCACTATTATGGTAATA 1167
QY 124 ValPheThrTyrVal-----GlyAlaLeuPheAsnGlyLeuThr 136
DB 1166 GCCTTTTTCGTTAATCAAGGGTGTACTACTGCGCAATTTGTTTCATCTGTCATT 1107
QY 137 Leu-----LeuIleLeuAlaLeuIleSerLeuPheSerIleProValIle 151
DB 1106 GTCTCTGCGCGTATTTCGCGGATCATTTTCGAATTTTCTTCTACATTATATC 1056
RESULT 80
US-09-247-373B-47/c
; Sequence 47, Application US/09247373B
; Patent No. 6168954
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEFE, DANIEL
; TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
; FILE REFERENCE: CL-1108-A
; CURRENT APPLICATION NUMBER: US/09/247,373B
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 08/924,747
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 47
; LENGTH: 859
; TYPE: DNA
; ORGANISM: SOYBEAN
US-09-247-373B-47
Alignment Scores:
Pred. No.: 0.333 Length: 859
Score: 80.00 Matches: 40
Percent Similarity: 38.92% Conservative: 25
Best Local Similarity: 23.95% Mismatches: 50
Query Match: 8.65% Indels: 52
DB: 3 Gaps: 9
US-09-830-972-2_COPY_975_1163 (1-189) x US-09-247-373B-47 (1-859)

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Db 707 TTATACATCTTGAATTAAGTGAATCTTCACTTTTTTAAATAATAATAATAATTAATTAAT 648
Qy 23 PheLeuLeuSerLeuThrVal----- 30
Db 647 TTTCATATATTAGTTTACCAATACGATATTCATCATTTTATTAAAGTTATGTAATAA 588
Qy 31 -----PheSerIleValSerValThrAlaTyriIleAlaLeuAlaLeuSer 46
Db 587 TCAGTTAAATCATCTTTTCAATAAAGCTCTAGGAATCATCTGCCATAATTTTATT--- 531
Qy 47 ValThrIleSerPheArgIleTyriLysGlyValIleGlnAlaIleGlnLysSerAspGlu 66
Db 530 ATAAAAATGATTTTAAATATATGCCTATAAAGATACAGATTTTAAA-----AACAA 477
Qy 67 GlyHisProPheArgAlaTyriLeuGluSerGluValAlaIleSerGluGluLeuValGln 86
Db 476 AGACACTTATACAAATGTTT-----GAATCATGTGTTT 444
Qy 87 LysTyriSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArgGlu 106
Db 443 AAATACAGTAATTTATCATTAATGAATAATTAAGTTTACAAATAAGTAAAGTTATCCAGTAC 384
Qy 107 PheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThr 126
Db 383 TTGTGATA-----ATTAATATCATAAAGTTTATCAATCTTTTAAATAGCACTTACA 333
RESULT 85
US-09-540-236-99
; Sequence 99, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; NUMBER OF SEQ. ID NOS: 2000-04-04
; SEQ ID NO 99
; LENGTH: 870
; TYPE: DNA
; ORGANISM: M. catarrhalis
US-09-540-236-99
Alignment Scores:
Pred. No.: 0.47 Length: 870
Score: 79.00 Matches: 16
Percent Similarity: 60.87% Conservativity: 12
Best Local Similarity: 34.78% Mismatches: 14
Query Match: 8.54% Indels: 4
Gaps: 1
Db:
US-09-830-972-2_COPY_975_1163 (1-189) x US-09-540-236-99 (1-870)
Qy 120 ValLeuMetTrpValPheThrTyriValGlyAlaLeu-----PheAsnGlyLeu 135
Db 577 GTCATCGCTGGCTAAATCCAAATCCAGCATTTAATCTACGCAATTCAGCAATTCAGCGGTG 636
Qy 136 ThrLeuLeuIleAlaLeuIleSerLeuPheSerIleProValIleTyriGluArgHis 155
Db 637 GTGACTACTCATATCAGGATAGCAAGTGCCTTTAGCATACCAATCATGCAAAATTACAT 696
Qy 156 GlnValGlnIleAspHis 161
Db 697 GCGTCACGCGCAACAT 714
RESULT 86
US-09-252-991A-11432
; Sequence 11432, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 11432
; LENGTH: 936
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11432
Alignment Scores:
Pred. No.: 0.529 Length: 936
Score: 79.00 Matches: 40
Percent Similarity: 41.32% Conservativity: 29
Best Local Similarity: 23.95% Mismatches: 56
Query Match: 8.54% Indels: 42
Gaps: 8
Db:
US-09-830-972-2_COPY_975_1163 (1-189) x US-09-252-991A-11432 (1-936)
Qy 15 GlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIleVal 34
Db 467 GCGCGGTGTTCCGCAAG-----CTGATCGAGCTGGCGGCTTCTCCGCTCC 514
Qy 35 SerValThrAlaTyriIleAlaLeu-----AlaLeuSerValThrIle 49
Db 515 ATCTGCGCGGCGGCGATCCGCTGTCGGCACCCGCGGCGATGTCGGCATGCTACTG 574
Qy 50 -----SerPheArgIleTyriLysGly-----ValIleGlnAlaIleGln 62
Db 575 GTCTGCGCGTGTCTACCTACGCGCGGCTCTGCTGTTGTTGTTGTTGTTGTTGTTGTTG 631
Qy 63 LysSerAspGluGlyHisProPheArgAlaTyriLeuGluSerGluValAlaIleSerGlu 82
Db 632 -----TACCCGTTCCGCGGAGATGTTCCGCCAGACGATCCCCAAG 676
Qy 83 GluLeuValGlnLysTyriSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102
Db 677 CGATTGATTCG-----GCAGACCATCGCCCTCGCGGCGGTTTCTCTCCATGACGCG 730
Qy 103 LeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122
Db 731 CTGCCCGGCAACCCCGCAGATCCAGAACATCATCCCTCGACCTTCTTCGGCACCCACGCC 790
Qy 123 TrpValPheThrTyriValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeuAlaLeu 142
Db 791 TGGCGCGGCGCTGCTGCGGAGCC-----CTCGCGCGG 823
Qy 143 IleSerLeuPheSerIleProValIleTyriGluArgHisGlnValGlnIleAspHisTyri 162
Db 824 CTGTTGCTCTCGCGGTGGGCTGCTCTACTCTGCGACGCCAG----- 865
Qy 163 LeuGlyLeuAlaAsnLysSer 169
Db 866 -----GCGAACAAGGCG 877
RESULT 87
US-09-252-991A-11439/c
; Sequence 11439, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
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Db 952 ATCTATAACAACACCATGGCCAC---GTGCACAGCCACTTCGACGGAGAGGTGTTGGG 1008  
Qy 79 AlalieserGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAenSer 98  
Db 1009 GCTGTCCTGGCCGACGAGACGGAGTTTTCACACAGAACACGACAGGTAACATCATGTCT 1068  
Qy 99 ThrilleysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPhe 118  
Db 1069 CGGGTAACAGAG---GACACGTCACCCCTGAGTGATCTCTGAGTGAGAACTG----- 1119  
Qy 119 AlavalLeuMetTrpValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeu 138  
Db 1120 AGCTTTATCTGTGTAC-----CTGGTCGAGGCGCTATGTCCTCTG 1161  
Qy 139 -----lLeuAlaLeuLeuSerLeuPheSerileProVal 150  
Db 1162 GGGATCATGCTCGGGATCATGTCCTCACCATGGTCACCCCTGATCACCCTGCTCTG 1221  
Qy 151 lletyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAenLysSerVal 170  
Db 1222 CTTTTCCTTCGCCCAAG---AAGGTGGGAAATGGTACCAGTTGCTCGAAGTGCAGGTG 1278  
Qy 171 LysAepAlaMetAlaLys 176  
Db 1279 CGGGAATCTCTGGCAAG 1296

## RESULT 93

US-09-585-858-1

; Sequence 1, Application US/09585858

; Patent No. 6492161

; GENERAL INFORMATION:

; APPLICANT: Sigridur Hjordleifsdottir

; APPLICANT: Gudmundur O. Hreggvidsson

; APPLICANT: Olafur H. Fridjonsson

; APPLICANT: Arnthor Aevartsson

; APPLICANT: Jakob K. Kristjansson

; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic

; FILE REFERENCE: 2739.1001-001

; CURRENT APPLICATION NUMBER: US/09/585,858

; CURRENT FILING DATE: 2000-12-18

; PRIOR APPLICATION NUMBER: 60/137,120

; PRIOR FILING DATE: 1999-06-02

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 129908

; TYPE: DNA

; ORGANISM: Bacteriophage RM378

US-09-585-858-1

Alignment Scores:  
Pred. No.: 1.77e+03 Length: 129908  
Score: 78.50 Matches: 41  
Percent Similarity: 41.62% Conservative: 36  
Best Local Similarity: 22.16% Mismatches: 61  
Query Match: 8.49% Indels: 47  
DB: 4 Gaps: 8

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-585-858-1 (1-129908)

Qy 8 TrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu----- 22  
Db 18117 TGGGAGGATCCAACTTCGGGACCACTTCGGGTGCCAATCTTATCAGCGTATCTCC 18176  
Qy 23 -----PheLeuLeuLeuSerLeuThrValPheSerile 33  
Db 18177 TTGTGTTACTGGATACCCGAAACAGTTTTCTTGCTATAGCTTTCGTTTACTCT--- 18233  
Qy 34 ValSerValThrAlaTyriLeAlaLeuAlaLeuLeuSerValThrileSerPheArgile 53  
Db 18234 GCTTCGCCGCAACCTAT-----CTTAACCTTAATGATGCTTACAGAAAT 18278

Qy 54 TyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyr 73  
Db 18279 TACGTAGGAACATTTTCGGCACCCCGCAATGGGAAGTTGGTTTACCGGTAGTTTCAGG 18338  
Qy 74 LeuGluSerGluValAlaIleSerGluGlu-----LeuValGlnLysTyrSer 89  
Db 18339 GTTTCGTCCGCTTCAATTTCTCACAAACGTTTTCAGGATTTTACTTCTTCTTAACATT 18398  
Qy 90 AenSerAlaLeuGlyHisValAenSerThr----- 99  
Db 18399 GATAGTCACCTTAATTTACTATATTACTACGTTTCAGCGCACCAGCATTCGCCTCACATTCA 18458  
Qy 100 lLelysGluLeuArgLeuPheLeuValAspLeu-----ValAspSer 115  
Db 18459 TTTCAAGTTATCAGGAAATATATGAGTTGAGCCACTTTCTGCTTACACAGTACCGTCT 18518  
Qy 116 LeuLysPheAlaValLeuMet-----TrpValPheThrTyrVal 128  
Db 18519 ATCGTGTGTTTCTACACGGTTTCAGTACTAACAGCTTCGGGTGGAGCTATTCCAATATA 18578  
Qy 129 -----GlyAlaLeuPheAenGlyLeuThrLeuLeuLeuAlaLeuLeuSerLeuPhe 146  
Db 18579 GAAATGGGGTCTCTTACAGAAATATCAACTATATGTCATTCTAAGTTATCTTACCCCTAC 18638  
Qy 147 SerileProValIle 151  
Db 18639 ACGGCACCGGCTATA 18653

## RESULT 94

US-10-270-878-1

; Sequence 1, Application US/10270878

; Patent No. 6818425

; GENERAL INFORMATION:

; APPLICANT: Sigridur Hjordleifsdottir

; APPLICANT: Gudmundur O. Hreggvidsson

; APPLICANT: Olafur H. Fridjonsson

; APPLICANT: Arnthor Aevartsson

; APPLICANT: Jakob K. Kristjansson

; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic

; FILE REFERENCE: 2739.1001-001

; CURRENT APPLICATION NUMBER: US/10/270,878

; CURRENT FILING DATE: 2002-10-11

; PRIOR APPLICATION NUMBER: US/09/585,858

; PRIOR FILING DATE: 2000-12-18

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 129908

; TYPE: DNA

; ORGANISM: Bacteriophage RM378

US-10-270-878-1

Alignment Scores:  
Pred. No.: 1.77e+03 Length: 129908  
Score: 78.50 Matches: 41  
Percent Similarity: 41.62% Conservative: 36  
Best Local Similarity: 22.16% Mismatches: 61  
Query Match: 8.49% Indels: 47  
DB: 4 Gaps: 8

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-270-878-1 (1-129908)

Qy 8 TrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu----- 22  
Db 18117 TGGGAGGATCCAACTTCGGGACCACTTCGGGTGCCAATCTTATCAGCGTATCTCC 18176  
Qy 23 -----PheLeuLeuLeuSerLeuThrValPheSerile 33  
Db 18177 TTGTGTTACTGGATACCCGAAACAGTTTTCTTGCTATAGCTTTCGTTTACTCT--- 18233  
Qy 34 ValSerValThrAlaTyriLeAlaLeuAlaLeuLeuSerValThrileSerPheArgile 53



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Db 277 GAGATGAATAAGCCGATTTAATAGCTTACTGCTCTTTCCTATTGCGTTTCCCATCTGTA 336
Qy 54 ---TyrLeuGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAla 72
Db 337 TTGTATAAAGAAACACCTACGCAATTCGCAAGATGGGATGGTGTCTATTCGCCATGGGT 396
Qy 73 TyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAla 92
Db 397 TTATTG-----GTGATTATGCAAGAGATTGGTGCAGTATTAT----- 435
Qy 93 LeuGlyHisValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeu 112
Db 436 TTGGAATATACGAAATATTTTGGCTTTTACAGAAAGATCAGTTGGCGCAT----- 489
Qy 113 ValAspSerLeuLysPheAlaValLeu-----MetThrVal 124
Db 490 ---AGAGAAATCTCTATGCTCTGCTATTTCCTTCTTATATATGTCCTTATGGGCA 546
Qy 125 PheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSer 144
Db 547 TTGAAAAAATCATTCGATAATTAATTGGCTTTTATTAAAGTGTGTAGCTATTATT 606
Qy 145 LeuPheSerIle 148
Db 607 TTATTGCAATC 618

RESULT 97
US-09-795-927-6
; Sequence 6, Application US/09795927
; Patent No. 6531309
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James A.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Revelli, Jean-Pierre
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6531309el Human Transporter Proteins and Polynucleotides Enc
; FILE REFERENCE: Same
; CURRENT APPLICATION NUMBER: US/09/795,927
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/185,956
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 2913
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-795-927-6

Alignment Scores:
Pred. No.: 4.56 Length: 2913
Score: 78.00 Matches: 48
Percent Similarity: 42.71% Conservative: 37
Best Local Similarity: 24.12% Mismatches: 68
Query Match: 8.43% Indels: 46
DB: 4 Gaps: 10

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-795-927-6 (1-2913)
Qy 21 SerLeuPheLeuLeuLeu-----SerLeuThrValPheSerIle 33
Db 1102 AGCTCCTTCTGCTCATATTTCTGGGCAAGAGATTGCCAGTCTTCAACATTACAGTGC 1161
Qy 34 ValSerValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerPhe----- 51
Db 1162 AATTCACACAGGATTAAATGACCATCGGCTTTCGAATGTCGTCAATTCATTTCAGA 1221
Qy 52 -----ArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAsp 65
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Db 1222 TCTTGTGTGTTTACTGGTGCTATTGCTAGGACTATTATCCAG-----GATAAATCTGGA 1275
Qy 66 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuVal 85
Db 1276 GGAAGACAAACAGTTTGCATCTCTGTAGCGCAGGTGTGATGCTGCTC-----CTGATG 1329
Qy 86 GlnLysTyrSerAsnSerAlaLeuGlyHis----- 95
Db 1330 GTGAAG-----ATGGGACACTTTTCTACACACTGCCAAATGCTGTGCTG 1374
Qy 96 -----ValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAspAsp 111
Db 1375 GCTGTATTATTCTGAGCAACGCTCATCTCCCTACCTTGAACCAATTTCTAACCTACCCAGC 1434
Qy 112 LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeu 131
Db 1435 CTGTGGAGGCGAGGACCAATATGACTGTGCTCTTTGGATGATGACATTTCTCATCTTCAATT 1494
Qy 132 PheAsnGlyLeuThrLeu---LeuIleLeuAlaLeuIleSerLeuPheSerIleProVal 150
Db 1495 TTCTGGGACTGGACATTTGGACTAATTAATCTCAGTAGTTTCTGCTTCTTCATCACCCT 1554
Qy 151 IleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsn----- 167
Db 1555 GTT---CGTTCACACAGAGCTAAGATTCTCTCTGGGTCAAATCCCTAACACCAACATT 1611
Qy 168 ---LysSerValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 185
Db 1612 TATAGAAGCATCAATGATTATCGGAGATCATC-----ACCATTTCTCTGGGTGAAA 1662

RESULT 98
US-09-328-352-932
; Sequence 932, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 932
; LENGTH: 3162
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-932

Alignment Scores:
Pred. No.: 5.2 Length: 3162
Score: 78.00 Matches: 34
Percent Similarity: 39.51% Conservative: 30
Best Local Similarity: 20.99% Mismatches: 54
Query Match: 8.43% Indels: 44
DB: 4 Gaps: 6

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-328-352-932 (1-3162)
Qy 5 LeuLeuTyrTrpArgAspIleLysLysThrGlyValValPhe----- 18
Db 2734 ATGATTCAGCTGAAGAGTTTGTCTCGGCAACAATTTGATTTTGTGCTGACCATTAGGC 2793
Qy 19 -----GlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerVal 36
Db 2794 TTAATTCGCGTGTGTTTATTTCTTACTTCTTATTAATAAACCAATTTGGTTTGTGCCATG 2853
Qy 37 ThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGly 56
Db 2854 CTAGAACCACTTCCTTATCCGGCATGATTAATGCGTAACCTCACTCATCTCTG----- 2904
Qy 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76
```



Alignment Scores:  
Pred. No.: 8.1 Length: 4162  
Score: 78.00 Matches: 44  
Percent Similarity: 39.42% Conservative: 38  
Best Local Similarity: 21.15% Mismatches: 66  
Query Match: 8.43% Indels: 60  
DB: 3 Gaps: 10

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-453-702B-259 (1-4162)

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QY 7 TyrTrp-----ArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22
Db 2364 TTCTGGAGTCTTTCGCTAAAGACTGGCGGCTACGCGATATTATGTCGCTCACTG 2423
QY 23 -----PheLeuLeuSerLeuThrValPheSer-----Ile 33
Db 2424 GTGGCGAAGCTGCTGGCTGGCGGCGATGATTTCTCGATGACGGTTTACGATCGGGTG 2483
QY 34 ValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerPheArgIle 53
Db 2484 GTTCGGGCGCAATCGTACCGGACGCTATGGTGCTT----- 2519
QY 54 TyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyr 73
Db 2520 TTCGCGGGGTGATGATGCGGATCCTGTTGAGTTCTGTATGCGCATGTCGTACGCAT 2579
QY 74 LeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeu 93
Db 2580 CTATCTGATGTGATCGGAAGCGGCGACACCTG-----CGTATTTTCGATCGCGT 2633
QY 94 GlyHis-----ValAsnSerThrIleLys 101
Db 2634 GGTCAATCGCTACGCTGAATAACACGTCGATCGAATCCACCGGATCGTTTATCTCG 2693
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSer----- 115
Db 2694 CAGATCCGGAACCTGGAATCAGTCGGGAGCTTATTAGTCCACCACCATCGGCGCGTG 2753
QY 116 -----LeuLysPheAlaValLeuMetTropValPheThrTyrValGly 129
Db 2754 GCGGACCTGCCATTCTTCTGCTGTTTGTCTTTATTGTTGGATG----- 2798
QY 130 AlaLeuPheAsnGlyLeuThrLeuIleLeuAlaLeuIleSerLeuPheSerIlePro 149
Db 2799 ---ATCGGCGGCTGGCTGGTGTGTTGTTGCTGGCGCTGCCGTTGCTGGTATCCCC 2855
QY 150 ---ValIleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsnLys 168
Db 2856 GGCCTGCTGTGTCAACGCCGCTGGCGCG-----CTGGCGAAGCAA 2897
QY 169 SerValLysAspAlaMetAlaLys 176
Db 2898 GGAATGCGGAGTCAGCGGTACGC 2921
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Job time : 1635.5 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 19, 2005, 03:56:06 ; Search time 445.5 Seconds  
(without alignments)  
2633.504 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 6054689 seqs, 3103772919 residues

Total number of hits satisfying chosen parameters: 12109378

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-MINLEN=0 -MAXLEN=2000000000  
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-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA.\*  
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22: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	925	100.0	4684	9	US-09-893-348-17	Sequence 17, Appl
2	925	100.0	4684	20	US-10-810-653-17	Sequence 17, Appl
3	922	99.7	2782	15	US-10-205-194-165	Sequence 165, App
4	908	98.2	600	21	US-10-956-157-9764	Sequence 9764, Ap
5	908	98.2	1400	21	US-10-956-157-9763	Sequence 9763, Ap
6	908	98.2	2883	21	US-10-956-157-4529	Sequence 4529, Ap
7	908	98.2	3478	21	US-10-956-157-4528	Sequence 4528, Ap
8	908	98.2	3579	9	US-09-789-386-1	Sequence 1, Appli
9	908	98.2	3579	9	US-09-893-348-22	Sequence 22, Appl
10	908	98.2	3579	18	US-10-267-502-212	Sequence 212, App
11	908	98.2	3579	19	US-10-327-213-8	Sequence 8, Appli
12	908	98.2	3579	19	US-10-466-258-8	Sequence 8, Appli
13	908	98.2	3579	20	US-10-810-653-22	Sequence 22, Appl
14	908	98.2	4053	9	US-09-758-140-5	Sequence 5, Appli
15	908	98.2	4053	9	US-09-972-599A-5	Sequence 5, Appli
16	908	98.2	4053	19	US-10-717-597-310	Sequence 310, App
17	908	98.2	4623	21	US-10-956-157-4532	Sequence 4532, Ap
18	908	98.2	4632	14	US-10-060-036-53	Sequence 53, Appl
19	906.5	98.0	3492	18	US-10-267-502-214	Sequence 214, App
20	904	97.7	799	18	US-10-660-946-2	Sequence 2, Appli
21	904	97.7	1122	9	US-09-789-386-5	Sequence 5, Appli
22	904	97.7	1160	14	US-10-175-523-156	Sequence 156, App
23	904	97.7	1609	21	US-10-956-157-4527	Sequence 4527, Ap
24	904	97.7	1610	9	US-09-765-205-5	Sequence 5, Appli
25	904	97.7	1610	21	US-10-347-669-5	Sequence 5, Appli
26	904	97.7	1785	17	US-10-439-388-62	Sequence 62, Appl
27	904	97.7	1785	21	US-10-956-157-1705	Sequence 1705, Ap
28	904	97.7	2050	21	US-10-956-157-4530	Sequence 4530, Ap
29	904	97.7	2052	19	US-10-466-258-3	Sequence 3, Appli
30	904	97.7	2226	21	US-10-956-157-4531	Sequence 4531, Ap
31	898	97.1	2235	14	US-10-060-036-54	Sequence 54, Appl
32	898	97.1	1980	17	US-10-220-891-22	Sequence 22, Appl
33	895	96.8	994	11	US-09-978-360A-110	Sequence 110, App
34	891	96.3	2610	18	US-10-641-643-382	Sequence 382, Appl
35	864	93.4	1798	18	US-10-466-258-10	Sequence 10, Appl
36	849	91.8	1400	21	US-10-956-157-9765	Sequence 9765, Ap
37	844	91.2	1514	9	US-09-823-245A-349	Sequence 349, App
38	782	84.5	1400	21	US-10-956-157-9762	Sequence 9762, Ap
39	782	84.5	1400	21	US-10-956-157-9767	Sequence 9767, Ap
40	695	75.1	1400	21	US-10-956-157-9766	Sequence 9766, Ap
41	679	73.4	1520	15	US-10-084-817-333	Sequence 333, App
42	679	73.4	2331	18	US-10-267-502-213	Sequence 213, App
43	679	73.4	3202	9	US-09-954-456-210	Sequence 210, App
44	679	73.4	3202	17	US-10-172-118-386	Sequence 386, App
45	679	73.4	3202	18	US-10-342-887-386	Sequence 386, App

ALIGNMENTS

RESULT 1  
US-09-893-348-17  
; Sequence 17, Application US/09893348  
; Patent No. US20020072493A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN, Irun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SCHWARTZ-2A  
; CURRENT APPLICATION NUMBER: US/09/893,348  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161

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; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 4684
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (253)..(3744)
; OTHER INFORMATION:
US-09-893-348-17

Alignment Scores:
Pred. No.: 1.29e-101 Length: 4684
Score: 925.00 Matches: 189
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-893-348-17 (1-4684)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
DB 3175 TCAGTTGTTGACCTCTCTACTGGAGAGACATTAAGAGACCTGGAGTGTGTTGGTCC 3234

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 3235 AGCTTATTCCTGCTGCTCTGACAGTGTTCAGCATTTGTCAGTGTAAAGCGCTACATT 3294

QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
DB 3295 GCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGT 3354

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 3355 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATA 3414

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
DB 3415 TCAGAGGAATGGTTCAGAAATACAGTAATTCCTGCTTGGTCATGTAACAGCAATA 3474

QY 101 LysGluLeuArgGluLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaVal 120
DB 3475 AAAGAACTGAGCGCGCTTTCTTAGTTGATGATTTAGTTGATTCCTGAAAGTTGCAAGT 3534

QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
DB 3535 TTGATGTGGGTGTTTACTTATGTTGTCCTGTTGTTCAATGGTCTGACACTACTGATTATA 3594

QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
DB 3595 GCTCTGATCTCACTTCTCAGTATTCCTGTTATTAAGCGCATCAGTCAGTCAGATAGAT 3654

QY 161 HisTyrLeuGlyLeuAlaIleLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
DB 3655 CATTTATCAGGACTTCGAAACAAGAGTGTAAAGGATGCGATGCGCAAAATCCAAAGCAAA 3714

QY 181 IleProGlyLeuLysArgLysAlaAsp 189
DB 3715 ATCCCTGGATTGAAGCGCAAGCAGAT 3741
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## RESULT 2

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US-10-810-653-17
; Sequence 17, Application US/10810653
; Publication No. US20040253218A1
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; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR US-
; FILE REFERENCE: EIS-SCHWARTZ-2A
; CURRENT APPLICATION NUMBER: US/10/810,653
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US/09/893,348
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 4684
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (253)..(3744)
; OTHER INFORMATION:
US-10-810-653-17

Alignment Scores:
Pred. No.: 1.29e-101 Length: 4684
Score: 925.00 Matches: 189
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-810-653-17 (1-4684)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
DB 3175 TCAGTTGTTGACCTCTCTACTGGAGAGACATTAAGAGACCTGGAGTGTGTTGGTCC 3234

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 3235 AGCTTATTCCTGCTGCTCTGACAGTGTTCAGCATTTGTCAGTGTAAAGCGCTACATT 3294

QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
DB 3295 GCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGT 3354

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 3355 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATA 3414

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
DB 3415 TCAGAGGAATGGTTCAGAAATACAGTAATTCCTGCTTGGTCATGTAACAGCAATA 3474

QY 101 LysGluLeuArgGluLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaVal 120
DB 3475 AAAGAACTGAGCGCGCTTTCTTAGTTGATGATTTAGTTGATTCCTGAAAGTTGCAAGT 3534

QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
DB 3535 TTGATGTGGGTGTTTACTTATGTTGTCCTGTTGTTCAATGGTCTGACACTACTGATTATA 3594

QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
DB 3595 GCTCTGATCTCACTTCTCAGTATTCCTGTTATTAAGCGCATCAGTCAGTCAGATAGAT 3654

QY 161 HisTyrLeuGlyLeuAlaIleLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
DB 3655 CATTTATCAGGACTTCGAAACAAGAGTGTAAAGGATGCGATGCGCAAAATCCAAAGCAAA 3714

QY 181 IleProGlyLeuLysArgLysAlaAsp 189
DB 3715 ATCCCTGGATTGAAGCGCAAGCAGAT 3741
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Qy		161	HistyrLeuGlyLeuAlaAsnLysSerValIysAspAlaMetAlatylsileGinAlaLys	180
Dd		3655	CATTATCTAGACATTGCAAAACAAGAGTGTTAAGGATCCCATGGCCAATAATCCAAGCAAAA	3714
Qy		181	IleProGlyLeuLysArgLysAlaAasp	189
Dd		3715	ATCCTCGGATTGAAGCGCAAAGCACAGAT	3741

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RESULT 3
US-10-205-194-165
; Sequence 165, Application US/10205194
; Publication No. US20030134301A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnock, Robert
; TITLE OF INVENTION: Identification and Use
; FILE REFERENCE: WL-A-018201
; CURRENT APPLICATION NUMBER: US/10/205,194
; CURRENT FILING DATE: 5200-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 165
; LENGTH: 2782
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Foccen-m2 reticulon
US-10-205-194-165

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Alignment Scores:		
Pred. No.:	1.33e-101	Length:
Score:	922.00	Matches:
Percent Similarity:	100.00%	Conservative:
Best Local Similarity:	99.47%	Mismatches:
Query Match:	99.68%	Indels:
DB:	15	Gaps:
		0
		0
		2782

US-09-830-972-2 COPY 975 1163 (1-189) x US-10-205-194-165 (1-2782)

Qy	1	SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla	20
Db	1271	GAAGTTGTTGACCTCTCTACTCGAGAGACATTAAAGAAGACTCGAGTGGTGTGGTGCC	1330
Qy	21	SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	1331	AGCTTATTTCTGCTGCTGCTCTGACACAGTGTTCAGCAATTGTCAGTGTAAAGCGGCTACATT	1390
Qy	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
Db	1391	GCCTTGGCCCTGCTCTCGTGACTATCAGCTTTAGGATATATAAGGCGGTGATCCAGGCT	1450
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
Db	1451	ATCCAGAAATCAGATGAAGGCCACCCATTCAAGGCGCATTTATTAGAAATCTGAAGTTGCTATA	1510
Qy	81	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValIleAsnSerThrIle	100
Db	1511	TCAGAGGAAATGGTTCAGAATAACAGTAATCTTGCTCTTGGTCATGTGAACACACACAATA	1570
Qy	101	LysGluLeuLeuArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal	120
Db	1571	AAAGAAGTCAAGCGCGCTTTTCTTAGTTGATGATTATTAGTTCCCTGAAAGTTTGAGTG	1630
Qy	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
Db	1631	TTGATGTGGGTGTTTACTTATGTTGGTGGCTCTGTTCAAATGGCTGCACACTACTGATTTTATA	1690

Qy	141	AlaLeuIleSerLeuPheSerIleProValIleTyrClnuArgHisGlnValGlnIleAsp	160
Db	1691	GCTCTGATCTCATCTCTTCAGTATCTCTGTTATTATGACGGCATCAGGTGCAGATAGAT	1750
Qy	161	HisTyrIleuGlyIleuAlaAsnLysServAllyAspAlaMetAlaIleGlnAlaLys	180
Db	1751	CATTATCTAGGACTTGCAACAAGAGTGTAAAGATGCCATGGCCAAATCCAGCAANA	1810
Qy	181	IleProGlyIleuLysArgLysAlaAsp	189
Db	1811	ATCCCTTGGATTGAAGCGCAAGACAGAT	1837

## RESULT 4

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US-10-956-157-9764
; Sequence 9764, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS A
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9764
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-9764

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Alignment Scores:	6.17e-101	Length:	600
Pred. No.:	908.00	Matches:	184
Score:	98.94%	Conservative:	3
Percent Similarity:	97.35%	Mismatches:	2
Best Local Similarity:	98.16%	Indels:	0
Query Match:	21	Gaps:	0
DB:			

US-09-830-972-2 COPY 975 1163 (1-189) x US-10-956-157-9764 (1-600)

Qy	1	SerValValAspLeuLeuTyrTrpArgAspIleIysLysThrGlyValValPheGlyAla	20
Db	31	TCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGCC	90
Qy	21	SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	91	AGCCTATTCTCGTCGCTTTCATTGACAGTATTTCAGCATTTGTGAGGCTAACGCCCTACATT	150
Qy	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
Db	151	GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTTAGTATATACAAGGGTGTGATCCAAGCT	210
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
Db	211	ATCCAGAAATCAGATGAAGGCCGCCCATTCAGGGGCGATATCTGGAATCTGAAAGTTGCTATA	270
Qy	81	SerGluLeuLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle	100
Db	271	TCTGAGGAGTTGGTTCAGNAGTACAGTAATTTCTGCTCTTGGTCATGTGNACTGCACGATA	330
Qy	101	LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal	120
Db	331	AAGGAACCTCAGGCGCCCTCTCTTAGTTGATGATTAGTTAGTTGATTTCTCTGAAGTTTGCAGTG	390
Qy	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
Db	391	TTGATGTGGGTATTACCTATGTTGGGCCCTTGTTTAATGGTCTGCACACTCTGATTTTG	450
Qy	141	AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp	160
Db	451	GCTCTCATTTTCATCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGT	510

QY 161 HisTyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 511 CATTATCTAGGACTTCAAAATAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAA 570  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
Db 571 ATCCCTGGATTGAAGCGCAAGCTGAA 597

## RESULT 5

US-10-956-157-9763  
; Sequence 9763, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9763  
; LENGTH: 1400  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-956-157-9763

Alignment Scores:  
Pred. No.: 2,33e-100 Length: 1400  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 21 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-956-157-9763 (1-1400)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 488 TCAGTTGTTGACCTCTGCTGACGAGACATTTAAGACATGAGCTGGTGTGGTGCC 547  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 548 AGCCTATTCTGCTGCTTTTCATTGACAGTATTTCAGCATTTGTGAGCGTAAACGCTACATT 607  
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 608 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCT 667  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 668 ATCCAGAAATCAGATGAAGCCACCCATTTCAGGCGATATCTGGAATCTGAAGTTGCTATA 727  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
Db 728 TCTGAGGAGTTGGTTTCAGAAAGTACAGTAATCTGCTCTTGGTTCATGTGAAGTTCACGATA 787  
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 788 AAGAACTCAGGCGCTCTCTTCTAGTTAGTATTTAGTATTTAGTATTTAGTATTTAGTATTTAGT 847  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 848 TTGATGTGGGTATTTACCTATGTTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 907  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db 908 GCTCTCATTTTCACTCTCTGAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 967  
QY 161 HisTyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180

Db 968 CATTATCTAGGACTTCAAAATAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAA 1027  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
Db 1028 ATCCCTGGATTGAAGCGCAAGCTGAA 1054

## RESULT 6

US-10-956-157-4529  
; Sequence 4529, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4529  
; LENGTH: 2883  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-956-157-4529

## Alignment Scores:

Pred. No.: 7.22e-100 Length: 2883  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 21 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-956-157-4529 (1-2883)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 2314 TCAGTTGTTGACCTCTGCTGACGAGACATTTAAGACATGAGCTGGTGTGGTGCC 2373  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 2374 AGCCTATTCTGCTGCTTTTCATTGACAGTATTTCAGCATTTGTGAGCGTAAACGCTACATT 2433  
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 2434 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCT 2493  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 2494 ATCCAGAAATCAGATGAAGCCACCCATTTCAGGCGATATCTGGAATCTGAAGTTGCTATA 2553  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
Db 2554 TCTGAGGAGTTGGTTTCAGAAAGTACAGTAATCTGCTCTTGGTTCATGTGAAGTTCACGATA 2613  
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 2614 AAGAACTCAGGCGCTCTCTTCTAGTTAGTATTTAGTATTTAGTATTTAGTATTTAGTATTTAGT 2673  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 2674 TTGATGTGGGTATTTACCTATGTTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2733  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db 2734 GCTCTCATTTTCACTCTCTGAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 2793  
QY 161 HisTyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 2794 CATTATCTAGGACTTCAAAATAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAA 2853  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189

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Db 2854 ATCCCTGGATTGAAGCGCAAGCTGAA 2880
RESULT 7
US-10-956-157-4528
; Sequence 4528, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 4528
; LENGTH: 3478
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4528
Alignment Scores:
Pred. No.: 9.69e-100 Length: 3478
Score: 908.00 Matches: 184
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.35% Mismatches: 2
Query Match: 21 Indels: 0
Gaps: 0
DB:
US-09-830-972-2_COPY_975_1163 (1-189) x US-10-956-157-4528 (1-3478)
Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleYsThrGlyValValPheGlyAla 20
Db 2566 TCAGTTGTGTGACCTCTGCTACTGCGAGACATTAAGAAGACTGGAGTGGTGTGGTCC 2625
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 2626 AGCTATTTCCTGCTGCTTTCATTGACAGTATTCAGCATTTGAGCGTGAACGCTACATT 2685
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 2686 GCCTTGGCCCTGCTCTGTCGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAGCT 2745
Qy 61 IleGlnIysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 2746 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAAGTTGCTATA 2805
Qy 81 SerGluGluLeuValGlnIysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 2806 TCTGAGGAGTTGGTTTCAGAGTACAGTANNTCTGCTTGTGTCATGTGAAGTGCACGATA 2865
Qy 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 2866 AAGAACTCAGCGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTGCAGTG 2925
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeu 140
Db 2926 TTGATGTGGGTATTTACCTATGTGGTGGCTTGTGTTAATGCTGCTGACACTACTGATTTTG 2985
Qy 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 2986 GCTCTCATTTTCACCTTCAGTGTTCCTGTTTATTTATGAACGGCATCAGGCACAGATAGAT 3045
Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 3046 CATTATCTAGGACTTGCAAAATAAGAAATGTTAAAGATGCTATGGCTGCTGAAATCCAGCAAAA 3105
Qy 181 IleProGlyLeuLysArgLysAlaAsp 189
Db 3106 ATCCCTGGATTGAAGCGCAAGCTGAA 3132
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RESULT 8
US-09-789-386-1
; Sequence 1, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: MICHALOVICH, DAVID
; APPLICANT: PRINJHA, RABINDER KUMAR
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-789-386-1
Alignment Scores:
Pred. No.: 1.01e-99 Length: 3579
Score: 908.00 Matches: 184
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.35% Mismatches: 2
Query Match: 21 Indels: 0
Gaps: 0
DB:
US-09-830-972-2_COPY_975_1163 (1-189) x US-09-789-386-1 (1-3579)
Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleYsThrGlyValValPheGlyAla 20
Db 3010 TCAGTTGTGTGACCTCTGCTACTGCGAGACATTAAGAAGACTGGAGTGGTGTGGTCC 3069
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 3070 AGCTATTTCCTGCTGCTTTCATTGACAGTATTCAGCATTTGAGCGTGAACGCTACATT 3129
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 3130 GCCTTGGCCCTGCTCTGTCGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAGCT 3189
Qy 61 IleGlnIysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 3190 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAAGTTGCTATA 3249
Qy 81 SerGluGluLeuValGlnIysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 3250 TCTGAGGAGTTGGTTTCAGAGTACAGTANNTCTGCTTGTGTCATGTGAAGTGCACGATA 3309
Qy 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 3310 AAGAACTCAGCGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTGCAGTG 3369
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeu 140
Db 3370 TTGATGTGGGTATTTACCTATGTGGTGGCTTGTGTTAATGCTGCTGACACTACTGATTTTG 3429
Qy 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 3430 GCTCTCATTTTCACCTTCAGTGTTCCTGTTTATTTATGAACGGCATCAGGCACAGATAGAT 3489
Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 3490 CATTATCTAGGACTTGCAAAATAAGAAATGTTAAAGATGCTATGGCTGCTGAAATCCAGCAAAA 3549
Qy 181 IleProGlyLeuLysArgLysAlaAsp 189
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Db 3550 ATCCCTGGATTGAGCGCAAGCTGAA 3576
RESULT 9
US-09-893-348-22
; Sequence 22, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 22
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3579)
; OTHER INFORMATION:
US-09-893-348-22
Alignment Scores:
Pred. No.: 1.01e-99 Length: 3579
Score: 908.00 Matches: 184
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.35% Mismatches: 2
Query Match: 98.16% Indels: 0
DB: 9 Gaps: 0
US-09-830-972-2_COPY_975_1163 (1-189) x US-09-893-348-22 (1-3579)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
Db 3010 TCAGTTGTTGACCTCTCTGACCATTTAGAGACATTAGAGACATTGAGTGGTGTGGTGC 3069
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 3070 AGCCTATTCTGCTGCTTTTCATTGACAGTATTGAGCATTTGAGCGTAAACAGCCTACATT 3129
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAla 60
Db 3130 GCCTTGGCCCTGCTCTCTGTGACCATTCAGCTTTAGGATATACAGGGTGTGATCCAAAGCT 3189
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 3190 ATCCAGAAATCAGATGAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3249
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 3250 TCTGAGGAGTTGGTTTCTGAGAGTACAGTAATTCCTGCTTTGGTTCATGTAAGTTCAGGAT 3309
QY 101 LysGluLeuArgGluPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 3310 AAGGAACCTCAGGCGCCTCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTCAGTG 3369
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 3370 TTGATGTGGGTATTTACCTATGTTGGTGCCTTGTCTTAAATGGTCTGACACTACTGATTTTG 3429
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 3430 GCTCTCATTTTCACTCTTCTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCGCAGATAGAT 3489
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QY 161 HistTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3490 CATTATCTAGGACTTGCAATTAAGAATGTTAAAGATGCTATGGCTAAATCCCAAGCAAAA 3549  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
Db 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

## RESULT 11

US-10-327-213-8  
; Sequence 8, Application US/10327213  
; Publication No. US20040121341A1  
; GENERAL INFORMATION:  
; APPLICANT: FILBIN, MARIE T.  
; APPLICANT: DOMENICONI, MARCO  
; APPLICANT: CAO, ZIXUAN  
; TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)  
; FILE REFERENCE: CUNY/003  
; CURRENT APPLICATION NUMBER: US/10/327,213  
; CURRENT FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 8  
; LENGTH: 3579  
; TYPE: DNA  
; ORGANISM: Homo sapiens

## US-10-327-213-8

Alignment Scores:  
Pred. No.: 1.01e-99 Length: 3579  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservatives: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 19 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-327-213-8 (1-3579)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
Db 3010 TCAGTTGTGGACCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGTCGCC 3069  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 3070 AGCTTATCTCTGCTCTTTCATGACGATTTAGGATATACAGGGGTGTGTCGCC 3129  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 3130 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGTCGCC 3189  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 3190 ATCCAGAAATCAGATGCAAGGCCACCCATTCAGGCGATATCTGGAATCTGAAATCTGCTATA 3249  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
Db 3250 TCTGAGGAGTTGGTTTCAGAGTACAGTAATCTCTCTTGTGTCATGTCACGACGATA 3309  
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3310 AAGGAACCTCAGCGGCTCTCTTACTGATGATTTAGTTGATTTCTGAGTTTGCAGTG 3369  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 3370 TTGATGGGTATTTACCTATGTTGGTCTTGTAAATGGTCTGACACTACTGATTTTG 3429  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db 3430 GCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGCGCATCAGGCGCAGATAGAT 3489  
QY 161 HistTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3490 CATTATCTAGGACTTGCAATTAAGAATGTTAAAGATGCTATGGCTAAATCCCAAGCAAAA 3549

Db 3490 CATTATCTAGGACTTGCAATTAAGAATGTTAAAGATGCTATGGCTAAATCCCAAGCAAAA 3549  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
Db 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

## RESULT 12

US-10-466-258-8  
; Sequence 8, Application US/10466258  
; Publication No. US20040132096A1  
; GENERAL INFORMATION:  
; APPLICANT: GLAXO GROUP LIMITED  
; TITLE OF INVENTION: ASSAY  
; FILE REFERENCE: P80966 GCW  
; CURRENT APPLICATION NUMBER: US/10/466,258  
; CURRENT FILING DATE: 2003-07-15  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 8  
; LENGTH: 3579  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3579)  
US-10-466-258-8

Alignment Scores:  
Pred. No.: 1.01e-99 Length: 3579  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservatives: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 19 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-466-258-8 (1-3579)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
Db 3010 TCAGTTGTGGACCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGTCGCC 3069  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 3070 AGCTTATCTCTGCTCTTTCATGACGATTTAGGATATACAGGGGTGTGTCGCC 3129  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 3130 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGTCGCC 3189  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 3190 ATCCAGAAATCAGATGCAAGGCCACCCATTCAGGCGATATCTGGAATCTGAAATCTGCTATA 3249  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
Db 3250 TCTGAGGAGTTGGTTTCAGAGTACAGTAATCTCTCTTGTGTCATGTCACGACGATA 3309  
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3310 AAGGAACCTCAGCGGCTCTCTTACTGATGATTTAGTTGATTTCTGAGTTTGCAGTG 3369  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 3370 TTGATGGGTATTTACCTATGTTGGTCTTGTAAATGGTCTGACACTACTGATTTTG 3429  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db 3430 GCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGCGCATCAGGCGCAGATAGAT 3489  
QY 161 HistTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3490 CATTATCTAGGACTTGCAATTAAGAATGTTAAAGATGCTATGGCTAAATCCCAAGCAAAA 3549

QY 181 ileProGlyLeuLysArgLysAlaAsp 189  
Db 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576  
RESULT 13  
US-10-810-653-22  
; Sequence 22, Application US/10810653  
; Publication No. US20040253218A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN, Irun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SCHWARTZ=2A  
; CURRENT APPLICATION NUMBER: US/10/810,653  
; CURRENT FILING DATE: 2004-03-29  
; PRIOR APPLICATION NUMBER: US/09/893,348  
; PRIOR FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 22  
; LENGTH: 3579  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3579)  
; OTHER INFORMATION:  
US-10-810-653-22  
Alignment Scores:  
Pred. No.: 1,01e-99 Length: 3579  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservatives: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 20 Gaps: 0  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-810-653-22 (1-3579)  
QY 1 SerValAlaAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 3010 TCAGTTGTTGACCTCTCTGTACTGAGAGACATTAAGAGACTGGAGTGGTGTGGCC 3069  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 3070 AGCCTATTCTCTGTCTTTTCATTGACAGTATTTCAGCATTTGTGAGCGTAACAGCCTACATT 3129  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 3130 GCCTTGGCCCTCTCTCTGTGACCATCAGCTTTTAGGATATACAAAGGTGTGATCCAGCT 3189  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 3190 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGCGCATATCTCGAATCTGAAGTTGCTATA 3249  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
Db 3250 TCTGAGGAGTGGTTCTCAGAGTAGTACGTAATTCCTGTCTTGGTCTATGTGAACCTCCAGATA 3309  
QY 101 LysGluLeuArgGluPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120

Db 3310 AAGGAACCTCAGCGCCCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTCAGTG 3369  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 3370 TTGATGTGGGTATTTTACCTATGTTGGTCTTGTAAATGTTTAAATGTTCTGACACTACTGATTTTG 3429  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluAtcHisGlnValGlnIleAsp 160  
Db 3430 GCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCAGCAGCGGAGATAGAT 3489  
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3490 CATTATCTAGGACTTGCAAAATAAGATGTTAAAGATGCTATGCTAAATCCACAGCANAA 3549  
QY 181 ileProGlyLeuLysArgLysAlaAsp 189  
Db 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576  
RESULT 14  
US-09-758-140-5  
; Sequence 5, Application US/09758140  
; Patent No. US20020012965A1  
; GENERAL INFORMATION:  
; APPLICANT: Strittmatter, Stephen M.  
; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth  
; FILE REFERENCE: 44574-5073-US  
; CURRENT APPLICATION NUMBER: US/09/758,140  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/175,707  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: US 60/207,366  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/236,378  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 4053  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (135)..(3710)  
; OTHER INFORMATION: Human mRNA for No. US20020012965A1o protein (K1AA0886, GenBank  
; OTHER INFORMATION: Accession No. US20020012965A1 AB020693)  
US-09-758-140-5  
Alignment Scores:  
Pred. No.: 1,23e-99 Length: 4053  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservatives: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 98.16% Indels: 0  
DB: 9 Gaps: 0  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-758-140-5 (1-4053)  
QY 1 SerValAlaAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 3144 TCAGTTGTTGACCTCTCTGTACTGAGAGACATTAAGAGACTGGAGTGGTGTGGTGGC 3203  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 3204 AGCCTATTCTCTCTCTCTTCATTGACAGTATTTCAGCATTTGTGAGCGTAACAGCCTACATT 3263  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 3264 GCCTTGGCCCTCTCTCTGTGACCATCAGCTTTTAGGATATACAAAGGTGTGATCCAGCT 3323  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 3324 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGCGCATATCTCGAATCTCGAAGTTGCTATA 3383

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrile 100  
 Db 3384 TCTGAGGAGTGGTTTCAGAGTACAGTAATCTCTGCTCTGGTCACTGACGCGATA 3443  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 3444 AAGGAACATCAGGCGCTCTCTCTAGTATGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTG 3503  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 Db 3504 TTGATGTGGTATTTACCTATGTTGGTGGCTTGTATGCTGACACTACTGATTTTG 3563  
 QY 141 AlaLeuLysSerLeuPheSerIleProValletyrGluArgHisGlnValGlnIleAsp 160  
 Db 3564 GCTCTCAATTCACCTCTCAGTGTCTCTGTTATTAAGATGCTATGGCTTAAATCCAGCAAAA 3683  
 QY 161 HistyLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlalys 180  
 Db 3624 CATTATCTAGGACTTGCATAAATAAGAAATGTTAAAGATGCTATGGCTTAAATCCAGCAAAA 3683  
 QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
 Db 3684 ATCCCTGGATTGAAGCGCAAGCTGAA 3710

## RESULT 15

US-09-972-599A-5  
 ; Sequence 5, Application US/09972599A  
 ; Patent No. US20020077295A1  
 ; GENERAL INFORMATION:

; APPLICANT: STRITTMATTER, STEPHEN M.  
 ; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH  
 ; FILE REFERENCE: C077 CIP US  
 ; CURRENT APPLICATION NUMBER: US/09/972,599A  
 ; PRIORITY FILING DATE: 2001-10-06  
 ; PRIOR APPLICATION NUMBER: PCT/US01/01041  
 ; PRIOR FILING DATE: 2001-01-12  
 ; PRIOR APPLICATION NUMBER: 09/758,140  
 ; PRIOR FILING DATE: 2001-01-12  
 ; PRIOR APPLICATION NUMBER: 60/236,378  
 ; PRIOR FILING DATE: 2000-09-29  
 ; PRIOR APPLICATION NUMBER: 60/207,366  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: 60/175,707  
 ; PRIOR FILING DATE: 2000-01-12  
 ; NUMBER OF SEQ ID NOS: 57  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 5

LENGTH: 4053

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (135)..(3710)

; OTHER INFORMATION: Human DNA encoding for No. US20020077295A1o protein (K1AA0886, GenBank accession No. U00001)  
 ; OTHER INFORMATION: Accession No. US20020077295A1 AB020693

US-09-972-599A-5

Alignment Scores:

Pred. No.:	1.23e-99	Length:	4053
Score:	908.00	Matches:	184
Percent Similarity:	98.94%	Conservative:	3
Best Local Similarity:	97.35%	Mismatches:	2
Query Match:	98.16%	Indels:	0
DB:	9	Gaps:	0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-972-599A-5 (1-4053)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 Db 3144 TCAGTTGTTGACCTCTCTACTGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGCC 3203  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40

Db 3204 AGCCTATTCTCTGCTGCTTTTCATTGACAGTATTTCAGCATTTGTCAGCGTAACAGCCTACATT 3263  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 3264 GCTTTGGCCCTGCTCTCTGTGACCATCAGCTTTTAGATATACAGGGTGTGATCCAGCT 3323  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 3324 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGAATCTGAAAGTTGCTATA 3383  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrile 100  
 Db 3384 TCTCAGGAGTGGTTCAGAGTACAGTAATCTCTCTTGTGTCATGTGAACCTGCACGATA 3443  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 3444 AAGGAACATCAGGCGCTCTCTCTAGTATGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTG 3503  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 Db 3504 TTGATGTGGTATTTACCTATGTTGGTGGCTTGTATGCTGACACTACTGATTTTG 3563  
 QY 141 AlaLeuLysSerLeuPheSerIleProValletyrGluArgHisGlnValGlnIleAsp 160  
 Db 3564 GCTCTCAATTCACCTCTCAGTGTCTCTGTTATTAAGATGCTATGGCTTAAATCCAGCAAAA 3683  
 QY 161 HistyLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlalys 180  
 Db 3624 CATTATCTAGGACTTGCATAAATAAGAAATGTTAAAGATGCTATGGCTTAAATCCAGCAAAA 3683  
 QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
 Db 3684 ATCCCTGGATTGAAGCGCAAGCTGAA 3710

## RESULT 16

US-10-717-597-310  
 ; Sequence 310, Application US/10717597  
 ; Publication No. US20040110221A1  
 ; GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Burczynski, Michael E.

APPLICANT: Twine, Natalie C.

APPLICANT: Dörner, Andrew J.

APPLICANT: Trepicchio, William L.

APPLICANT: Slonim, Donna K.

APPLICANT: Stover, Jennifer A.

; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS  
 ; FILE REFERENCE: AM101080L  
 ; CURRENT APPLICATION NUMBER: US/10/717,597  
 ; CURRENT FILING DATE: 2003-11-21  
 ; PRIOR APPLICATION NUMBER: US 60/459,782  
 ; PRIOR FILING DATE: 2003-04-03  
 ; PRIOR APPLICATION NUMBER: US 60/427,982  
 ; PRIOR FILING DATE: 2002-11-21  
 ; NUMBER OF SEQ ID NOS: 4904  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 310

LENGTH: 4053

TYPE: DNA

ORGANISM: Homo sapiens

US-10-717-597-310

Pred. No.:	1.23e-99	Length:	4053
Score:	908.00	Matches:	184
Percent Similarity:	98.94%	Conservative:	3
Best Local Similarity:	97.35%	Mismatches:	2
Query Match:	98.16%	Indels:	0
DB:	19	Gaps:	0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-717-597-310 (1-4053)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20

```
Db 3144 TCAGTTGTTGACCTCTGCTGCTGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGC 3203
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 3204 AGCCTATTCTGCTGCTCTTCATTGACAGATTTCAGCATTTGAGCGTAAACAGCTACATT 3263
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60
Db 3264 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT 3323
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 3324 ATCCAGAAATCAGATGAAGCCACCATTTCAGGCAATATCTGGAATCTGAAGTTGCTATA 3383
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 3384 TCTGAGGACTTGGTTCAGAAAGTACAGTAATCTGCTCTTGGTCACTGTAAGTGCAGATA 3443
Qy 101 LysGluLeuArgGluPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 3444 AAGGAACCTCAGCGCCCTCTCTCTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTG 3503
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 3504 TTGATGTGGGTATTTACCTATGTTGGTGCCTTGTGTTTAAATGGTCTGACACTACTGATTTTG 3563
Qy 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 3564 GCTCTCATTTCACTCTTCAGTGTCTCTGTTTATTAAGACGGCATCAGGCACAGATAGAT 3623
Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 3624 CATTATCTAGGACTTGCATAATGAAGATGTTAAAGATGCTATGGCTAAATAATCCAAGCAAAA 3683
Qy 181 IleProGlyLeuLysArgLysAlaAsp 189
Db 3684 ATCCCTGGATTGAAGCGCAAAAGCTGAA 3710

RESULT 17
US-10-956-157-4532
; Sequence 4532, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4532
; LENGTH: 4623
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4532

Alignment Scores:
Pred. No.: 1 51e-99 Length: 4623
Score: 908.00 Matches: 184
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.35% Mismatches: 2
Query Match: 98.16% Indels: 0
DB: 21 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-956-157-4532 (1-4623)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysIleThrGlyValValPheGlyAla 20
Db 3151 TCAGTTGTTGACCTCTGCTGCTGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGC 3210
```

```
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 3211 AGCCTATTCTGCTGCTCTTCATTGACAGATTTCAGCATTTGAGCGTAAACAGCTACATT 3270
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60
Db 3271 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT 3330
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 3331 ATCCAGAAATCAGATGAAGCCACCATTTCAGGCAATATCTGGAATCTGAAGTTGCTATA 3390
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 3391 TCTGAGGAGTTGGTTCAGAAAGTACAGTAATCTGCTCTTGGTCACTGTAAGTGCAGATA 3450
Qy 101 LysGluLeuArgGluPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 3451 AAGGAACCTCAGCGCCCTCTCTCTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTG 3510
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 3511 TTGATGTGGGTATTTACCTATGTTGGTGCCTTGTGTTTAAATGGTCTGACACTACTGATTTTG 3570
Qy 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 3571 GCTCTCATTTCACTCTTCAGTGTCTCTGTTTATTAAGACGGCATCAGGCACAGATAGAT 3630
Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 3631 CATTATCTAGGACTTGCATAATGAAGATGTTAAAGATGCTATGGCTAAATAATCCAAGCAAAA 3690
Qy 181 IleProGlyLeuLysArgLysAlaAsp 189
Db 3691 ATCCCTGGATTGAAGCGCAAAAGCTGAA 3717

RESULT 18
US-10-060-036-53
; Sequence 53, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 4632
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-53

Alignment Scores:
Pred. No.: 1 52e-99 Length: 4632
Score: 908.00 Matches: 184
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.35% Mismatches: 2
Query Match: 98.16% Indels: 0
DB: 14 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-060-036-53 (1-4632)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysIleThrGlyValValPheGlyAla 20
Db 3151 TCAGTTGTTGACCTCTGCTGCTGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGC 3210
```



QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 3211 AGCTATTCTCTGCTCTTTCATTGACAGTATTGAGGAGTAAAGGCTACATT 3270  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
DB 3271 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCT 3330  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
DB 3331 ATCCAGAAATCAGATGAAGGCCACCCATTGAGGATATCTGGAATCTGAAGTTGCTATA 3390  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
DB 3391 TCTGAGGAGTTGTTTTCAGAGTACAGTAATCTCTGCTTGGTCATGTGAAGTGCACGATA 3450  
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
DB 3451 AAGGAACCTCAGCGGCTCTCTTCTAGTTGATGATTTAGTTGATTTCTCTGAAGTTGACGTG 3510  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
DB 3511 TTGATGTGGGTATTTTACCTATGTTGGTGGCTTTGTTTAAATGGTCTGACACTACTGATTTG 3570  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
DB 3571 GCTCTCATTTTCTCTTCTGAGTCTCTCTGTTCTTATTTATGACGGCATCAGGCACAGTAGT 3630  
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
DB 3631 CATTATCTAGGACTTGCATAAAGAAATGTTAAAGATGCTATGGCTAAATAATCCAGCAAAA 3690  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
DB 3691 ATCCCTGGATTGAAGCGCAAGAGCTGAA 3717

## RESULT 19

US-10-267-502-214  
; Sequence 214, Application US/10267502  
; Publication No. US20040071700A1

## GENERAL INFORMATION:

; APPLICANT: Kim, Jaeseob  
; APPLICANT: Galant, Ron  
; TITLE OF INVENTION: Obesity Linked Genes  
; FILE REFERENCE: LSD-07416  
; CURRENT APPLICATION NUMBER: US/10/267,502  
; CURRENT FILING DATE: 2003-01-27  
; NUMBER OF SEQ ID NOS: 439  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 214  
; LENGTH: 3492  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-267-502-214

## Alignment Scores:

Pred. No.:	1.49e-99	Length:	3492
Score:	306.50	Matches:	187
Percent Similarity:	98.95%	Conservative:	1
Best Local Similarity:	98.42%	Mismatches:	1
Query Match:	98.00%	Indels:	1
DB:	18	Gaps:	1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-267-502-214 (1-3492)

QY 1 SerValAlaSerLeuLeuTyrTrpArgAspIleLysThrGlyValVal---PheGly 19  
DB 2920 TCAGTTGTTGACTCTCTGCTACTGAGACATTAAGAGACTGGAGTGTGTTTGGT 2979  
QY 20 AlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr 39  
DB 2980 GCCAGCTTATTCTCTGCTGCTCTCTGACAGTGTTCAGCAATTTGTCAGTGAACGCGCTAC 3039

QY 40 IleAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGln 59  
DB 3040 ATTGCTTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAA 3099  
QY 60 AlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAla 79  
DB 3100 GCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGATATTTGGAATCTGAAGTTGCC 3159  
QY 80 IleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThr 99  
DB 3160 ATATCAGAGGAATTTGGTTTCAGAAATATAGTAATTTCTGCTCTTGGTCTGATGAACAGACA 3219  
QY 100 IleLysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAla 119  
DB 3220 ATAAAGAAATGAGCGGCTCTCTTCTTAGTTGATGATTTAGTTGCTCCCTGAAGTTTGA 3279  
QY 120 ValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIle 139  
DB 3280 GTGTTGATGTGGGTATTTACTTACGTTGGTGGCTTGTTCATGTTTGCACACTACTGATT 3339  
QY 140 LeuAlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIle 159  
DB 3340 TTAGCTCTGATCTCACCTCTTCAGTATTTCTGTTATATATGAACGCGCATCAGCGCGAGATA 3399  
QY 160 AspHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAla 179  
DB 3400 GATCATTTATCTAGGACTTGCATAACAGAGCGTTAAGGATGCGATGGCCAAATCCAGACA 3459  
QY 180 LysIleProGlyLeuLysArgLysAlaAsp 189  
DB 3460 AAAATCCCTGGATTGAAGCGCAAGAGCAAA 3489

## RESULT 20

US-10-660-946-2  
; Sequence 2, Application US/10660946  
; Publication No. US2004006313A1

## GENERAL INFORMATION:

; APPLICANT: Bandman, Olga  
; Au-Young, Janice  
; Goli, Surya K.  
; Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/660,946  
FILING DATE: 12-Sep-2003  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/228,213A  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/700,607  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0114 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:

LENGTH: 799 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: Consensus  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-660-946-2

Alignment Scores:  
Pred. No.: 2,98e-100 Length: 799  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: 18 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-660-946-2 (1-799)

```
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 108 GTTGTGACCTCTCTGACTGGAGACATTAAAGACCTGGAGTGGTGTGGTGGCCAGC 167
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 168 CTATTCCTCTGCTTTCATTCAGATGATTCAGCATTTGTGAGCGTAACAGCCTACATTTGCC 227
QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 228 TTGGCCCTGCTCTCTGTGACCATTCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 287
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 288 CAGAAATCAGATGAAGCCACCCATTCAGGCATATCTGGAATCTGAAGTTGCTATATCT 347
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 348 GAGGAGTTGGTTTCAGAAATACAGTAATCTCTGCTCTTGGTCTGTGAACTGCACGATAAAG 407
QY 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 408 GAACCTCAGGCGCTCTCTTAGTGAATGATTTAGTTGATTTCTGAAAGTTTCAGAGTTTG 467
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 468 ATGTGGGTATTTACCTATGTTGGTCTGCTTTTAAATGGTCTGACACTACTGATTTTGGCT 527
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 528 CTCATTTTCATCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 587
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 588 TATCTAGGACTTGCAATTAAGAATGTTAAAGATGCTATGGCTAAATCCAGCAAAATTC 647
QY 182 ProGlyLeuLysArgLysAlaAsp 189
Db 648 CCTGGATTGAAGCGCAAGCTGAA 671
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## RESULT 21

US-09-789-386-5  
Sequence 5, Application US/09789386  
Patent No. US20020010324A1  
GENERAL INFORMATION:  
APPLICANT: MICHALOVICH, DAVID  
TITLE OF INVENTION: NOVEL COMPOUNDS  
FILE REFERENCE: GP-30165-C1  
CURRENT APPLICATION NUMBER: US/09/789,386  
CURRENT FILING DATE: 2001-02-21  
PRIOR APPLICATION NUMBER: U.K. 9916898.1

PRIOR FILING DATE: 1999-07-19  
PRIOR APPLICATION NUMBER: U.K. 9816024.5  
PRIOR FILING DATE: 1998-07-22  
PRIOR APPLICATION NUMBER: US 09/359,208  
PRIOR FILING DATE: 1999-07-22  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 5  
LENGTH: 1122  
TYPE: DNA  
ORGANISM: HOMO SAPIENS  
US-09-789-386-5

Alignment Scores:  
Pred. No.: 5,08e-100 Length: 1122  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: 9 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-789-386-5 (1-1122)

```
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 556 GTTGTGACCTCTCTGACTGGAGACATTAAAGACCTGGAGTGGTGTGGTGGCCAGC 615
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 616 CTATTCCTCTGCTTTCATTCAGATGATTCAGCATTTGTGAGCGTAACAGCCTACATTTGCC 675
QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 676 TTGGCCCTGCTCTCTGTGACCATTCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 735
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 736 CAGAAATCAGATGAAGCCACCCATTCAGGCATATCTGGAATCTGAAGTTGCTATATCT 795
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 796 GAGGAGTTGGTTTCAGAAATACAGTAATCTCTGCTCTTGGTCTGTGAACTGCACGATAAAG 855
QY 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 856 GAACCTCAGGCGCTCTCTTAGTGAATGATTTAGTTGATTTCTGAAAGTTTCAGAGTTTG 915
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 916 ATGTGGGTATTTACCTATGTTGGTCTGCTTTTAAATGGTCTGACACTACTGATTTTGGCT 975
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 976 CTCATTTTCATCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1035
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 1036 TATCTAGGACTTGCAATTAAGAATGTTAAAGATGCTATGGCTAAATCCAGCAAAATTC 1095
QY 182 ProGlyLeuLysArgLysAlaAsp 189
Db 1096 CCTGGATTGAAGCGCAAGCTGAA 1119
```

## RESULT 22

US-10-175-523-156  
Sequence 156, Application US/10175523  
Publication No. US20030096264A1  
GENERAL INFORMATION:  
APPLICANT: Brockman, Jeffrey  
TITLE OF INVENTION: NOVEL COMPOUNDS  
FILE REFERENCE: GP-30165-C1  
CURRENT APPLICATION NUMBER: US/09/789,386  
CURRENT FILING DATE: 2001-02-21  
PRIOR APPLICATION NUMBER: U.K. 9916898.1

```
; APPLICANT: Palfreyman, Michael
; APPLICANT: Rajan, Prithi
; TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
; FILE REFERENCE: 3235/1J795-US3
; CURRENT APPLICATION NUMBER: US 10/175,523
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/299,151
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/317,828
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/325,150
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/333,047
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 60/349,936
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/361,834
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 156
; LENGTH: 1160
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-175-523-156

Alignment Scores:
Pred. No.: 5,35e-100 Length: 1160
Score: 904.00 Matches: 183
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.73% Indels: 0
DB: 14 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-175-523-156 (1-1160)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleYsThrGlyValValPheGlyAlaSer 21
Db 228 GTTGTGACCTCCTCTGTGACCATCAGCTTTAGAGATATACAGGGTGTGTTGGTCCAGC 287
Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 288 CTATTCTCGCTCTTCTTTCATTTGACAGTATTGACGATTTGAGCGTTAACGCGCTACATTGCC 347
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 348 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGAGATATACAGGGTGTGATCCAGCTATC 407
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 408 CAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGAATCTGGAAGTTGCTATATCT 467
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 468 GAGGAGTTGGTTTCAAGATACAGTAATTTCTGCTTGTGTCATGTGAAGTGCACGATAAG 527
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 528 GAACTCAGCGCCCTCTTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTGCGAGTGTG 587
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 588 ATGTGGGTATTTACCTATGTTGGTGGCTTGTGTTAATGTTCTGACACTACTGATTTGGCT 647
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 648 CTCATTTCACTCTTCAGTGTCTCTTCTTAGTTGATTTAGTGTGATTTCTGAAAGTTGCGAGTGTG 707
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 708 TATCTAGGACTTGCATAATGAAGATGTTAAAGATGCTATGGCTTAAATCCAAAGCAAAATC 767
Qy 182 ProGlyLeuLysArgLysAlaAsp 189
```

```
Db 768 CTTGATTGAAGCGCAAGCTGAA 791

RESULT 23
US-10-956-157-4527
; Sequence 4527, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4527
; LENGTH: 1609
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4527

Alignment Scores:
Pred. No.: 8,93e-100 Length: 1609
Score: 904.00 Matches: 183
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.73% Indels: 0
DB: 21 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-956-157-4527 (1-1609)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleYsThrGlyValValPheGlyAlaSer 21
Db 140 GTTGTGACCTCCTCTGTGACCATCAGCTTTAGAGATATACAGGGTGTGTTGGTCCAGC 199
Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 200 CTATTCTCGCTCTTCTTTCATTTGACAGTATTGACGATTTGAGCGTTAACGCGCTACATTGCC 259
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 260 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGGTGTGATCCAGCTATC 319
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 320 CAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGAATCTGGAAGTTGCTATATCT 379
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 380 GAGGAGTTGGTTTCAAGATACAGTAATTTCTGCTTGTGTCATGTGAAGTGCACGATAAG 439
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 440 GAACTCAGCGCCCTCTTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTGCGAGTGTG 499
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 500 ATGTGGGTATTTACCTATGTTGGTGGCTTGTGTTAATGTTCTGACACTACTGATTTGGCT 559
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 560 CTCATTTCACTCTTCAGTGTCTCTGTTGATTTATGACCGCATCAGGCACAGATAGATCAT 619
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 620 TATCTAGGACTTGCATAATGAAGATGTTAAAGATGCTATGGCTTAAATCCAAAGCAAAATC 679
Qy 182 ProGlyLeuLysArgLysAlaAsp 189
Db 680 CTTGATTGAAGCGCAAGCTGAA 703
```

```
RESULT 24
US-09-765-205-5
; Sequence 5, Application US/09765205
; Patent No. US2002003480A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/09/765,205
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1610
; TYPE: DNA
; ORGANISM: human
US-09-765-205-5

Alignment Scores:
Pred. No.:      8,94e-100      Length:      1610
Score:          904.00      Matches:      183
Percent Similarity: 98.94%      Conservative: 3
Best Local Similarity: 97.34%      Mismatches: 2
Query Match:      97.73%      Indels:      0
DB:              9          Gaps:      0

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-765-205-5 (1-1610)

QY      2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db      687 GTTGTGACCTCTCTGACAGTATTAGAGACATTAAAGACTGGAGTGGTGTGGTCCAGC 746

QY      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db      747 CTATTCTCTGCTTTCATTGACAGTATTACAGATTGTGAGGTAAACACCTACATTGCC 806

QY      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db      807 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 866

QY      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db      867 CAGAAATCAGATGAAGCCACCCATTTCAGGCATATCTGGAATCTGGAATCTGATATCT 926

QY      82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db      927 GAGGAGTTGGTTTCAGAAATACAGTAAATCTCTGCTTTGGTTCATGTCACGATTAAG 986

QY      102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db      987 GAACTCAGGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAAGTTTCAGTGTG 1046

QY      122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
Db      1047 ATGTGGGTATTTACCTATGTTGGTCTGTTTAAATGGTCTGACACTACTGATTTGGCT 1106

QY      142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db      1107 CTCAATTCATCTTCTAGTGTCTCTGTTTATTATGAACGGCATCAGGCACAGATAGCAT 1166

QY      162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      1167 TATCTAGGACTTGCATAAAGATGTTAAAGATGCTATGGCTAAATATCCAAAGCAAAATC 1226

QY      182 ProGlyLeuLysArgLysAlaAsp 189
Db      1227 CCTGGATTGAAGCGCAAGCTGAA 1250

RESULT 25
US-10-439-388-62
; Sequence 62, Application US/10439388
; Publication NO. US20030228617A1
; GENERAL INFORMATION:
; APPLICANT: Aune, Thomas M
```

```
; Publication No. US20050084850A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/10/347,669
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1610
; TYPE: DNA
; ORGANISM: human
US-10-347-669-5

Alignment Scores:
Pred. No.:      8,94e-100      Length:      1610
Score:          904.00      Matches:      183
Percent Similarity: 98.94%      Conservative: 3
Best Local Similarity: 97.34%      Mismatches: 2
Query Match:      97.73%      Indels:      0
DB:              21          Gaps:      0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-347-669-5 (1-1610)

QY      2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db      687 GTTGTGACCTCTCTGACAGTATTAGAGACATTAAAGACTGGAGTGGTGTGGTCCAGC 746

QY      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db      747 CTATTCTCTGCTTTCATTGACAGTATTACAGATTGTGAGGTAAACACCTACATTGCC 806

QY      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db      807 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 866

QY      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db      867 CAGAAATCAGATGAAGCCACCCATTTCAGGCATATCTGGAATCTGGAATCTGATATCT 926

QY      82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db      927 GAGGAGTTGGTTTCAGAAATACAGTAAATCTCTGCTTTGGTTCATGTCACGATTAAG 986

QY      102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db      987 GAACTCAGGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAAGTTTCAGTGTG 1046

QY      122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
Db      1047 ATGTGGGTATTTACCTATGTTGGTCTGTTTAAATGGTCTGACACTACTGATTTGGCT 1106

QY      142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db      1107 CTCAATTCATCTTCTAGTGTCTCTGTTTATTATGAACGGCATCAGGCACAGATAGCAT 1166

QY      162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      1167 TATCTAGGACTTGCATAAAGATGTTAAAGATGCTATGGCTAAATATCCAAAGCAAAATC 1226

QY      182 ProGlyLeuLysArgLysAlaAsp 189
Db      1227 CCTGGATTGAAGCGCAAGCTGAA 1250

RESULT 26
US-10-439-388-62
; Sequence 62, Application US/10439388
; Publication NO. US20030228617A1
; GENERAL INFORMATION:
; APPLICANT: Aune, Thomas M
```

APPLICANT: Olsen, Nancy J  
TITLE OF INVENTION: Method for Predicting Autoimmune Disease  
FILE REFERENCE: 1242/68  
CURRENT APPLICATION NUMBER: US/10/439,388  
CURRENT FILING DATE: 2003-05-16  
PRIOR APPLICATION NUMBER: US 60/381,055  
PRIOR FILING DATE: 2002-03-16  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 62  
LENGTH: 1785  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-439-388-62

Alignment Scores:  
Pred. No.: 1,05e-99 Length: 1785  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservatives: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: 17 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-439-388-62 (1-1785)

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QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
DB 247 GTTGTGGACCTCTCTACTGGAGACATTAAGAGACTGGAGTGGTGTGGTCCAGC 306
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 307 CTATTCTCGCTGCTTTTCATTCAGCATTTAGCATTTGAGCGTTAAGCGCTACATTGCC 366
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 367 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGGTGTGATCCAAGCTATC 426
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 427 CAGAAATCAGATGAAGCCACCCATTCAGGCGATATCTGGAATCTGGAAGTTGCTATATCT 486
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
DB 487 GAGGAGTTGGTTTCAGAGTACAGTAATCTCTCTTGTGTCATGTGAACTGCACGATAAAG 546
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 547 GAACCTCAGCGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 606
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
DB 607 ATGTGGGTATTACCTATGTTGGTGCCTTGTAAATGTCCTGACACTACTGATTTGGCT 666
QY 142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
DB 667 CTCATTTTCACCTCTTTCAGTGTCTCTGTTATTATGAACGGCATCAGGCACATAGATCAT 726
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
DB 727 TATCTAGGACTTGCATAATTAAGATGTTAAGATGCTATGGCTAAATAATCAAGCAAAATC 786
QY 182 ProGlyLeuLysArgLysAlaAsp 189
DB 787 CCTGGATTGAAGCGCAAGCTGAA 810
```

## RESULT 27

US-10-956-157-1705  
Sequence 1705, Application US/10956157  
Publication No. US20050118625A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
MOUNTS, William  
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
FILE REFERENCE: 031896-043000 (AM 101081)  
CURRENT APPLICATION NUMBER: US/10/956,157  
CURRENT FILING DATE: 2004-10-04  
NUMBER OF SEQ ID NOS: 319805  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1705  
LENGTH: 1785  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-956-157-1705

Alignment Scores:  
Pred. No.: 1,05e-99 Length: 1785  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservatives: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: 21 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-956-157-1705 (1-1785)

```
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
DB 247 GTTGTGGACCTCTCTACTGGAGACATTAAGAGACTGGAGTGGTGTGGTCCAGC 306
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 307 CTATTCTCGCTGCTTTTCATTCAGCATTTAGCATTTGAGCGTTAAGCGCTACATTGCC 366
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 367 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGGTGTGATCCAAGCTATC 426
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 427 CAGAAATCAGATGAAGCCACCCATTCAGGCGATATCTGGAATCTGGAAGTTGCTATATCT 486
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
DB 487 GAGGAGTTGGTTTCAGAGTACAGTAATCTCTCTTGTGTCATGTGAACTGCACGATAAAG 546
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 547 GAACCTCAGCGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 606
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
DB 607 ATGTGGGTATTACCTATGTTGGTGCCTTGTAAATGTCCTGACACTACTGATTTGGCT 666
QY 142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
DB 667 CTCATTTTCACCTCTTTCAGTGTCTCTGTTATTATGAACGGCATCAGGCACATAGATCAT 726
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
DB 727 TATCTAGGACTTGCATAATTAAGATGTTAAGATGCTATGGCTAAATAATCAAGCAAAATC 786
QY 182 ProGlyLeuLysArgLysAlaAsp 189
DB 787 CCTGGATTGAAGCGCAAGCTGAA 810
```

## RESULT 28

US-10-956-157-4530  
Sequence 4530, Application US/10956157  
Publication No. US20050118625A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
MOUNTS, William  
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
FILE REFERENCE: 031896-043000 (AM 101081)  
CURRENT APPLICATION NUMBER: US/10/956,157

; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4530  
; LENGTH: 2050  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-956-157-4530

Alignment Scores:  
Pred. No.: 1,31e-99 Length: 2050  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservatives: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: 21 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-956-157-4530 (1-2050)

```
QY 2 ValValAspLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 622 GTTGTGACCTCTCTGACTCGAGACATTAAGACACTCGAGTGGTGTGGTCCACG 681
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 682 CTATTCCTGCTCTTCATTGACAGTATTACAGATTGTGAGCGTAACAGCCTACATTGCC 741
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 742 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 801
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 802 CAGAAATCAGATGAGCGCCACCCATTTCAGGGCATATCTGGAATCTCGAAGTTGCTATATCT 861
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 862 GAGGAGTTGGTTCAGAAAGTACAGTAATCTGCTCTTGGTCATGTGAAGTGCACGATAAG 921
QY 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 922 GAACCTCAGCGGCTCTCTTAGTTGATGATTTAGTTGATCTCTGAAGTTTCAGTGTG 981
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 982 ATGTGGGTATTTACCTATGTTGGTCTGCTTTAATGGTCTGACACTACTGATTTGGCT 1041
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 1042 CTCATTTCACTCTTCAGTGTCTCTGTTATTATGAACGCGATCAGGCACAGATAGATCAT 1101
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 1102 TATCTAGGACTTGCAAAATGAAGTGTAAAGATGCTATGCTTAAATCCAGCAAAATC 1161
QY 182 ProGlyLeuLysArgLysAlaAsp 189
Db 1162 CTGTGATTGAAGCGCAAGCTGAA 1185
```

RESULT 29  
US-10-466-258-3  
; Sequence 3, Application US/10466258  
; Publication No. US20040132096A1  
; GENERAL INFORMATION:  
; APPLICANT: GLAXO GROUP LIMITED  
; TITLE OF INVENTION: ASSAY  
; FILE REFERENCE: P80966 GCW  
; CURRENT APPLICATION NUMBER: US/10/466,258  
; CURRENT FILING DATE: 2003-07-15  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 2052

; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (67)..(1188)  
US-10-466-258-3

Alignment Scores:  
Pred. No.: 1,31e-99 Length: 2052  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservatives: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: 19 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-466-258-3 (1-2052)

```
QY 2 ValValAspLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 622 GTTGTGACCTCTCTGACTCGAGACATTAAGACACTCGAGTGGTGTGGTCCACG 681
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 682 CTATTCCTGCTCTTCATTGACAGTATTACAGATTGTGAGCGTAACAGCCTACATTGCC 741
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 742 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 801
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 802 CAGAAATCAGATGAGCGCCACCCATTTCAGGGCATATCTGGAATCTCGAAGTTGCTATATCT 861
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 862 GAGGAGTTGGTTCAGAAAGTACAGTAATCTGCTCTTGGTCATGTGAAGTGCACGATAAG 921
QY 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 922 GAACCTCAGCGGCTCTCTTAGTTGATGATTTAGTTGATCTCTGAAGTTTCAGTGTG 981
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 982 ATGTGGGTATTTACCTATGTTGGTCTGCTTTAATGGTCTGACACTACTGATTTGGCT 1041
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 1042 CTCATTTCACTCTTCAGTGTCTCTGTTATTATGAACGCGATCAGGCACAGATAGATCAT 1101
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 1102 TATCTAGGACTTGCAAAATGAAGTGTAAAGATGCTATGCTTAAATCCAGCAAAATC 1161
QY 182 ProGlyLeuLysArgLysAlaAsp 189
Db 1162 CTGTGATTGAAGCGCAAGCTGAA 1185
```

RESULT 30  
US-10-956-157-4531  
; Sequence 4531, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4531  
; LENGTH: 2226

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4531

Alignment Scores:
Pred. No.: 1.49e-99 Length: 2226
Score: 904.00 Matches: 183
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.73% Indels: 0
DB: 21 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-956-157-4531 (1-2226)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 697 GTTGTGACCTCTCTGACTGAGAGACATTAAAGACTGGAGTGGTGTGGTGGCCAGC 756
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 757 CTATTCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 816
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 817 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 876
Qy 62 GlnLysSerAspGluGlyHisPropheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 877 CAGAAATCAGATGAAGGCCACCCATTGAGGCGATATCTGGAATCTGAAAGTTGCTATATCT 936
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 937 GAGGAGTTGGTTCAAGATACAGTAATCTGCTCTTGTGTCATGTGAACCTGCACGATAAG 996
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 997 GAACCTCAGCGCGCTCTCTTGTAGTGTGATTTAGTTGATCTCTGAAGTTTGCAGTGTG 1056
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 1057 ATGGGGTATTACCTATGTTGGTGGCTGTTTAAATGCTGACACTACTGATTTGGCT 1116
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 1117 CTCAATTCACCTTCAGTGTTCCCTGTTATTATGAACGCGATCAGGCACAGATAGATCAT 1176
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 1177 TATCTAGGACTTGCAAAATAAGAATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAAATC 1236
Qy 182 ProGlyLeuLysArgLysAlaAsp 189
Db 1237 CCTGATTGAAGCGCAAGCTGAA 1260

RESULT 31
US-10-060-036-54
; Sequence 54, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT FILING DATE: 2002-01-30
; CURRENT APPLICATION NUMBER: US/10/060.036
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
```

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; LENGTH: 2235
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-54

Alignment Scores:
Pred. No.: 1.5e-99 Length: 2235
Score: 904.00 Matches: 183
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.73% Indels: 0
DB: 14 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-060-036-54 (1-2235)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 697 GTTGTGACCTCTCTGACTGAGAGACATTAAAGACTGGAGTGGTGTGGTGGCCAGC 756
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 757 CTATTCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 816
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 817 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 876
Qy 62 GlnLysSerAspGluGlyHisPropheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 877 CAGAAATCAGATGAAGGCCACCCATTGAGGCGATATCTGGAATCTGAAAGTTGCTATATCT 936
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 937 GAGGAGTTGGTTCAAGATACAGTAATCTGCTCTTGTGTCATGTGAACCTGCACGATAAG 996
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 997 GAACCTCAGCGCGCTCTCTTGTAGTGTGATTTAGTTGATCTCTGAAGTTTGCAGTGTG 1056
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 1057 ATGGGGTATTACCTATGTTGGTGGCTGTTTAAATGCTGACACTACTGATTTGGCT 1116
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 1117 CTCAATTCACCTTCAGTGTTCCCTGTTATTATGAACGCGATCAGGCACAGATAGATCAT 1176
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 1177 TATCTAGGACTTGCAAAATAAGAATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAAATC 1236
Qy 182 ProGlyLeuLysArgLysAlaAsp 189
Db 1237 CCTGATTGAAGCGCAAGCTGAA 1260

RESULT 32
US-10-220-891-22
; Sequence 22, Application US/10220891
; Publication No. US20030207286A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWARA, AKIRA
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES HAVING CHARACTERISTICS OF ENHANCED
; TITLE OF INVENTION: EXPRESSION IN HUMAN NEUROBLASTOMA WITH FAVORABLE PROGNOSIS
; TITLE OF INVENTION: BASED ON COMPARISON BETWEEN HUMAN NEUROBLASTOMA WITH FAVORABLE
; TITLE OF INVENTION: PROGNOSIS AND HUMAN NEUROBLASTOMA WITH UNFAVORABLE PROGNOSIS
; FILE REFERENCE: 7388-73435
; CURRENT FILING DATE: 2003-03-07
; CURRENT APPLICATION NUMBER: US/10/220.891
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: JP 2000/140387
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: JP 2000/159195
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 108
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; SOFTWARE: Patentin version 3.2
; SEQ ID NO 22
; LENGTH: 1980
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-220-891-22

Alignment Scores:
Pred. No.: 6,7e-99 Length: 1980
Score: 898.00 Matches: 182
Percent Similarity: 98.41% Conservative: 4
Best Local Similarity: 96.30% Mismatches: 3
Query Match: 97.08% Indels: 0
DB: 17 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-220-891-22 (1-1980)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 1006 TCAGTTGTTGACCTCTCTGCTGAGAGACATTAGAGACTGGAGTGGTGGTGGTCC 1065

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 1066 AGCCTATTCAGCTGCTTTTCATTGCAGTATTCAGCATTTGAGCGTAAACGCTACATT 1125

QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 1126 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT 1185

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 1186 ATCCAGAAATCAGATGAAGCCACCAATTCAGGCAATATCTGGAATCTGAAGTTGCTATA 1245

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 1246 TCTGAGGAGTTGTTTCTGAGAGTACAGTAATCTGCTCTTGGTTCATGTGAACTGCAGATA 1305

QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 1306 AAGGAACCTCAGCGGCTCTCTCTAGTTGATGATTTAGTTGATTTCTCTGAGTTTTCAGTG 1365

QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db 1366 TTGATGTGGGTATTTACCTATGTTGGTGGCTGTTGTTTAAATGGTCTGACACTACTGATTTG 1425

QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 1426 GCTCTCATTTCACTCTTCTAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 1485

QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 1486 CATTATCTAGGACTTGCAAAATAGATGTTAAAGATGCTATGGCTAAATAATCCAGCAAAA 1545

QY 181 IleProGlyLeuLysArgLysAlaAsp 189
Db 1546 ATCCCTGGATTGAGCCCAAGCTGAA 1572

RESULT 33
US-09-978-360A-110
; Sequence 110, Application US/09978360A
; Publication No. US20040110939A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56.04.CIP
; CURRENT APPLICATION NUMBER: US/09/978,360A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/IB98/02122
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.pm
; SEQ ID NO 110
; LENGTH: 994
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 35..631
; FEATURE:
; NAME/KEY: sig peptide
; LOCATION: 35..160
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 8.6
; OTHER INFORMATION: seq ASLFLLLSLTVFS/IV
; FEATURE:
; NAME/KEY: polyA signal
; LOCATION: 901...906
; FEATURE:
; NAME/KEY: polyA site
; LOCATION: 979..994
US-09-978-360A-110

Alignment Scores:
Pred. No.: 5,29e-99 Length: 994
Score: 895.00 Matches: 182
Percent Similarity: 98.40% Conservative: 3
Best Local Similarity: 96.81% Mismatches: 3
Query Match: 96.76% Indels: 0
DB: 11 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-978-360A-110 (1-994)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 68 GTTGTGGTACCTCTCTGCTGAGAGACATTAGAGACTGGAGTGGTGGTGGTGGCAGC 127

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 128 CTATTCTGCTGCTTTTCATTGCAGTATTCAGCATTTGAGCGTAAACGCTACATTGCC 187

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 188 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 247

QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 248 CAGAAATCAGATGAAGCCACCAATTCAGGCGATATCTGGAATCTGGAATCTGATATCT 307

QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 308 GAGGAGTTGGTTGAGAGTACAGTAAATTTCTGCTCTTGGTCTGTGAACTGCACGATAAG 367

QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
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Db 368 GAACTCAGCGCCTCTCTTAGTGTGATTTAGTGTGATTTCTGAAAGTTGTCAGTGTG 427  
Qy 122 MetTTPValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuLeuAla 141  
Db 428 ATGTGGGTATTTACCTATGTGTGTCCTCTGTTTAAATGTCGACACTACTGATTTGGCT 487  
Qy 142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
Db 488 CTCATTTTCACCTTCAGTGTTCCTCTGTTTATGAAAGGTCATCAGGCACAGATAGATCAT 547  
Qy 162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 548 TATCTAGTACTGCAATAAGAAATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAATC 607  
Qy 182 ProGlyLeuLysArgLysAlaAsp 189  
Db 608 CCTGGATTGAAGCGCAAGCTGAA 631

RESULT 34

US-10-641-643-382  
; Sequence 382, Application US/10641643  
; Publication No. US20040077003A1  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; Susan G. Stuart  
; Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL  
; GENE EXPRESSION

NUMBER OF SEQUENCES: 1508  
CORRESPONDENCE ADDRESS:  
ADDRESS: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/641,643  
FILING DATE: 14-Aug-2003  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 382:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2610 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: LUNGNOT14  
CLONE: 1508778

SEQUENCE DESCRIPTION: SEQ ID NO: 382 :

US-10-641-643-382  
Alignment Scores:  
Pred. No.: 7,41e-98 Length: 2610  
Score: 891.00 Matches: 183  
Percent Similarity: 98.41% Conservative: 3  
Best Local Similarity: 96.83% Mismatches: 2

Query Match: 96.32% Indels: 1  
DB: 18 Gaps: 0  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-641-643-382 (1-2610)  
Qy 2 ValValAspLeuLeuTyrTTPArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 1311 GTTGTGACCTCCTGTACTGAGAGACATTAAAGAACTGGAGTGGTGTGGTCCACG 1370  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr-IleAl 41  
Db 1371 CTATTCCTGCTGCTTTCAATGACAGATATTCAGCATTGTGAGCGTAACAGCCTACAAATGC 1430  
Qy 41 aLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaI 61  
Db 1431 CTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAAGCTAT 1490  
Qy 61 eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 81  
Db 1491 CCAGAAATCAGATGAAGGCCACCCATTCAAGGCATATCTGGAATCTGAAGTTGCTATATC 1550  
Qy 81 rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLy 101  
Db 1551 TGAGGAGTTGGTTCAGAAAGTACAGTAATTCCTGCTTCTTGGTCTATGTGAACCTGCACATAA 1610  
Qy 101 sGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValIle 121  
Db 1611 GGAATCTAGGCGCCTCTCTTAGTTAGTATGATTTAGTTAGTTCTCTGAAGTTTGCAGTGT 1670  
Qy 121 uMetTTPValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuLeuAl 141  
Db 1671 GATGTGGGTATTTACCTATGTTGGTGCCTCTTTAATGGTCTGACACTACTGATTTTGGC 1730  
Qy 141 aLeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHi 161  
Db 1731 TCTCATTTCACTTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCA 1790  
Qy 161 sTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysI 181  
Db 1791 TTATCTAGGACTTCGCAATAGAAATGTTAAAGATGCTATGCTAAATCCAAAGCAAAAT 1850  
Qy 181 eProGlyLeuLysArgLysAlaAsp 189  
Db 1851 CCCTGGGTTGAAGCGCAAGCTGAA 1875  
RESULT 35  
US-10-466-258-10  
; Sequence 10, Application US/10466258  
; Publication No. US20040132096A1  
; GENERAL INFORMATION:  
; APPLICANT: GLAXO GROUP LIMITED  
; TITLE OF INVENTION: ASSAY  
; FILE REFERENCE: P80966 GCW  
; CURRENT APPLICATION NUMBER: US/10/466,258  
; CURRENT FILING DATE: 2003-07-15  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10  
; LENGTH: 1798  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (215)..(814)  
US-10-466-258-10  
Alignment Scores:  
Pred. No.: 8,28e-95 Length: 1798  
Score: 864.00 Matches: 182  
Percent Similarity: 97.88% Conservative: 3  
Best Local Similarity: 96.30% Mismatches: 3  
Query Match: 93.41% Indels: 2  
DB: 19 Gaps: 0



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Qy 13 LysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSer 32
Db 3 AAGACTGGAGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGC 62
Qy 33 IleValSerValThrAlaTyrIleAlaLeuLeuSerValThrIleSerPheArg 52
Db 63 ATTGTGAGCGTAACAGCCTACATTGCCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG 122
Qy 53 IleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAla 72
Db 123 ATATCAAGGGTGTGATCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA 182
Qy 73 TyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAla 92
Db 183 TATCTCGAATCTGAAGTTGCTATATCTCGAGGTTGGTTCAGAGTACAGTAATCTGCT 242
Qy 93 LeuGlyHisValAsnSerThrIleLysGluLeuArgLeuPheLeuValAspLeu 112
Db 243 CTGTGCTATGTGAATCGACAGCAATAAGAACTCAGCGCCTCTCTTAGTTGATGATTTA 302
Qy 113 ValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPhe 132
Db 303 GTTGATCTCTGAAGTTGCAAGTTGATGGGTATTTACTATGTTGGTGCCTTGTGT 362
Qy 133 AsnGlyLeuThrLeuLeuIleAlaLeuLeuSerLeuPheSerIleProValIleTyr 152
Db 363 AATGCTCTGACACTACTGATTTGGCTCTCATTCACCTTCAGTGTTCTTGTATTTAT 422
Qy 153 GluArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerValLysAsp 172
Db 423 GAACGGCATCAGGCACAGATAGATCATTTATCTAGGACTTGCAATAAGAAATGTTAAAGAT 482
Qy 173 AlaMetAlaLysIleGlnAlaLysIleProGlyLeuLysArgLysAlaAsp 189
Db 483 GCTATGGCTAAATCCAGCAAAAATCCCTGGATTGAAGCGCAAGCTGAA 533

RESULT 38
US-10-956-157-9762
; Sequence 9762, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9762
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-9762

Alignment Scores:
Pred. No.: 5,96e-85 Length: 1400
Score: 782.00 Matches: 159
Percent Similarity: 98.78% Conservative: 3
Best Local Similarity: 96.95% Mismatches: 2
Query Match: 84.54% Indels: 0
DB: 21 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-956-157-9762 (1-1400)
Qy 26 LeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLeu 45
Db 3 CTTTCATTGACAGTATTCAGCATTTGAGCGGTAAACAGCCTACATTCCTTGGCCCTGCTC 62
Qy 46 SerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAsp 65
Db 63 TCTGTGACCATCAGCTTTAGGATATCAAGGGTGTGATCCAAGCTATCCAGAAATCAGAT 122
Qy 66 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuVal 85
Db 123 GAAGCCACCCATTCAGGCGCATATCTGAAATCTGAAATCTGAAATCTGAGGAGTTGGTT 182
Qy 86 GlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArg 105
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Db 63 TCTGTGACCATCAGCTTTAGGATATCAAGGGTGTGATCCAAGCTATCCAGAAATCAGAT 122
Qy 66 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuVal 85
Db 123 GAAGCCACCCATTCAGGCGCATATCTGAAATCTGAAATCTGAAATCTGAGGAGTTGGTT 182
Qy 86 GlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArg 105
Db 183 CAGAAGTACAGTAATCTGCTCTTGGTCATCTGAACTGCACGATAAAGAACTCAGGCGC 242
Qy 106 LeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPhe 125
Db 243 CTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTTCATGTGGGTATTT 302
Qy 126 ThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeuIleSerLeu 145
Db 303 ACCATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTC 362
Qy 146 PheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeu 165
Db 363 TTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCATTTACTAGACTT 422
Qy 166 AlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 185
Db 423 GCAATAAAGAAATGTTAAAGATGCTATGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAG 482
Qy 186 ArgLysAlaAsp 189
Db 483 CGCAAAAGCTGAA 494

RESULT 39
US-10-956-157-9767
; Sequence 9767, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9767
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-9767

Alignment Scores:
Pred. No.: 5,96e-85 Length: 1400
Score: 782.00 Matches: 159
Percent Similarity: 98.78% Conservative: 3
Best Local Similarity: 96.95% Mismatches: 2
Query Match: 84.54% Indels: 0
DB: 21 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-956-157-9767 (1-1400)
Qy 26 LeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLeu 45
Db 3 CTTTCATTGACAGTATTCAGCATTTGAGCGGTAAACAGCCTACATTCCTTGGCCCTGCTC 62
Qy 46 SerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAsp 65
Db 63 TCTGTGACCATCAGCTTTAGGATATCAAGGGTGTGATCCAAGCTATCCAGAAATCAGAT 122
Qy 66 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuVal 85
Db 123 GAAGCCACCCATTCAGGCGCATATCTGAAATCTGAAATCTGAAATCTGAGGAGTTGGTT 182
Qy 86 GlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArg 105
```

Db 183 CAGAGTACAGTAATTTCTGCTCTTGTGTCATGTGAAGTGCACGATTAAGGAATCAGGCC 242  
Qy 106 LeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPhe 125  
Db 243 CTCCTCTTAGTTGATGATTAGTTGATTTCTCTGAAGTTTGAGTGTGGTATTT 302  
Qy 126 ThrTyrValGlyAlaLeuPheAnGlyLeuThrLeuLeuLeuAlaLeuLeuSerLeu 145  
Db 303 ACCTATGTTGGTGCCTGTTGTTAATGGTCTGACACTACTGATTTGGCTCTCATTTCACTC 362  
Qy 146 PheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeu 165  
Db 363 TTCAGTGTCTCTGTTATTTATGAACGCAATCAGGCATAGATAGATCATTTCTAGACTT 422  
Qy 166 AlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 185  
Db 423 GCAATAAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAATCCCTGGATTGAAG 482  
Qy 186 ArgLysAlaAsp 189  
Db 483 CGCAAGCTGAA 494

## RESULT 40

US-10-956-157-9766  
; Sequence 9766, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 9766  
; LENGTH: 1400  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-956-157-9766

Alignment Scores:  
Pred. No.: 2,598-74 Length: 1400  
Score: 695.00 Matches: 139  
Percent Similarity: 98.61% Conservative: 3  
Best Local Similarity: 96.53% Mismatches: 2  
Query Match: 75.14% Indels: 0  
DB: 21 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-956-157-9766 (1-1400)

Qy 46 SerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAsp 65  
Db 3 TCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATCCAGAAATCAGAT 62  
Qy 66 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluVal 85  
Db 63 GAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCTCAGGAGTTGGTT 122  
Qy 86 GlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlnLeuArgArg 105  
Db 123 CAGAAGTACAGTAATTTCTGCTCTTGTGTCATGTGAAGTGCACGATTAAGGAATCAGGCC 182  
Qy 106 LeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPhe 125  
Db 183 CTCCTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTGACGTTGTGATGTGGTATTT 242  
Qy 126 ThrTyrValGlyAlaLeuPheAnGlyLeuThrLeuLeuLeuAlaLeuLeuSerLeu 145  
Db 243 ACCTATGTTGGTGCCTTGTGTTAATGGTCTGACACTACTGATTTGGCTCTCATTTCACTC 302

Qy 146 PheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeu 165  
Db 303 TTCAGTGTCTCTGTTATTTATGAACGCAATCAGGCATAGATAGATCATTTCTAGACTT 362  
Qy 166 AlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 185  
Db 363 GCAATAAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAATCCCTGGATTGAAG 422  
Qy 186 ArgLysAlaAsp 189  
Db 423 CGCAAGCTGAA 434

## RESULT 41

US-10-084-817-333  
; Sequence 333, Application US/10084817  
; Publication No. US20030119009A1  
; GENERAL INFORMATION:  
; APPLICANT: Susan Stuart  
; APPLICANT: Jed G. Nuchtern  
; APPLICANT: Sharon E. Plon  
; APPLICANT: Jason M. Shohet  
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION  
; FILE REFERENCE: PA-0046 US  
; CURRENT APPLICATION NUMBER: US/10/084,817  
; CURRENT FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: 60/270,784  
; PRIOR FILING DATE: 2001-02-23  
; NUMBER OF SEQ ID NOS: 365  
; SOFTWARE: PERL Program  
; SEQ ID NO 333  
; LENGTH: 1520  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030119009A1 092267CB1  
US-10-084-817-333

Alignment Scores:  
Pred. No.: 2,678-72 Length: 1520  
Score: 679.00 Matches: 127  
Percent Similarity: 84.49% Conservative: 31  
Best Local Similarity: 67.91% Mismatches: 29  
Query Match: 73.41% Indels: 0  
DB: 15 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-084-817-333 (1-1520)

Qy 3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22  
Db 176 ATTGACCTGTTGTTATTTGGCGGACATCAAGCAGCGGCATCTGTTTGGAGTTCTCTG 235  
Qy 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
Db 236 CTGTGCTCTTCTCTCCCTGACCCAGTTTCAGCGTGTGAGCGTCTGTCGCCCTACCTGGCCCTG 295  
Qy 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
Db 296 GCGGCACCTCTCAGCCACCATCATGTTTCGCACTCAAGATCTGTTTACACGACGTGCAG 355  
Qy 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
Db 356 AAAACCGACGAAGGCCACCCCTTTCAAGGCTACTTGGAGCTTGAGATCAACCTTCTCAG 415  
Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102  
Db 416 GAGCAGATTTCAGAGTACACGACCTCCCTGCGACTTACGTGACACGACACTTAAGGAA 475  
Qy 103 LeuArgArgLeuPheLeuValAspSerLeuLysPheAlaValLeuMet 122  
Db 476 CTGAGAGGCTCTTCTCTGTCAGGACCTGGTGGATTCCTAAATTTTCAGTCTCTGATG 535  
Qy 123 TrpValPheThrTyrValGlyAlaLeuPheAnGlyLeuThrLeuLeuLeuAlaLeu 142

```
Db 536 TGGCTCCTGACCTACCTGTTGGGCGCTCTCTTCAATGGCGCTGACCGCTGCTCATGGCTGTG 595
Qy 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162
Db 596 GTTTCATGTTTACTCTACCTGTAGTGATGTGTTAAGCACGAGGACACGATTGACCAATAT 655
Qy 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
Db 656 CTGGGACTTGTGAGGACTCACATAATGCTGTGTGGCAAGATTCAGGCTAAATCCCA 715
Qy 183 GlyLeuLysArgLysAlaAsp 189
Db 716 GCGCGTAAGAGCGACGCTGAG 736

RESULT 42
US-10-267-502-213
; Sequence 213, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 213
; LENGTH: 2331
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-267-502-213

Alignment Scores:
Pred. No.: 5,22e-72 Length: 2331
Score: 679.00 Matches: 127
Percent Similarity: 84.49% Conservative: 31
Best Local Similarity: 67.91% Mismatches: 29
Query Match: 73.41% Indels: 0
DB: 18 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-267-502-213 (1-2331)
Qy 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22
Db 1768 ATTGACCTGTTGTTATTGGCGGACATCAAGCAGCGGCATCGTGTGGGAGTTCCTG 1827
Qy 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
Db 1828 CTGCTGCTCTCTCCCTGACCCAGTTTCAGCGTGGTGGAGCGTGGCGCTACCTGGCCCTG 1887
Qy 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62
Db 1888 GCGGACACTCTCAGCCACCATCATGTTTCGCGATCTACAAGTCTGTTTTCACAGCAGTGCG 1947
Qy 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
Db 1948 AAAACCGAGAGGCCACCCCTTTCAGGCGCTTTCAGGCGCTTTCAGATCACCCCTTCTCAG 2007
Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102
Db 2008 GAGCAGATTTCAGAGTACACGAGCTCCGCGAGTTCCTACGTGACGACGACACTTAAGGAA 2067
Qy 103 LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet 122
Db 2068 CTGAGGAGGCTCTCTCTTGTCCAGGACCTGGTGGATTCTCTTAAATTTTCAGTCTCTGATG 2127
Qy 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeu 142
Db 2128 TGGCTCTCGACTAGTGTGGCGCTCTCTTCAATGGCGCTGACCCCTGCTCTCATGGCTGTG 2187
Qy 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162
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Db 2188 GTTTCATGTTTACTCTACCTGTAGTGATGTGTTAAGCACGAGGACACGATTGACCAATAT 2247
Qy 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
Db 2248 CTGGGACTTGTGAGGACTCACATAATGCTGTGTGGCAAGATTCAGGCTAAATCCCA 2307
Qy 183 GlyLeuLysArgLysAlaAsp 189
Db 2308 GCGCGTAAGAGCGACGCTGAG 2328

RESULT 43
US-09-954-456-210
; Sequence 210, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 210
; LENGTH: 3202
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-210

Alignment Scores:
Pred. No.: 8,58e-72 Length: 3202
Score: 679.00 Matches: 127
Percent Similarity: 84.49% Conservative: 31
Best Local Similarity: 67.91% Mismatches: 29
Query Match: 73.41% Indels: 0
DB: 9 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-954-456-210 (1-3202)
Qy 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22
Db 1890 ATTGACCTGTTGTTATTGGCGGACATCAAGCAGCGGCATCGTGTGGGAGTTCCTG 1949
Qy 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
Db 1950 CTGCTGCTCTCTCTCCCTGACCCAGTTCAGCGTGGTGGAGCGTGGCGCTACCTGGCCCTG 2009
Qy 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62
Db 2010 GCGGACACTCTCAGCCACCATCATGTTTCGCGATCTACAAGTCTGTTTTCACAGCAGTGCG 2069
Qy 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
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Db 2070 AAAACGAGAGGCGCCCTTTCAAGGCTTACTTGAGCTTGAGATCAACCTTTCTCAG 2129
Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102
Db 2130 GAGCAGATTGAGAGTACAGGACTGCTGCGAGTCTACGTGACAGCACACATTAAAGGA 2189
Qy 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122
Db 2190 CTGAGGAGGCTCTTCTGCTCCAGGACCTGCTGGATTCCTTAAATTTGCAGTCTCTGATG 2249
Qy 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuLeuAlaLeu 142
Db 2250 TGCTCTCTGACCTACCTGCGCTCTCTCAATGGCTGACCTGCTGCTCAAGGCTG 2309
Qy 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162
Db 2310 GTTTCATGTTTACTCTACCTGTAGTGTATGTTAAGCACCAGGCACAGATTGACCAATAT 2369
Qy 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
Db 2370 CTGGGACTTGTGAGGACTCACATAATGCTGTTGTGGCAAGATTTCAGGCTAAATCCCA 2429
Qy 183 GlyLeuLysArgLysAlaAsp 189
Db 2430 GCGCTAAGAGGACGCTGAG 2450

RESULT 44
US-10-172-118-386
; Sequence 386, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 386
; LENGTH: 3202
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: L10333
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-386

Alignment Scores:
Pred. No.: 8.58e-72 Length: 3202
Score: 679.00 Matches: 127
Percent Similarity: 84.49% Conservative: 31
Best Local Similarity: 67.91% Mismatches: 29
Query Match: 73.41% Indels: 0
DB: 17 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-172-118-386 (1-3202)

Qy 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22
Db 1890 ATTGACCTGTGTATTGGCGGACATCAAGCAGAGCGGCTGTTGGGATTTCTTCG 1949
Qy 23 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
Db 1950 CTGCTGCTCTTCTCCCTGACCCAGTTTCAGGCTGTTGAGGCTTACCTGCGCCCTG 2009
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Qy 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaLeuGln 62
Db 2010 GCGCAGCTCTTCAGCCACCATCAGTTTCCGCATCTACAAGTCTGTGTTTACAGCAGTGCAG 2069
Qy 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
Db 2070 AAAACCGAGAGGCGCCCTTTCAAGGCTTACTTGAGCTTGAGATCAACCTTTCTCAG 2129
Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102
Db 2130 GAGCAGATTGAGAGTACAGGACTGCTGCGAGTCTACGTGACAGCACACATTAAAGGA 2189
Qy 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122
Db 2190 CTGAGGAGGCTCTTCTGCTCCAGGACCTGCTGGATTCCTTAAATTTGCAGTCTCTGATG 2249
Qy 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuLeuAlaLeu 142
Db 2250 TGCTCTCTGACCTACCTGCGCTCTCTCAATGGCTGACCTGCTGCTCAAGGCTG 2309
Qy 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162
Db 2310 GTTTCATGTTTACTCTACCTGTAGTGTATGTTAAGCACCAGGCACAGATTGACCAATAT 2369
Qy 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
Db 2370 CTGGGACTTGTGAGGACTCACATAATGCTGTTGTGGCAAGATTTCAGGCTAAATCCCA 2429
Qy 183 GlyLeuLysArgLysAlaAsp 189
Db 2430 GCGCTAAGAGGACGCTGAG 2450

RESULT 45
US-10-342-887-386
; Sequence 386, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 386
; LENGTH: 3202
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-386

Alignment Scores:
Pred. No.: 8.58e-72 Length: 3202
Score: 679.00 Matches: 127
Percent Similarity: 84.49% Conservative: 31
Best Local Similarity: 67.91% Mismatches: 29
Query Match: 73.41% Indels: 0
DB: 18 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-342-887-386 (1-3202)
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Qy	3	ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu	22
Db	1890	ATTGACCTGTTGTATGCGGGACATCAAGCAGCAGCGGCATCGTGTGTGGAGATTTCCGT	1949
Qy	23	PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu	42
Db	1950	CTGCTGCTTCTCCCTGACCCAGTTTCAGCGTGTGAGCGTCGTGGCGCTACCTTGGCCCTG	2009
Qy	43	AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln	62
Db	2010	GCGGCATCTCTCAGCCACCATCAGTTTCGCGCATCTACAAGTCGTGTTTACAAGCAGTCGAC	2069
Qy	63	LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu	82
Db	2070	AAACCCAGCAGGCCACCCCTTTCAAGCCCTACTTGGAGCTGTGAGATCAACCCCTTCTCTCAG	2129
Qy	83	GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu	102
Db	2130	GAGCAGATTTCAGAAGTACAGCATCGCTGCAGTTCTACGTGAACACGACACTTAAAGAA	2189
Qy	103	LeuArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet	122
Db	2190	CTGAGGAGGCTTTCCTTGTGCCAGCACTGGTGCATTCCTTAAATTTGCAGTCTCATG	2249
Qy	123	TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu	142
Db	2250	TGGCTCCTGCACCTACGTTGGCGCTCTCTTCAATGGCCTGCACCCCTGCTGCTCATGGCTGTG	2309
Qy	143	IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr	162
Db	2310	GTTTCAATGTTTACTCTACCTGTAGTGTATGTTAAGCACCAGGCACAGATTGACCAATAT	2369
Qy	163	LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro	182
Db	2370	CTGGGACTTGTGAGGACTCACAATAAATGCTGTTGTGCAAAAGATTTCAGGCTAAAATCCCA	2429
Qy	183	GlyLeuLysArgLysAlaAsp	189
Db	2430	GGCGCTAAGAGGCACGCTGAG	2450

RESULT 46

```

RES001 48
US-10-723-860-1480
; Sequence 1480, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1480
; LENGTH: 3202
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-1480

```

Alignment Scores:		
Pred. No.:	8,586-72	Length:
Score:	679.00	Matches:
Percent Similarity:	84.4%	Conservative:
Best Local Similarity:	67.91%	Mismatches:
Query Match:	73.41%	Indels:
DB:	20	Gaps:
		3202
		127
		31
		29
		0
		0

US-09-830-972-2 COPY 975 1163 (1-189) x US-10-723-860-1480 (1-3202)

Qy 3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22  
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::  
1890 ATTGCACCTGTGTATTGGCGGGACATCAAGCAGACGGGCATCGTGTTGGAGATTTCCTG 1949

Qy 23 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::  
1950 CTGCTGCTCTTCCTCCAGCCCATCAGTTTCGGCGTGGTGGCGTCTGGCCCTACCTGGGCCCTG 2009

Qy 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::  
2010 GCCGCATCTCCAGCCACCATCAGTTTCGGCATCTACAAGTCTGTTTTACAGCAGTGCAG 2069

Qy 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::  
2070 AAAACCCAGCAGAGCCACCCCTTTCAAGGCCCTACTTGGAGCTTGAGATCACCCCTTCTCAG 2129

Qy 83 GluLeuValGlnLysTyrSerAasnSerAlaLeuGlyHisValAasnSerThrIleLysGlu 102  
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::  
2130 GAGCAGATTAGAAGTACACGGACTCCCTGCAGTCTTACGTGAACAGCACACTTAAGGAA 2189

Qy 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::  
2190 CTGAGGAGGCTCTCTCTGTTCAGGACCTGGTGGAATCTCTAAAATTTGCAGTCTCTGATG 2249

Qy 123 TrpValPheThrTyrValGlyAlaLeuPheAasnGlyLeuThrLeuLeuIleLeuAlaLeu 142  
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::  
2250 TGGCTCTGACCTACGTTGGCGCTCTCTTCAATGGCTGACCCCTGCTGCTCATGGCTGTG 2309

Qy 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162  
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::  
2310 GTTTCATGTATTACTCTACCTGTAGTGTATGTTAAGCACCAGCAGATTCACCAATAT 2369

Qy 163 LeuGlyLeuAlaAasnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::  
2370 CTGGACTTGTGAGGACTCACATAATGCTGTTGTGCGAAAGATTGAGCTAAATATCCA 2429

Qy 183 GlyLeuLysArgLysAlaAsp 189  
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::  
2430 GGCGCTAAGAGGCACGCTGAG 2450

RESULT 47  
US-10-843-641A-3237  
; Sequence 3237, Application US/10843641A  
; Publication No. US20050064454A1  
; GENERAL INFORMATION:  
; APPLICANT: Avalon Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using  
; TITLE OF INVENTION: Signature Gene Sets  
; FILE REFERENCE: 689290-189  
; CURRENT FILING DATE: US/10/843,641A  
; PRIOR APPLICATION NUMBER: US/09/873,367  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US/09/954,531  
; PRIOR FILING DATE: 2001-09-18  
; PRIOR APPLICATION NUMBER: US/09/954,456  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US/09/962,436  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US/09/962,832  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US/09/964,824  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: US/09/967,768  
; PRIOR FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: US/09/968,007  
; PRIOR FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US/09/969,347  
; PRIOR FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US/09/969,708  
; PRIOR FILING DATE: 2001-10-03  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 8447

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3237
; LENGTH: 3202
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-3237

Alignment Scores:
Pred. No.:      8,58e-72      Length:      3202
Score:          679.00      Matches:      127
Percent Similarity: 84.49%      Conservative: 31
Best Local Similarity: 67.91%      Mismatches:  29
Query Match:      73.41%      Indels:       0
DB:              21          Gaps:       0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-843-641A-3237 (1-3202)

QY  3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22
Db  1890 ATTGACCTGTTGATTTGGCGGACATCAAGCAGACGGGCATCGTGTGGAGTTCCCG 1949
QY  23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
Db  1950 CTGCTGCTCTTCTCCCTGACCCAGTTTCAGCGTGGTGAGCGTCTGGCCCTACCTGGGCCCTG 2009
QY  43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaLeuGln 62
Db  2010 GCGGCACCTCTCAGCCACCATCATGATTTCCGCATCTACAAGTCTGTTTTACAAGCAGTGCAG 2069
QY  63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
Db  2070 AAACCGACGAGGCCACCCCTTTCAAGGCTTACTTGGAGCTTGAGATCACCCCTTCTCAG 2129
QY  83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102
Db  2130 GAGCAGATTTCAGAGTACACGAGCTGCCTGCAGTTCTACGTGAAACAGCACACTTAAGGAA 2189
QY  103 LeuArgArgLeuPheLeuValAspLeuValAspLeuValAspLeuPheAlaValLeuMet 122
Db  2190 CTGAGAGAGCTCTTCCTCTGTCAGGACCTGGTGGATTCCTTAAATTTTCAGTCTCTGATG 2249
QY  123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu 142
Db  2250 TGGCTCTGACCTACCTTGGCGCTCTCTTCATGGCTGACCTGCTGCTGCTGCTGCTGCTG 2309
QY  143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162
Db  2310 GTTCAATGTTTACTCTACCTGATGTATGTTAAGCACAGGACAGATTCACCAATAT 2369
QY  163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaIleGlnAlaLysIlePro 182
Db  2370 CTGGGACTTTGTGAGGACTCACATAAATGCTGTGTGGCAAGATTCAGGCTAAATCCCA 2429
QY  183 GlyLeuLysArgLysAlaAsp 189
Db  2430 GCGGCTAAGAGGACGCTGAG 2450

RESULT 49
US-10-205-219-94
; Sequence 94, Application US/10205219
; Publication No. US20030138803A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018200
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3237
; LENGTH: 3202
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-3237

Alignment Scores:
Pred. No.:      8,58e-72      Length:      3202
Score:          679.00      Matches:      127
Percent Similarity: 84.49%      Conservative: 31
Best Local Similarity: 67.91%      Mismatches:  29
Query Match:      73.41%      Indels:       0
DB:              21          Gaps:       0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-843-641A-3237 (1-3202)

QY  3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22
Db  1890 ATTGACCTGTTGATTTGGCGGACATCAAGCAGACGGGCATCGTGTGGAGTTCCCG 1949
QY  23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
Db  1950 CTGCTGCTCTTCTCCCTGACCCAGTTTCAGCGTGGTGAGCGTCTGGCCCTACCTGGGCCCTG 2009
QY  43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaLeuGln 62
Db  2010 GCGGCACCTCTCAGCCACCATCATGATTTCCGCATCTACAAGTCTGTTTTACAAGCAGTGCAG 2069
QY  63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
Db  2070 AAACCGACGAGGCCACCCCTTTCAAGGCTTACTTGGAGCTTGAGATCACCCCTTCTCAG 2129
QY  83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102
Db  2130 GAGCAGATTTCAGAGTACACGAGCTGCCTGCAGTTCTACGTGAAACAGCACACTTAAGGAA 2189
QY  103 LeuArgArgLeuPheLeuValAspLeuValAspLeuValAspLeuPheAlaValLeuMet 122
Db  2190 CTGAGAGAGCTCTTCCTCTGTCAGGACCTGGTGGATTCCTTAAATTTTCAGTCTCTGATG 2249
QY  123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu 142
Db  2250 TGGCTCTGACCTACCTTGGCGCTCTCTTCATGGCTGACCTGCTGCTGCTGCTGCTGCTG 2309
QY  143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162
Db  2310 GTTCAATGTTTACTCTACCTGATGTATGTTAAGCACAGGACAGATTCACCAATAT 2369
QY  163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaIleGlnAlaLysIlePro 182
Db  2370 CTGGGACTTTGTGAGGACTCACATAAATGCTGTGTGGCAAGATTCAGGCTAAATCCCA 2429
QY  183 GlyLeuLysArgLysAlaAsp 189
Db  2430 GCGGCTAAGAGGACGCTGAG 2450

RESULT 48
US-10-723-860-5926
; Sequence 5926, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
```



; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 94  
; LENGTH: 1502  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: rs-Rex-s  
US-10-205-219-94

Alignment Scores:  
Pred. No.: 3,478-72 Length: 1502  
Score: 678.00 Matches: 126  
Percent Similarity: 84.4% Conservative: 32  
Best Local Similarity: 87.3% Mismatches: 29  
Query Match: 73.3% Indels: 0  
DB: 15 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-205-219-94 (1-1502)

```
Qy 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22
Db 179 ATTGACCTTCTGTACTGGCGGACATCAAGCAGCGGATGTGTTTCGGAGCTTCCTG 238

Qy 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
Db 239 CTGCTGCTCTCTCCCTGACCCAGTTTACGGTTGTGAGCGTGTGCTTACCTGCGCCCTG 298

Qy 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62
Db 299 GCTGCGCCCTCTGCGCACCATCAGCTTCGCGCATCTCAAGTCCGTTTCTACAAGCTGTGCAG 358

Qy 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
Db 359 AAAACAGATGAGGGTACACCTTTCAAGGCTTACCTGGAGCTGGAGATCACCTGTGCCAG 418

Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102
Db 419 GAGCAGATCCAGAGTACACAGACTCGCTGCAGCTATACGTGAACAGCAGCTCTGAAGGAG 478

Qy 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122
Db 479 CTACGGAGGCTCTTCCTGGTCAGACCTCTGTTGGATTCCTTAAATTTTGCAGTCTCATG 538

Qy 123 TrpValPheThrTyrValGlyAlaLeuPheGlnGlyLeuThrLeuLeuIleAlaLeu 142
Db 539 TGGCTCTGACCTACGTGGCGGCACTCTCAATGGCCCTGACCCCTGCTTATGGCTGTG 598

Qy 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162
Db 599 GTTTCGATGTTTACTTACCTGCTGTATATGTTAAGCACCAGGACAGGTTGACCAATAT 658

Qy 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
Db 659 CTGGGACTTGTGAGGACTCACATAAACACCGTTGTGGCAAGATCCAGGCTAAATATCCCC 718

Qy 183 GlyLeuLysArgLysAlaAsp 189
Db 719 GCGGCCAAGAGGACGCTGAG 739
```

## RESULT 50

US-10-267-502-215  
; Sequence 215, Application US/10267502  
; Publication No. US20040071700A1  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Jaeseob  
; APPLICANT: Galant, Ron  
; TITLE OF INVENTION: Obesity Linked Genes  
; FILE REFERENCE: LSD-07416  
; CURRENT APPLICATION NUMBER: US/10/267,502  
; CURRENT FILING DATE: 2003-01-27  
; NUMBER OF SEQ ID NOS: 439  
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 215  
; LENGTH: 2343  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-267-502-215

Alignment Scores:  
Pred. No.: 6,978-72 Length: 2343  
Score: 678.00 Matches: 126  
Percent Similarity: 84.4% Conservative: 32  
Best Local Similarity: 87.3% Mismatches: 29  
Query Match: 73.3% Indels: 0  
DB: 18 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-267-502-215 (1-2343)

```
Qy 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22
Db 1780 ATTGACCTTCTGTACTGGCGGACATCAAGCAGACTGGGATGTGTTTCGGGAGCTTCCTG 1839

Qy 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
Db 1840 CTGCTGCTCTCTCCCTGACCCAGTTTACGGTTGTGAGCGTGTGCTTACCTGCGCCCTG 1899

Qy 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62
Db 1900 GCGGCCCTCTCTGCGCACCATCAGCTTCGCGCATCTACAAGTCCGTTTCTACAAGCTGTGCAG 1959

Qy 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
Db 1960 AAAACAGATGAGGGTACACCTTTCAAGGCTTACCTGGAGCTGGAGATCACCTGTGCCAG 2019

Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102
Db 2020 GAGCAGATCCAGAGTACACAGACTCGCTGCAGCTGTATGTGAACAGCAGCTCTGAAGGAG 2079

Qy 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122
Db 2080 CTACGGAGGCTTTTCTGCTGGTCAGGACCTGTGGATTCCTTAAATTTTGCAGTCTCATG 2139

Qy 123 TrpValPheThrTyrValGlyAlaLeuPheGlnGlyLeuThrLeuLeuIleAlaLeu 142
Db 2140 TGGCTCTGACCTACGTGGCGGCTCTTCAATGGCCCTGACCCCTGCTTATGGCTGTG 2199

Qy 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162
Db 2200 GTTTCGATGTTTACTTACCTGCTGTGTGTTAGCACCAGGACCAAGTTGACCAATAT 2259

Qy 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
Db 2260 CTGGGACTTGTGAGGACTCACATAAACACCGCTCGTGGCAAGATCCAGGCTAAATATCCCC 2319

Qy 183 GlyLeuLysArgLysAlaAsp 189
Db 2320 GCGGCCAAGAGGACGCTGAG 2340
```

## RESULT 51

US-09-960-352-8477  
; Sequence 8477, Application US/09960352  
; Patent No. US20020137139A1  
; GENERAL INFORMATION:  
; APPLICANT: Warren, Wesley C.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Byatt, John C.  
; APPLICANT: Mathialagan, Nagappan  
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
; FILE REFERENCE: 16511.006/37-21(10298)C  
; CURRENT APPLICATION NUMBER: US/09/960,352  
; CURRENT FILING DATE: 2001-09-24  
; NUMBER OF SEQ ID NOS: 15112  
; SEQ ID NO 8477  
; LENGTH: 422

; TYPE: DNA  
; ORGANISM: Bos taurus  
; OTHER INFORMATION: Clone ID: 36-LIB34-048-Q1-E1-A8  
US-09-960-352-8477

Alignment Scores:  
Pred. No.: 1,11e-72 Length: 422  
Score: 675.00 Matches: 136  
Percent Similarity: 98.57% Conservative: 2  
Best Local Similarity: 97.14% Mismatches: 2  
Query Match: 72.97% Indels: 0  
DB: 9 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-960-352-8477 (1-422)

```
QY 37 ThrAlaTyrIleAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGly 56
DB 2 ACGGCCTACATTGCCCTTGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATAAGGCT 61
QY 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76
DB 62 GTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTCAGGCGCATATTTGGAATCT 121
QY 77 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal 96
DB 122 GAAGTTGCTATATCTCAGGAGTTGGTTCAAGAGTACGCAATCTGCTCTTGGTCATGTT 181
QY 97 AsnSerThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeu 116
DB 182 AACTGCACAATAAAGAACTCAGAGCCCTCTCTTAGTTGATGATTTAGTTCATCTCTG 241
QY 117 LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr 136
DB 242 AAGTTTGCACTGTGATGGGTATTTACCTATGTTGGTGCCTTGTTCATGCTCTGACA 301
QY 137 LeuLeuIleLeuAlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGln 156
DB 302 CTACTAATTTGGCTCTGATTTTCACCTCTCAGTGTTCTCTGTTATTTATGACGGCATCAG 361
QY 157 ValGlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLys 176
DB 362 GCGCAATAGATCATTTCTGGACTTGCATAAAGATGTTAAAGATGCTATGGCTAAA 421
```

## RESULT 52

US-10-205-194-128  
; Sequence 128, Application US/10205194  
; Publication No. US20030134301A1  
; GENERAL INFORMATION:  
; APPLICANT: Warner-Lambert Company  
; APPLICANT: Lee, Kevin  
; APPLICANT: Dixon, Alistair  
; APPLICANT: Brooksbank, Robert  
; APPLICANT: Pimnock, Robert  
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain  
; FILE REFERENCE: WL-A-018201  
; CURRENT APPLICATION NUMBER: US/10/205,194  
; CURRENT FILING DATE: 5200-07-24  
; PRIOR APPLICATION NUMBER: GB 0118354.0  
; PRIOR FILING DATE: 2001-07-27  
; NUMBER OF SEQ ID NOS: 177  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 128  
; LENGTH: 1473  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: C1-13 protein  
US-10-205-194-128

Alignment Scores:  
Pred. No.: 1.31e-70 Length: 1473  
Score: 665.00 Matches: 126  
Percent Similarity: 84.49% Conservative: 32

Best Local Similarity: 67.38% Mismatches: 29  
Query Match: 71.89% Indels: 1  
DB: 15 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-205-194-128 (1-1473)

```
QY 3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22
DB 146 ATTGACCTTCTGTACTGCGGACATCAAGCAGACGGGATTTGTTCGGAGCTTCCTCG 205
QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
DB 206 CTGCTGCTCTCTCTCCCTGACCCAGTTCAGCGTTGTGAGCGTCTCGCCTACCTGGCCCTG 265
QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaLeuGln 62
DB 266 GCTGCCCTCTCTGCCACCATCAGCTTCGCGCATCTACAAGTCCGTCTTACAAGCTGTGCAG 325
QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
DB 326 AAAACAGATGAGGGTCACCCCTTCAAGGCTACCTGGAGCTGGAGATCACCTGTCCCCAG 385
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102
DB 386 GAGCAGATCCAGAAGTACACAGACTGCCTGCAGCTATACGTGAACAGACACTCTGAAGGAG 445
QY 103 LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet 122
DB 446 CTACGAGGCTCTCTCTGTCACAGACCTAGTGGATTCTTAAAAATTTGCAGTCTCATG 505
QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuLeuLeuLeuAlaLeu 142
DB 506 TGCTCTCTGACCTAGCTGGCGCACTCTCAATGGCCTGACCTGCTGTATGGCTGTG 565
QY 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162
DB 566 GTTTCGATGTTTACTCTACTCTGTTGTTATATGTTAAGCACCAGGCACAGGTTCACCAATAT 625
QY 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
DB 626 CTGGGACTTGTGAGGACTCACATAAACCCGTTGTGGCAAGATCCAGGCTAAATCCCC 685
QY 183 GlyLeuLysArgLysAlaAsp 189
DB 686 GCGGC-AAGAGGCTGCTGAG 705
```

## RESULT 53

US-09-960-352-11567  
; Sequence 11567, Application US/09960352  
; Patent No. US20020137139A1  
; GENERAL INFORMATION:  
; APPLICANT: Warren, Wesley C.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Byatt, John C.  
; APPLICANT: Mathialagan, Nagappan  
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
; FILE REFERENCE: 16511.006/37-21(10298)C  
; CURRENT APPLICATION NUMBER: US/09/960,352  
; CURRENT FILING DATE: 2001-09-24  
; NUMBER OF SEQ ID NOS: 15112  
; SEQ ID NO 11567  
; LENGTH: 422  
; TYPE: DNA  
; ORGANISM: Bos taurus  
; OTHER INFORMATION: Clone ID: 50-BOVMS1-005-Q1-E1-E6  
US-09-960-352-11567

Alignment Scores:  
Pred. No.: 1.76e-70 Length: 422  
Score: 657.00 Matches: 135  
Percent Similarity: 98.56% Conservative: 2  
Best Local Similarity: 97.12% Mismatches: 2

Query Match: 71.03% Indels: 0  
DB: 9 Gaps: 0  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-960-352-11567 (1-422)  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 4 AACTGTTCTCTGCTCTCGTCAGTATTCAGCAATTCAGCAATTCAGTGTACGGCCTACATT 63  
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
DB 64 GCCTTGGCCCTCTCTCTGACTATCAGCTTAGGATATATAAGGGTGTGATCCAGGCT 123  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
DB 124 ATCCAGAAATCTGATGAAGGCCACCAATTCAGGCAATATTCGAAATCTGAGTTCGTATA 183  
QY 81 SerGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAsnSerThrIle 100  
DB 184 TCTGAGGAGTTGGTTTTCAGAAAGTACAGCAATTCCTGCTCTTGGTCAATGTTAACTGCACAATA 243  
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
DB 244 AAAGAACTCAGACGCCCTCTCTTAGTGTAGTATTTAGTTGATCTCTGAAAGTTTCAGTG 303  
QY 121 LeuMetTyrValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuIleLeu 140  
DB 304 TTGATGTGGTATTTACCTATGTTGGTGGCTTGTTCATGCTGACACTACTAATTTTG 363  
QY 141 AlaLeuLysSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIle 159  
DB 364 GCTCTGATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGCATCAGGCGCAATA 420

## RESULT 54

## US-10-408-967-1

; Sequence 1, Application US/10408967  
; Publication NO. US20040063161A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacia & Upjohn Company  
; APPLICANT: Yan, Riqiang  
; APPLICANT: Lu, Yifeng  
; TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease  
; FILE REFERENCE: 00925  
; CURRENT APPLICATION NUMBER: US/10/408,967  
; PRIOR FILING DATE: 2003-04-08  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 711  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-408-967-1

## Alignment Scores:

Pred. No.: 6,596-66 Length: 711  
Score: 622.50 Matches: 113  
Percent Similarity: 81.05% Conservative: 41  
Best Local Similarity: 59.47% Mismatches: 35  
Query Match: 67.30% Indels: 1  
DB: 18 Gaps: 1

## US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-408-967-1 (1-711)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
DB 139 CGGGTGCACGATCTCATTTTCTGGAGAGATGTGAAGAAGACTGGGTTGTCTTTGGCACC 198  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 199 AGCTGATCATGCTCTCTTCCCTGGCAGCTTTCAGTGTTCATGTCAGTGTGTTCTTACTTC 258  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60

DB 259 ATCTGGGCTCTTCTCTGTCCACATCAGCTTCAGGATCTCAAGTCCGTCATCAAGCT 318  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
DB 319 GTACAGAAGTTCAGAAGAAGGCCATCCATTCAAAGCCTACCTGGAGCTAGACATTACTCTG 378  
QY 81 SerGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAsnSerThrIle 100  
DB 379 TCCTCAGAAGCTTTTCCATAATTACATGAATGTCGCCATCGTCACATCAACAGGGCCCTG 438  
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
DB 439 AAACATCATTTCTGCTCTCTTCTGTAGAAGACTCTGGTTGACTCTCTTGAAGCTGGCTGC 498  
QY 121 LeuMetTyrValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuIleLeu 140  
DB 499 TTCATGTGGCTGTAGTACCTATGTTGGTGTCTTTTAAACGGAATCACCCCTCTTAATCTT 558  
QY 141 AlaLeuLysSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
DB 559 GCTGAACGTCTCATTTTTCAGTGTCCCGATTGCTATGAGAAGTACAGACCCAGATTGAT 618  
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
DB 619 CACTATGTGGCATCGCCCGAGATCAGACCAAGTCAATTTGTTGAAAAGATCCAAGCAAAA 678  
QY 181 IleProGlyLeu---LysArgLysAlaAsp 189  
DB 679 CTCCCTGGAATCGCCCAAAAAAAGGCAGAA 708

## RESULT 55

## US-10-106-698-1945

; Sequence 1945, Application US/10106698  
; Publication NO. US20030109690A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides  
; FILE REFERENCE: PA005P1  
; CURRENT APPLICATION NUMBER: US/10/106,698  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: PCT/US00/26524  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US 60/157,137  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: US 60/163,280  
; PRIOR FILING DATE: 1999-11-03  
; NUMBER OF SEQ ID NOS: 8564  
; SOFTWARE: PatentIn Ver. 3.0  
; SEQ ID NO 1945  
; LENGTH: 1330  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-106-698-1945

## Alignment Scores:

Pred. No.: 1,766-65 Length: 1330  
Score: 622.50 Matches: 113  
Percent Similarity: 81.05% Conservative: 41  
Best Local Similarity: 59.47% Mismatches: 35  
Query Match: 67.30% Indels: 1  
DB: 15 Gaps: 1

## US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-106-698-1945 (1-1330)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
DB 297 CGGGTGCACGATCTCATTTTCTGGAGAGATGTGAAGAAGACTGGGTTGTCTTTGGCACC 356  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 357 ACGTGTATCATGCTCTTCCCTGGCAGCTTTCAGTGTTCATGTCAGTGTGTTCTTACTTC 416  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60

Db 417 ATCTGGCTCTTCTCTCTGTCCACCATCAGCTTCCAGGATCTACAAAGTCCCTCATCCAAGCT 476  
QY 61 lIeGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 477 GTACAGAGTCAGAGAGAGGCCATCCATTCAAAGCTTACTGGACGTAGACATTACTCTG 536  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGluGlyHisValAsnSerThrile 100  
Db 537 TCTCAGAAAGCTTTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 596  
QY 101 LysGluLeuArgArgGluPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
Db 597 AAATCAATATTCT 656  
QY 121 LeuMetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
Db 657 TTCATGTGGCTGATGACCTATGTTGGTGTCTGTTTAAACGGAATCACCCTTCTAATTCCT 716  
QY 141 AlaLeuLysSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnLysLeu 160  
Db 717 GCTGAATCTGCTCATTTTCACTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 776  
QY 161 HisTyrLeuGluLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 777 CACTATGTTGGCATCGCCGAGATCAGACCAAGTCAATGTTGAAAGATCAAGCAAAA 836  
QY 181 lIeProGlyLeu---LysArgLysAlaAsp 189  
Db 837 CTCCTCGGAATCGCCCAAAAAAAGGCAGAA 866

## RESULT 56

US-09-729-674-19  
; Sequence 19, Application US/09729674  
; Patent No. US20010039335A1  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: McCoy, John M.  
; APPLICANT: LaVallie, Edward R.  
; APPLICANT: Collins-Racie, Lisa A.  
; APPLICANT: Evans, Cheryl  
; APPLICANT: Merberg, David  
; APPLICANT: Treacy, Maurice  
; APPLICANT: Agostino, Michael J.  
; APPLICANT: Steininger II, Robert J.  
; APPLICANT: Spaulding, Vikki  
; APPLICANT: Wong, Gordon G.  
; APPLICANT: Clark, Hilary  
; APPLICANT: Fechtel, Kim  
; APPLICANT: Genetics Institute, Inc.  
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
; FILE REFERENCE: 6055-64X  
; CURRENT APPLICATION NUMBER: US/09/729,674  
; CURRENT FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: 09/539,330  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 283  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 1656  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-729-674-19  
Alignment Scores:  
Pred. No.: 2 48e-65 Length: 1656  
Score: 622.50 Matches: 113  
Percent Similarity: 81.05% Conservative: 41  
Best Local Similarity: 59.47% Mismatches: 35  
Query Match: 67.30% Indels: 1  
DB: Gaps: 1  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-729-674-19 (1-1656)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 165 GCGGTGTCAGATCT 224  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 225 AGCTGTATCATCT 284  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 285 ATCTCTGGCT 344  
QY 61 lIeGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 345 GTACAGAAAGTCAGAGAGAGGCCATCCATTCAAAGCTTACTGGACGTAGACATTACTCTG 404  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrile 100  
Db 405 TCTCAGAAAGCTTTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 464  
QY 101 LysGluLeuArgArgGluPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
Db 465 AAATCAATATTCT 524  
QY 121 LeuMetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
Db 525 TTCATGTGGCTGATGACCTATGTTGGTGTCTGTTTAAACGGAATCACCCTTCTAATTCCT 584  
QY 141 AlaLeuLysSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnLysLeu 160  
Db 585 GCTGAATCTGCTCATTTTCACTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 644  
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 645 CACTATGTTGGCATCGCCGAGATCAGACCAAGTCAATGTTGAAAGATCAAGCAAAA 704  
QY 181 lIeProGlyLeu---LysArgLysAlaAsp 189  
Db 705 CTCCTCGGAATCGCCCAAAAAAAGGCAGAA 734  
RESULT 57  
US-10-913-553-19  
; Sequence 19, Application US/10913553  
; Publication No. US20050003491A1  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: McCoy, John M.  
; APPLICANT: LaVallie, Edward R.  
; APPLICANT: Collins-Racie, Lisa A.  
; APPLICANT: Evans, Cheryl  
; APPLICANT: Merberg, David  
; APPLICANT: Treacy, Maurice  
; APPLICANT: Agostino, Michael J.  
; APPLICANT: Steininger II, Robert J.  
; APPLICANT: Spaulding, Vikki  
; APPLICANT: Wong, Gordon G.  
; APPLICANT: Clark, Hilary  
; APPLICANT: Fechtel, Kim  
; APPLICANT: Genetics Institute, Inc.  
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
; FILE REFERENCE: 6055-64X  
; CURRENT APPLICATION NUMBER: US/10/913,553  
; CURRENT FILING DATE: 2004-08-09  
; PRIOR APPLICATION NUMBER: US/09/539,330  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 283  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 1656  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-913-553-19

Alignment Scores:  
 Pred. No.: 2,48e-65 Length: 1656  
 Score: 622.50 Matches: 113  
 Percent Similarity: 81.05% Conservatives: 41  
 Best Local Similarity: 59.47% Mismatches: 35  
 Query Match: 67.30% Indels: 1  
 DB: 21 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-913-553-19 (1-1656)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
 Db 165 GCGGTGCAGATCTGATTTCTGAGAGATGTGAAGAAGACTGGGTGCTTTGGCACC 224  
 Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValAlaTyrIle 40  
 Db 225 AGCTGTATCATCTGCTTCCCTGGCAGCTTTCAGTGTCTCAGTGTGGTTTCTTACCTC 284  
 Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 285 ATCTGGCTCTTCTCTGTCAACATCAGCTTCAGATCTACAAGTCCGTATCAAGCT 344  
 Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 345 GTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCTACCTGGACCTAGACATTACTCTG 404  
 Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 Db 405 TCCTCAGAAGCTTCCATAATACATGAATGCTGCCATGCTGCATCAACAGGCCCTG 464  
 Qy 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 465 AAATCATATTATTCGTTCTCTTCTGTGAGAGATCTGGTTGACTCTTGAAGCTGCTCTC 524  
 Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 Db 525 TTCATGTGGCTGATGACCTATGTTGGTGTCTGTTTAAACGGAATCACCCTTCTAATTCT 584  
 Qy 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 585 GCTGAACGTCTCATTTTCAGTGTCCGATTTGCTATGAGAAGTACAGACCCAGATTGAT 644  
 Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 645 CACTATGTGGATCGCCCAAAAAAAGGACAGAA 734  
 Qy 181 IleProGlyLeu---LysArgLysAlaAsp 189  
 Db 705 CTCCTCGAATCGCCCAAAAAAAGGACAGAA 734

RESULT 58  
 US-09-765-205-25  
 ; Sequence 25, Application US/09765205  
 ; Patent No. US20020034800A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cao, Li  
 ; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES  
 ; FILE REFERENCE: 1458.004/200130.449  
 ; CURRENT APPLICATION NUMBER: US/09/765,205  
 ; CURRENT FILING DATE: 2001-01-17  
 ; PRIOR APPLICATION NUMBER: US/09/212,440  
 ; PRIOR FILING DATE: 1998-12-16  
 ; NUMBER OF SEQ ID NOS: 46  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 25  
 ; LENGTH: 1668  
 ; TYPE: DNA  
 ; ORGANISM: human  
 US-09-765-205-25

Alignment Scores:  
 Pred. No.: 2,51e-65 Length: 1668  
 Score: 622.50 Matches: 113  
 Percent Similarity: 81.05% Conservatives: 41  
 Best Local Similarity: 59.47% Mismatches: 35

Score: 622.50 Matches: 113  
 Percent Similarity: 81.05% Conservatives: 41  
 Best Local Similarity: 59.47% Mismatches: 35  
 Query Match: 67.30% Indels: 1  
 DB: 9 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-765-205-25 (1-1668)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
 Db 237 GCGGTGCAGATCTGATTTCTGAGAGATGTGAAGAAGACTGGGTGCTTTGGCACC 296  
 Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValAlaTyrIle 40  
 Db 297 AGCTGTATCATCTGCTTCCCTGGCAGCTTTCAGTGTCTCAGTGTGGTTTCTTACCTC 356  
 Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 357 ATCTGGCTCTTCTCTGTCAACATCAGCTTCAGATCTACAAGTCCGTATCAAGCT 416  
 Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 417 GTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCTACCTGGACCTAGACATTACTCTG 476  
 Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 Db 477 TCCTCAGAAGCTTCCATAATACATGAATGCTGCCATGCTGCATCAACAGGCCCTG 536  
 Qy 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 537 AAATCATATTATTCGTTCTCTTCTGTGAGAGATCTGGTTGACTCTTGAAGCTGCTCTC 596  
 Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 Db 597 TTCATGTGGCTGATGACCTATGTTGGTGTCTGTTTAAACGGAATCACCCTTCTAATTCT 656  
 Qy 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 657 GCTGAACGTCTCATTTTCAGTGTCCGATTTGCTATGAGAAGTACAGACCCAGATTGAT 716  
 Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 717 CACTATGTGGATCGCCCAAAAAAAGGACAGAA 776  
 Qy 181 IleProGlyLeu---LysArgLysAlaAsp 189  
 Db 777 CTCCTCGAATCGCCCAAAAAAAGGACAGAA 806

RESULT 59  
 US-10-347-669-25  
 ; Sequence 25, Application US/10347669  
 ; Publication No. US20050084850A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cao, Li  
 ; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES  
 ; FILE REFERENCE: 1458.004/200130.449  
 ; CURRENT APPLICATION NUMBER: US/10/347,669  
 ; CURRENT FILING DATE: 2003-01-16  
 ; PRIOR APPLICATION NUMBER: US/09/212,440  
 ; PRIOR FILING DATE: 1998-12-16  
 ; NUMBER OF SEQ ID NOS: 46  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 25  
 ; LENGTH: 1668  
 ; TYPE: DNA  
 ; ORGANISM: human  
 US-10-347-669-25

Alignment Scores:  
 Pred. No.: 2,51e-65 Length: 1668  
 Score: 622.50 Matches: 113  
 Percent Similarity: 81.05% Conservatives: 41  
 Best Local Similarity: 59.47% Mismatches: 35



1 PRIOR APPLICATION NUMBER: 60/047,615  
2 PRIOR FILING DATE: 1997-05-23  
3 PRIOR APPLICATION NUMBER: 60/047,597  
4 PRIOR FILING DATE: 1997-05-23  
5 PRIOR APPLICATION NUMBER: 60/047,502  
6 PRIOR FILING DATE: 1997-05-23  
7 PRIOR APPLICATION NUMBER: 60/047,633  
8 PRIOR FILING DATE: 1997-05-23  
9 PRIOR APPLICATION NUMBER: 60/047,583  
10 PRIOR FILING DATE: 1997-05-23  
11 PRIOR APPLICATION NUMBER: 60/047,617  
12 PRIOR FILING DATE: 1997-05-23  
13 PRIOR APPLICATION NUMBER: 60/047,618  
14 PRIOR FILING DATE: 1997-05-23  
15 PRIOR APPLICATION NUMBER: 60/047,503  
16 PRIOR FILING DATE: 1997-05-23  
17 PRIOR APPLICATION NUMBER: 60/047,592  
18 PRIOR FILING DATE: 1997-05-23  
19 PRIOR APPLICATION NUMBER: 60/047,581  
20 PRIOR FILING DATE: 1997-05-23  
21 PRIOR APPLICATION NUMBER: 60/047,584  
22 PRIOR FILING DATE: 1997-05-23  
23 PRIOR APPLICATION NUMBER: 60/047,500  
24 PRIOR FILING DATE: 1997-05-23  
25 PRIOR APPLICATION NUMBER: 60/047,587  
26 PRIOR FILING DATE: 1997-05-23  
27 PRIOR APPLICATION NUMBER: 60/047,492  
28 PRIOR FILING DATE: 1997-05-23  
29 PRIOR APPLICATION NUMBER: 60/047,598  
30 PRIOR FILING DATE: 1997-05-23  
31 PRIOR APPLICATION NUMBER: 60/047,613  
32 PRIOR FILING DATE: 1997-05-23  
33 PRIOR APPLICATION NUMBER: 60/047,582  
34 PRIOR FILING DATE: 1997-05-23  
35 PRIOR APPLICATION NUMBER: 60/047,596  
36 PRIOR FILING DATE: 1997-05-23  
37 PRIOR APPLICATION NUMBER: 60/047,612  
38 PRIOR FILING DATE: 1997-05-23  
39 PRIOR APPLICATION NUMBER: 60/047,632  
40 PRIOR FILING DATE: 1997-05-23  
41 PRIOR APPLICATION NUMBER: 60/047,601  
42 PRIOR FILING DATE: 1997-05-23  
43 PRIOR APPLICATION NUMBER: 60/043,580  
44 PRIOR FILING DATE: 1997-04-11  
45 PRIOR APPLICATION NUMBER: 60/043,568  
46 PRIOR FILING DATE: 1997-04-11  
47 PRIOR APPLICATION NUMBER: 60/043,314  
48 PRIOR FILING DATE: 1997-04-11  
49 PRIOR APPLICATION NUMBER: 60/043,569  
50 PRIOR FILING DATE: 1997-04-11  
51 PRIOR APPLICATION NUMBER: 60/043,311  
52 PRIOR FILING DATE: 1997-04-11  
53 PRIOR APPLICATION NUMBER: 60/043,671  
54 PRIOR FILING DATE: 1997-04-11  
55 PRIOR APPLICATION NUMBER: 60/043,674  
56 PRIOR FILING DATE: 1997-04-11  
57 PRIOR APPLICATION NUMBER: 60/043,669  
58 PRIOR FILING DATE: 1997-04-11  
59 PRIOR APPLICATION NUMBER: 60/043,312  
60 PRIOR FILING DATE: 1997-04-11  
61 PRIOR APPLICATION NUMBER: 60/043,313  
62 PRIOR FILING DATE: 1997-04-11  
63 PRIOR APPLICATION NUMBER: 60/043,672  
64 PRIOR FILING DATE: 1997-04-11  
65 PRIOR APPLICATION NUMBER: 60/043,315  
66 PRIOR FILING DATE: 1997-04-11  
67 PRIOR APPLICATION NUMBER: 60/048,974  
68 PRIOR FILING DATE: 1997-06-06  
69 PRIOR APPLICATION NUMBER: 60/056,886  
70 PRIOR FILING DATE: 1997-08-22  
71 PRIOR APPLICATION NUMBER: 60/056,877  
72 PRIOR FILING DATE: 1997-08-22  
73 PRIOR APPLICATION NUMBER: 60/056,889

74 PRIOR FILING DATE: 1997-08-22  
75 PRIOR APPLICATION NUMBER: 60/056,893  
76 PRIOR FILING DATE: 1997-08-22  
77 PRIOR APPLICATION NUMBER: 60/056,630  
78 PRIOR FILING DATE: 1997-08-22  
79 PRIOR APPLICATION NUMBER: 60/056,878  
80 PRIOR FILING DATE: 1997-08-22  
81 PRIOR APPLICATION NUMBER: 60/056,662  
82 PRIOR FILING DATE: 1997-08-22  
83 PRIOR APPLICATION NUMBER: 60/056,872  
84 PRIOR FILING DATE: 1997-08-22  
85 PRIOR APPLICATION NUMBER: 60/056,882  
86 PRIOR FILING DATE: 1997-08-22  
87 PRIOR APPLICATION NUMBER: 60/056,637  
88 PRIOR FILING DATE: 1997-08-22  
89 PRIOR APPLICATION NUMBER: 60/056,903  
90 PRIOR FILING DATE: 1997-08-22  
91 PRIOR APPLICATION NUMBER: 60/056,888  
92 PRIOR FILING DATE: 1997-08-22  
93 PRIOR APPLICATION NUMBER: 60/056,879  
94 PRIOR FILING DATE: 1997-08-22  
95 PRIOR APPLICATION NUMBER: 60/056,880  
96 PRIOR FILING DATE: 1997-08-22  
97 PRIOR APPLICATION NUMBER: 60/056,894  
98 PRIOR FILING DATE: 1997-08-22  
99 PRIOR APPLICATION NUMBER: 60/056,911  
100 PRIOR FILING DATE: 1997-08-22  
101 PRIOR APPLICATION NUMBER: 60/056,636  
102 PRIOR FILING DATE: 1997-08-22  
103 PRIOR APPLICATION NUMBER: 60/056,874  
104 PRIOR FILING DATE: 1997-08-22  
105 PRIOR APPLICATION NUMBER: 60/056,910  
106 PRIOR FILING DATE: 1997-08-22  
107 PRIOR APPLICATION NUMBER: 60/056,864  
108 PRIOR FILING DATE: 1997-08-22  
109 PRIOR APPLICATION NUMBER: 60/056,631  
110 PRIOR FILING DATE: 1997-08-22  
111 PRIOR APPLICATION NUMBER: 60/056,845  
112 PRIOR FILING DATE: 1997-08-22  
113 PRIOR APPLICATION NUMBER: 60/056,892  
114 PRIOR FILING DATE: 1997-08-22  
115 PRIOR APPLICATION NUMBER: 60/057,761  
116 PRIOR FILING DATE: 1997-08-22  
117 PRIOR APPLICATION NUMBER: 60/047,595  
118 PRIOR FILING DATE: 1997-05-23  
119 PRIOR APPLICATION NUMBER: 60/047,599  
120 PRIOR FILING DATE: 1997-05-23  
121 PRIOR APPLICATION NUMBER: 60/047,588  
122 PRIOR FILING DATE: 1997-05-23  
123 PRIOR APPLICATION NUMBER: 60/047,585  
124 PRIOR FILING DATE: 1997-05-23  
125 PRIOR APPLICATION NUMBER: 60/047,586  
126 PRIOR FILING DATE: 1997-05-23  
127 PRIOR APPLICATION NUMBER: 60/047,590  
128 PRIOR FILING DATE: 1997-05-23  
129 PRIOR APPLICATION NUMBER: 60/047,594  
130 PRIOR FILING DATE: 1997-05-23  
131 PRIOR APPLICATION NUMBER: 60/047,589  
132 PRIOR FILING DATE: 1997-05-23  
133 PRIOR APPLICATION NUMBER: 60/047,593  
134 PRIOR FILING DATE: 1997-05-23  
135 PRIOR APPLICATION NUMBER: 60/047,614  
136 PRIOR FILING DATE: 1997-05-23  
137 PRIOR APPLICATION NUMBER: 60/043,578  
138 PRIOR FILING DATE: 1997-04-11  
139 PRIOR APPLICATION NUMBER: 60/043,576  
140 PRIOR FILING DATE: 1997-04-11  
141 PRIOR APPLICATION NUMBER: 60/047,501  
142 PRIOR FILING DATE: 1997-05-23  
143 PRIOR APPLICATION NUMBER: 60/043,670  
144 PRIOR FILING DATE: 1997-04-11  
145 PRIOR APPLICATION NUMBER: 60/056,632  
146 PRIOR FILING DATE: 1997-08-22

; PRIOR APPLICATION NUMBER: 60/056,664  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,876  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,881  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,909  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,875  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,862  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,887  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,908  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/048,964  
 ; PRIOR FILING DATE: 1997-06-06  
 ; PRIOR APPLICATION NUMBER: 60/057,650  
 ; PRIOR FILING DATE: 1997-09-05  
 ; PRIOR APPLICATION NUMBER: 60/056,884  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/057,669  
 ; PRIOR FILING DATE: 1997-09-05

Alignment Scores:  
 Pred. No.: 2,74e-65 Length: 1766  
 Score: 622.50 Matches: 113  
 Percent Similarity: 81.05% Conservative: 41  
 Best Local Similarity: 59.47% Mismatches: 35  
 Query Match: 67.30% Indels: 1  
 DB: 10 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-882-171-254 (1-1766)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
 Db 287 GCGGTGCAGATCTGATTTCTGGAGAGATGTGAAGAGCTGGTGTCTTTGGCACC 346  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 347 ACGCTGATCATGTCTCTTCCCTGGCAGCTTTTCAGTGTCTCATCGTGTGTTCTTACCTC 406  
 QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAla 60  
 Db 407 ATCTGGCTCTTCTCTCTCACCATCAGCTTTCAGGATCTACAAGTCCGTCATCCAAGCT 466  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 467 GTACAGAGTCAGAAGAGCCATCCATTCAGGCTTACCTGGACGTAGACATTACTCTG 526  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 Db 527 TCCTCAGAAGCTTTCATTAATATACATGAATGTGCTGCTGACATCAACAGGCGCCCTG 586  
 QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 587 AAACCTATTATTCTCTTCTGTTAGAGATCTGTTGACTCTCTTGAAGCTGGCTGTC 646  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 Db 647 TTCATGTGGCTGATGACCTATGTTGTGCTGTTTAAACGGAATCACCTTCTTAATCTT 706  
 QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 707 GCTGAACCTGCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGATTGAT 766  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 767 CACTATGTTGGATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCACAGCAAA 826  
 QY 181 IleProGlyLeu---LysArgLysAlaAsp 189  
 Db 827 CTCCTCGAATCGCCCAAAAAAAGGCAGAA 856

Db 827 CTCCTCGAATCGCCCAAAAAAAGGCAGAA 856

RESULT 62  
 ; Sequence 254, Application US/10164861  
 ; Publication No. US20030225248A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: 186 Human Secreted proteins  
 ; FILE REFERENCE: PZ002P1  
 ; CURRENT APPLICATION NUMBER: US/10/164,861  
 ; CURRENT FILING DATE: 2002-06-10  
 ; PRIOR APPLICATION NUMBER: US/09/149,476  
 ; PRIOR FILING DATE: 1998-09-08  
 ; PRIOR APPLICATION NUMBER: PCT/US98/04493  
 ; PRIOR FILING DATE: 1998-03-06  
 ; NUMBER OF SEQ ID NOS: 757  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 254  
 ; LENGTH: 1766  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-164-861-254

Alignment Scores:  
 Pred. No.: 2,74e-65 Length: 1766  
 Score: 622.50 Matches: 113  
 Percent Similarity: 81.05% Conservative: 41  
 Best Local Similarity: 59.47% Mismatches: 35  
 Query Match: 67.30% Indels: 1  
 DB: 17 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-164-861-254 (1-1766)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
 Db 287 GCGGTGCAGATCTGATTTCTGGAGAGATGTGAAGAGCTGGTGTCTTTGGCACC 346  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 347 ACGCTGATCATGTCTCTTCCCTGGCAGCTTTTCAGTGTCTCATCGTGTGTTCTTACCTC 406  
 QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 407 ATCTGGCTCTTCTCTCTCACCATCAGCTTTCAGGATCTACAAGTCCGTCATCCAAGCT 466  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 467 GTACAGAGTCAGAAGAGCCATCCATTCAGGCTTACCTGGACGTAGACATTACTCTG 526  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 Db 527 TCCTCAGAAGCTTTCATTAATATACATGAATGTGCTGCTGACATCAACAGGCGCCCTG 586  
 QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 587 AAACCTATTATTCTCTTCTGTTAGAGATCTGTTGACTCTCTTGAAGCTGGCTGTC 646  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 Db 647 TTCATGTGGCTGATGACCTATGTTGTGCTGTTTAAACGGAATCACCTTCTTAATCTT 706  
 QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 707 GCTGAACCTGCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGATTGAT 766  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 767 CACTATGTTGGATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCACAGCAAA 826  
 QY 181 IleProGlyLeu---LysArgLysAlaAsp 189  
 Db 827 CTCCTCGAATCGCCCAAAAAAAGGCAGAA 856



## RESULT 63

US-10-276-774-980  
; Sequence 980, Application US/10276774  
; Publication No. US20040053245A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-030  
; CURRENT APPLICATION NUMBER: US/10/276,774  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/560,875  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 09/496,914  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 2700  
; SOFTWARE: Custom  
; SEQ ID NO 980  
; LENGTH: 1915  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-276-774-980

## Alignment Scores:

Pred. No.:	3,11e-65	Length:	1915
Score:	622.50	Matches:	113
Percent Similarity:	81.05%	Conservative:	41
Best Local Similarity:	59.47%	Mismatches:	35
Query Match:	67.30%	Indels:	1
DB:	18	Gaps:	1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-276-774-980 (1-1915)

Qy	1	SerValValAspLeuLeuTyrTrpArgAspLeuLeuLysThrGlyValValPheGlyAla	20
Db	287	CGGGTGCAGATCTGATTTCTCGGAGAGATGTGAAGAGACTGGGTTGTCTTTGGCACC	346
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	347	ACGCTGATCATGCTCTTCCCTGGCAGCTTTCAGTGTCATCAGTGTGTTCTTACCTC	406
Qy	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
Db	407	ATCTGGCTCTTCTCTGTCCACATCAGCTTCAGATCTCAAGTCCGTCATCCAGCT	466
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
Db	467	GTACAGAAGTCAGAGAAGGGCCATCCATTCAAAGCCTACCTGGAGCTAGACATTACTCTG	526
Qy	81	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle	100
Db	527	TCCTCAGAAGCTTTCATAATATACATGATGTCGTCATGTCATCAACAGGGCCCTG	586
Qy	101	LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal	120
Db	587	AAACTATTATTCGCTCTTCTGTTAGAGATCTGGTTGACTCTTGAAGCTGGCTGTC	646
Qy	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
Db	647	TTTATGTGGCTGATGACCTATGTTGCTGTGTTTAAACGGAATCACCTTCTTAATCTT	706
Qy	141	AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp	160
Db	707	GCTGAACCTGCTATTTTCAGTGTCCGATTTGCTATGAGAAGTACAAACCCAGATTGAT	766
Qy	161	HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys	180
Db	767	CACATATGTTGGATCGCCCGAGATCAGACCAAGTCAATTGTTGAAGATCCAGCANA	826
Qy	181	IleProGlyLeu---LysArgLysAlaAsp	189
Db	827	CTCCCTGGAATCGCCAAAAAAGGCAGAA	856

## RESULT 64

US-09-809-391-255  
; Sequence 255, Application US/09809391  
; Publication No. US20030049618A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P2  
; CURRENT APPLICATION NUMBER: US/09/809,391  
; CURRENT FILING DATE: 2001-03-16  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 761  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 255  
; LENGTH: 2664  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (2623)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2640)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2652)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (2662)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-809-391-255

## Alignment Scores:

Pred. No.:	5,22e-65	Length:	2664
Score:	622.50	Matches:	113
Percent Similarity:	81.05%	Conservative:	41
Best Local Similarity:	59.47%	Mismatches:	35
Query Match:	67.30%	Indels:	1
DB:	10	Gaps:	1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-809-391-255 (1-2664)

Qy	1	SerValValAspLeuLeuTyrTrpArgAspLeuLeuLysThrGlyValValPheGlyAla	20
Db	262	CGGGTGCAGATCTGATTTCTGGAGAGATGTGAAGAGACTGGGTTGTCTTTGGCACC	321
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	322	ACGCTGATCATGCTCTTCCCTGGCAGCTTTCAGTGTCATCAGTGTGTTCTTACCTC	381
Qy	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
Db	382	ATCTGGCTCTTCTCTGTCCACATCAGCTTCAGGATCTCAAGTCCGTCATCCAGCT	441
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
Db	442	GTACAGAAGTCAGAGAAGGGCCATCCATTCAAAGCCTACCTGGAGCTAGACATTACTCTG	501
Qy	81	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle	100
Db	502	TCCTCAGAAGCTTTCATAATATACATGATGTCGTCATGTCATCAACAGGGCCCTG	561
Qy	101	LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal	120
Db	562	AAACTATTATTCGCTCTTCTGTTAGAGATCTGGTTGACTCTTGAAGCTGGCTGTC	621
Qy	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
Db	622	TTTATGTGGCTGATGACCTATGTTGCTGTGTTTAAACGGAATCACCTTCTTAATCTT	681
Qy	141	AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp	160

Db 682 GCTGAAGTCTATTTTCAGTGTCCGATTTCTATGAGAGTACAGACCCAGATTGAT 741  
Qy 161 HisTyrLeuGlyeulalenLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
|||:::|||||:::|  
Db 742 CACTATGTTGGCAGTCCCGAGATCAGACCAAGTCAATTGTTGAAAGATCCAGCAAAA 801  
Qy 181 IleProGlyLeu---LysArgLysAlaAsp 189  
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Db 802 CTCCTGGAATCGCCAAAAAAGGCGAGAA 831  
RESULT 65  
US-09-882-171-255  
; Sequence 255, Application US/09882171  
; Publication No. US20030175858A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P2  
; CURRENT APPLICATION NUMBER: US/09/882,171  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 09/809,391  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 09/149,476  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: PCT/US98/04493  
; PRIOR FILING DATE: 1998-03-06  
; PRIOR APPLICATION NUMBER: 60/040,162  
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; PRIOR APPLICATION NUMBER: 60/038,621  
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; PRIOR FILING DATE: 1997-03-07  
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; PRIOR FILING DATE: 1997-05-23  
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; PRIOR FILING DATE: 1997-05-23  
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; PRIOR FILING DATE: 1997-08-22  
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; PRIOR APPLICATION NUMBER: 60/056,874  
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7	PRIOR APPLICATION NUMBER: 60/056,845	
8	PRIOR FILING DATE: 1997-08-22	
9	PRIOR APPLICATION NUMBER: 60/056,892	
10	PRIOR FILING DATE: 1997-08-22	
11	PRIOR APPLICATION NUMBER: 60/057,761	
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15	PRIOR APPLICATION NUMBER: 60/047,599	
16	PRIOR FILING DATE: 1997-05-23	
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18	PRIOR FILING DATE: 1997-05-23	
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23	PRIOR APPLICATION NUMBER: 60/047,590	
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26	PRIOR FILING DATE: 1997-05-23	
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28	PRIOR FILING DATE: 1997-05-23	
29	PRIOR APPLICATION NUMBER: 60/047,593	
30	PRIOR FILING DATE: 1997-05-23	
31	PRIOR APPLICATION NUMBER: 60/047,614	
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33	PRIOR APPLICATION NUMBER: 60/043,578	
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40	PRIOR FILING DATE: 1997-04-11	
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42	PRIOR FILING DATE: 1997-08-22	
43	PRIOR APPLICATION NUMBER: 60/056,664	
44	PRIOR FILING DATE: 1997-08-22	
45	PRIOR APPLICATION NUMBER: 60/056,876	
46	PRIOR FILING DATE: 1997-08-22	
47	PRIOR APPLICATION NUMBER: 60/056,881	
48	PRIOR FILING DATE: 1997-08-22	
49	PRIOR APPLICATION NUMBER: 60/056,909	
50	PRIOR FILING DATE: 1997-08-22	
51	PRIOR APPLICATION NUMBER: 60/056,875	
52	PRIOR FILING DATE: 1997-08-22	
53	PRIOR APPLICATION NUMBER: 60/056,862	
54	PRIOR FILING DATE: 1997-08-22	
55	PRIOR APPLICATION NUMBER: 60/056,887	
56	PRIOR FILING DATE: 1997-08-22	
57	PRIOR APPLICATION NUMBER: 60/056,908	
58	PRIOR FILING DATE: 1997-08-22	
59	PRIOR APPLICATION NUMBER: 60/048,964	
60	PRIOR FILING DATE: 1997-06-06	
61	PRIOR APPLICATION NUMBER: 60/057,650	
62	PRIOR FILING DATE: 1997-09-05	
63	PRIOR APPLICATION NUMBER: 60/056,884	
64	PRIOR FILING DATE: 1997-08-22	
65	PRIOR APPLICATION NUMBER: 60/057,669	
66	PRIOR FILING DATE: 1997-09-05	

Alignment Scores:	
Pred. No.:	5.22e-65
Score:	622.50
Percent Similarity:	81.05%
Best Local Similarity:	59.47%
Query Match:	67.30%
	Length: 2664
	Matches: 113
	Conservative: 41
	Mismatches: 35
	Indels: 1

[illegible]

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; NAME/KEY: SITE
; LOCATION: (2652)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2662)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-164-861-255

Alignment Scores:
Pred. No.: 5,22e-65 Length: 2664
Score: 622.50 Matches: 113
Percent Similarity: 81.05% Conservative: 41
Best Local Similarity: 59.47% Mismatches: 35
Query Match: 67.30% Indels: 1
DB: 17 Gaps: 1

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-164-861-255 (1-2664)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 262 GCGGTGCAGCATCTGATTTCTGGAGAGATGTGAGAGAGACTGGGTTTCTTTGGCACC 321
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 322 ACCTCATCATCTGCTCTCCCTGGCAGCTTTTCAGTGTCTACGATGTGTTCTTACCTC 381
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 382 ATCTCGCTCTCTCTCTGTCACCATCAGCTTCAGGATCTACAGTCCGTCATCCAGCT 441
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 442 GTACAGAGTCAGAGAGAGCCATCCATTTCAAAGCCTTACCTGACGCTAGACATTACTCTG 501
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 502 TCTCAGAGCTTTCATTAATACATGAATGCTGCTGATGTCGATGACATCAACAGGCCCCCTG 561
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 562 AAATCATATTATTCGCTCTCTCTGTTAGAGATCTGTTGACTCTCTTGAAGCTGGCTGTC 621
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 622 TTCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 681
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 682 GCTGAACCTGCTATTTTCAGTGTCCCGATGCTATGAGAGATGATGATGATGATGATGATGAT 741
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 742 CACTATGTTGGCATCGCCGAGATCAGACCAAGTCAATGTTGAAAAGATCCCAAGCAAAA 801
QY 181 IleProGlyLeu---LysArgLysAlaAsp 189
Db 802 CTCCTCGGAATCGCCAAAAGAGGAGAA 831

RESULT 67
US-10-723-860-6867
; Sequence 6867, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739

; NAME/KEY: SITE
; LOCATION: (2652)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2743)..(2747)
; OTHER INFORMATION: n is a, c, g, or t
US-10-723-860-6867

Alignment Scores:
Pred. No.: 5,54e-65 Length: 2768
Score: 622.50 Matches: 113
Percent Similarity: 81.05% Conservative: 41
Best Local Similarity: 59.47% Mismatches: 35
Query Match: 67.30% Indels: 1
DB: 20 Gaps: 1

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-723-860-6867 (1-2768)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 320 GCGGTGCAGCATCTGATTTCTGGAGAGATGTGAGAGAGACTGGGTTTCTTTGGCACC 379
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 380 ACCTCATCATCTGCTCTCCCTGGCAGCTTTTCAGTGTCTACGATGTGTTCTTACCTC 439
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 440 ATCTCGCTCTCTCTCTGTCACCATCAGCTTCAGGATCTACAGTCCGTCATCCAGCT 499
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 500 GTACAGAGTCAGAGAGAGCCATCCATTTCAAAGCCTTACCTGACGCTAGACATTACTCTG 559
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 560 TCTCAGAGCTTTCATTAATACATGAATGCTGCTGATGTCGATGACATCAACAGGCCCCCTG 619
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 620 AAATCATATTATTCGCTCTCTCTGTTAGAGATCTGTTGACTCTCTTGAAGCTGGCTGTC 679
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 680 TTCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 739
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 740 GCTGAACCTGCTATTTTCAGTGTCCCGATGCTATGAGAGATGATGATGATGATGATGATGAT 799
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 800 CACTATGTTGGCATCGCCGAGATCAGACCAAGTCAATGTTGAAAAGATCCCAAGCAAAA 859
QY 181 IleProGlyLeu---LysArgLysAlaAsp 189
Db 860 CTCCTCGGAATCGCCAAAAGAGGAGAA 889

RESULT 68
US-10-108-260A-449
; Sequence 449, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
```

; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 449  
; LENGTH: 3637  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-108-260A-449

Alignment Scores:  
Pred. No.: 3 47e-64 Length: 3637  
Score: 617.50 Matches: 113  
Percent Similarity: 80.53% Conservative: 40  
Best Local Similarity: 59.47% Mismatches: 36  
Query Match: 66.76% Indels: 1  
DB: 17 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-108-260A-449 (1-3637)

```
Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1379 TCAGTGCAGCATCTGATTTCTGGAGAGATGGAAGAGACTGGGTTGTCTTTGGCACC 1438
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1439 ACGCTGATCATGCTCTTCCCTGGCAGCTTTCAGTGTCTCATCAGTGTGGTTCTTACCTC 1498
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1499 ATCTGGCTCTTCTCTGTCCATCATCAGTCTCAGGATCTACAGTCCGTCTATCAAGCT 1558
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1559 GTACAGAAGTCAGAGAAGGCCATTCATTCAAAGCTTACCTGGAGCTAGACATTACTCTG 1618
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1619 TCCTCAGAAGCTTTCATTAATACATGAATGCTGCATGTGTCATCAACAGAGGCCCTG 1678
Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1679 AAATCATATTTCGTCTCTTCTGTGAAGAAGTCTGGTTGACTCTCTGAAGCTGGCTGTC 1738
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1739 TTCAATGGCTGATGACCTATGTTGTGCTGTTTAAACGGAATCACCTCTTAATCTT 1798
Qy 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1799 GCTGAACCTGCTCATTTTCAGTGTCCCGATTTGTCTATGAGAAGTACAAGACCCAGATTGAT 1858
Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1859 CACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCAAGCAAAA 1918
Qy 181 IleProGlyLeu---LysArgLysAlaAsp 189
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1919 CTCCTGGATCGCCAAAAGAGGAGCAAA 1948
```

## RESULT 69

US-10-159-563-443  
; Sequence 443, Application US/10159563  
; Publication No. US20040009154A1

## GENERAL INFORMATION:

; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus  
; APPLICANT: Peterson, Carsten  
; APPLICANT: Meltzer, Paul  
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR  
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS  
; FILE REFERENCE: 11613.56US11  
; CURRENT APPLICATION NUMBER: US/10/159,563  
; CURRENT FILING DATE: 2002-12-09  
; PRIOR APPLICATION NUMBER: US 10/133,937

; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 444  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 443  
; LENGTH: 3637  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-159-563-443

Alignment Scores:  
Pred. No.: 3 47e-64 Length: 3637  
Score: 617.50 Matches: 113  
Percent Similarity: 80.53% Conservative: 40  
Best Local Similarity: 59.47% Mismatches: 36  
Query Match: 66.76% Indels: 1  
DB: 17 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-159-563-443 (1-3637)

```
Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1379 TCAGTGCAGCATCTGATTTCTGGAGAGATGGAAGAGACTGGGTTGTCTTTGGCACC 1438
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1439 ACGCTGATCATGCTCTTCCCTGGCAGCTTTCAGTGTCTCATCAGTGTGGTTCTTACCTC 1498
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1499 ATCTGGCTCTTCTCTGTCCATCATCAGTCTCAGGATCTACAGTCCGTCTATCAAGCT 1558
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1559 GTACAGAAGTCAGAGAAGGCCATTCATTCAAAGCTTACCTGGAGCTAGACATTACTCTG 1618
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1619 TCCTCAGAAGCTTTCATTAATACATGAATGCTGCATGTGTCATCAACAGAGGCCCTG 1678
Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1679 AAATCATATTTCGTCTCTTCTGTGAAGAAGTCTGGTTGACTCTCTGAAGCTGGCTGTC 1738
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1739 TTCAATGGCTGATGACCTATGTTGTGCTGTTTAAACGGAATCACCTCTTAATCTT 1798
Qy 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1799 GCTGAACCTGCTCATTTTCAGTGTCCCGATTTGTCTATGAGAAGTACAAGACCCAGATTGAT 1858
Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1859 CACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCAAGCAAAA 1918
Qy 181 IleProGlyLeu---LysArgLysAlaAsp 189
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1919 CTCCTGGATCGCCAAAAGAGGAGCAAA 1948
```

## RESULT 70

US-09-823-245A-510  
; Sequence 510, Application US/09823245A  
; Publication No. US20020039760A1

## GENERAL INFORMATION:

; APPLICANT: Wong, Gordon G.  
; APPLICANT: Clark, Hilary  
; APPLICANT: Fechtel, Kim  
; APPLICANT: Agostino, Michael J.  
; APPLICANT: Howes, Steven H.  
; APPLICANT: Resnick, Richard J.  
; APPLICANT: Gulukota, Kamalakari  
; APPLICANT: Graham, James R.  
; APPLICANT: Genetics Institute, Inc.

```
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6401
; CURRENT APPLICATION NUMBER: US/09/823,245A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/194,941
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 510
; LENGTH: 1636
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-823-245A-510

Alignment Scores:
Pred. No.: 4,87e-62 Length: 1636
Score: 595.50 Matches: 112
Percent Similarity: 80.53% Conservative: 41
Best Local Similarity: 58.95% Mismatches: 36
Query Match: 64.38% Indels: 2
DB: Gaps: 9

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-823-245A-510 (1-1636)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 248 GCGGTGCAGATCTGATTTCTGGAGAGATGGAAGAGACTGGGTGCTTTGGCACC 307
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 308 ACGTGATCATGCTGCTTC-CTGGCAGCTTTCAGTGTCATCAGTGTGGTTCTTACCTC 366
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAla 60
Db 367 ATCTTGCTCTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAACT 426
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 427 GTACAGAGTCAGAAGAGCCATCCATTCAAAGCCCTACTGGACGTAGACATTACTCTG 486
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
Db 487 TCTCAGAGCTTTCCTCAATATACATGAATGCTGCCATGTCACATCAACAGGGCCCTG 546
QY 101 LysGluLeuArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 547 AAATCATATTGCTCTCTCTGTTGTTAGAGATCTGGTTGACTCTCTTGAAGCTGGCTGC 606
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db 607 TTCATGTGGCTGATGACCTATGTTGGTGTCTGTTTTTAACGGATACCCCTTCAATCTT 666
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
Db 667 GCTGAAGTCTCATTTTCAGTGTCCGATGTTCTATGAGAAGTACAAGACCCAGATTGAT 726
QY 161 HisTyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 727 CACTATGTTGGCATCCCGCAGATCAGACCAAGTCAATTGTTGAAAAGATCCCAAGCAAAA 786
QY 181 IleProGlyLeu--LysArgLysAlaAsp 189
Db 787 CTCCTCGGAATCCCAAAAAAAGGCGAGAA 816

RESULT 71
US-09-960-352-5154
; Sequence 5154, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 9092
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 39-LIB3058-023-Q1-K1-B4
US-09-960-352-9092

Alignment Scores:
Pred. No.: 2.84e-57 Length: 423
Score: 549.00 Matches: 423
Percent Similarity: 98.28% Conservative: 4
```

```
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 5154
; LENGTH: 389
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 22-LIB34-043-Q1-E1-F5
US-09-960-352-5154

Alignment Scores:
Pred. No.: 4.83e-59 Length: 389
Score: 563.00 Matches: 116
Percent Similarity: 99.15% Conservative: 1
Best Local Similarity: 98.31% Mismatches: 1
Query Match: 60.86% Indels: 0
DB: Gaps: 9

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-960-352-5154 (1-389)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 34 GTTGTGACCTCTCTACTGGAGACATTAAGAGACTGGAGTGGTGTTCGTGCCACG 93
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 94 TTGTTCTCTGCTCTCTGTCAGCATTTACGATTTGAGTGTAAACGGCTTACATTCG 153
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 154 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 213
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 214 CAGAATCTGATGAGGCCACCCATTCAGGCATATTTGGAATCTGAAGTTCGTATCT 273
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 274 GAGGAGTTGGTTTCAGAAAGTACAGCAATTCCTCTTGGTTCATGTTAACTGCACAATAAAA 333
QY 102 GluLeuArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAla 119
Db 334 GAATCAGACGCTCTCTTCTAGTATGATTTAGTTGATTTCTCTGAAGTTTGCA 387

RESULT 72
US-09-960-352-9092
; Sequence 9092, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 9092
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 39-LIB3058-023-Q1-K1-B4
US-09-960-352-9092

Alignment Scores:
Pred. No.: 2.84e-57 Length: 423
Score: 549.00 Matches: 423
Percent Similarity: 98.28% Conservative: 4
```

Best Local Similarity: 94.83%  
Query Match: 59.35%  
DB: 9

Mismatches: 2  
Indels: 0  
Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-960-352-9092 (1-423)

Qy 74 LeuGluSerGluValAlaIleSerGluLeuValGlnLysTyrSerAsnSerAlaLeu 93  
Db 3 TTGGAATCTGAAGTTGCTATATCTGATGAGTTGGTTCAGAGTACAGCAATTCGCTCT 62  
Qy 94 GlyHisValAsnSerThrIleLysGluLeuArgArgLeuPheValAspLeuVal 113  
Db 63 GGTGATGTTAACTGCACAAATAAAGAACTCAGACGCCCTCTTCTAGTTGATGATTTAGTT 122  
Qy 114 AspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyValAlaLeuPheAsn 133  
Db 123 GATTCCTGAAGTTGCTAGTTGATGTTGGTATTTACATATGTTGGTCTTGTTCAT 182  
Qy 134 GlyLeuThrLeuLeuLeuAlaLeuLysSerLeuPheSerIleProValIleTyrGlu 153  
Db 183 GGTCTGACACTACTAAATTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTTATTATGAA 242  
Qy 154 ArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAla 173  
Db 243 CGGCATCAGCGCGCAATAATAGATCATTTCTGGGACTTGCATAAATAAGAAATGTTAAAGATGCT 302  
Qy 174 MetAlaLysIleGlnAlaLysIleProGlyLeuLysArgLysAlaAsp 189  
Db 303 ATGCTAATAATCCAAAGCAAAATCCCTGATGTAAGCGTTAAAGCTGAA 350

## RESULT 73

US-10-302-172-111  
; Sequence 111, Application US/10302172  
; Publication No. US20040053250A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Xue, Aidong J.  
; TITLE OF INVENTION: Drmanac, Radolje T.  
; TITLE OF INVENTION: No. US20040053250A1 Arginine-rich Protein-like Nucleic Acids and  
; FILE REFERENCE: 803.1GNC  
; CURRENT APPLICATION NUMBER: US/10/302,172  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/225,251  
; PRIOR FILING DATE: 2002-08-20  
; PRIOR APPLICATION NUMBER: PCT US02/05095  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US 09/799,451  
; PRIOR FILING DATE: 2001-03-05  
; NUMBER OF SEQ ID NOS: 950  
; SOFTWARE: pt FL\_genes Version 2.0  
; SEQ ID NO 111  
; LENGTH: 3517  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (196)..(654)  
US-10-302-172-111

Alignment Scores:  
Pred. No.: 7.46e-55 Length: 3517  
Score: 541.00 Matches: 102  
Percent Similarity: 68.97% Conservative: 38  
Best Local Similarity: 50.25% Mismatches: 35  
Query Match: 58.49% Indels: 28  
DB: 18 Gaps: 2

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-302-172-111 (1-3517)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 2906 GTGCACGATCTGATTTCTCGAGAGATGTGAAGAAGACTGGGTTGTCTTTGGCACCACG 2965

Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 2966 CTGATCATGCTGCTTTCCTGGCAGCTTTCAGTGCATCAGTGTGGTCTTCTTACTCATC 3025  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 3026 CTGGCTCTTCTCTGTCCATCAGCTTCAAGATCTCAAGATCGTGCATCCAGCTGTA 3085  
Qy 62 GlnLysSerAspGluGlyHisProPheArgIleTyrLeuGluSerGluValAlaIleSer 81  
Db 3086 CAGAAGTCAGAGAAGGCCATCCATTCAAGCCCTACCTGGAGCTAGACATTACTCTGTCC 3145  
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
Db 3146 TCAGAGCTTTCATATATACATGATGCTGCCATGTCACATCAACAGGCCCTGAAA 3205  
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 3206 CTCAATTATTCGCTCTTCTGTTAGAGATCTGGTGTGACTCTTGAAGCTGGCTGTCTTC 3265  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheArgGlyLeuThrLeuIleLeuAla 141  
Db 3266 ATGTGGCTGATGACCTATGTTGGTGTCTTTTAAACGGAATCACCCCTTCTAATCTTGT 3325  
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGln----- 156  
Db 3326 GAATGCTCATTTTCAGTGTCCGATGTCATATGAGAAGTACAGGATGCAGCTGTGCTA 3385  
Qy 157 -----ValGlnIle----- 159  
Db 3386 GCGCTGAGCAGGCAAGAGTCCACACTGAAGTATCAGAGAAGCTCCAGGCAAAAGCAA 3445  
Qy 160 -----AspHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAla 173  
Db 3446 GAGCACCAGCACCAGATGATGATCTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATT 3505  
Qy 174 MetAlaLys 176  
Db 3506 GTTGAAAAG 3514

## RESULT 74

US-10-660-946-4  
; Sequence 4, Application US/10660946  
; Publication No. US2004006313A1  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; Au-Young, Janice  
; Goli, Surya K.  
; Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/660,946  
; FILING DATE: 12-Sep-2003  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/228,213A  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/700,607  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:

```
/
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0114 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ INFORMATION FOR SEQ ID NO: 4:
/   SEQUENCE CHARACTERISTICS:
/     LENGTH: 1095 base pairs
/     TYPE: nucleic acid
/     STRANDEDNESS: single
/     TOPOLOGY: linear
/     MOLECULE TYPE: cDNA
/     IMMEDIATE SOURCE:
/     LIBRARY: TBPINOBO1
/     CLONE: 31870
/   SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-660-946-4
Alignment Scores:
Pred. No.: 1.25e-53 Length: 1095
Score: 524.50 Matches: 102
Percent Similarity: 72.7% Conservative: 37
Best Local Similarity: 53.4% Mismatches: 30
Query Match: 56.7% Indels: 22
DB: 18 Gaps: 2
US-09-830-972-2_COPY_975_1163 (1-189) x US-10-660-946-4 (1-1095)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
DB 329 GCGGTGCAGCATCTGATTCTTGGAGAGATGTGAAGAGACTGGGTGTCTTTGGCACC 388
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 389 AGCGTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTGATCATGTTGGTTTCTACCTC 448
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
DB 449 ATCTGGCTCTCTCTCTGTCACCATCAGCTTCAGGATCTCAAGTCCGTCATCCAAGCT 508
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 509 GTACAGAAAGTCAGAGAGAGCCATTCATTCAGAGCTTCCCTGGAGTACGATTAATCTGTG 568
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100
DB 569 TCCTCAGAGCTTTCATTAATACATGATGTCGATGTCACATCAACAGGCGCTG 628
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
DB 629 AAACATCATATTTCGTCTCTTCTGTGTAGAGATCTGTTGACTCTCCTTGAAGCTGGCTGC 688
QY 121 LeuMetTrpValPheThrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
DB 689 TTCATGTGGCTGATGACCTATGTTGGTGTGTTTAAAGGAATCACCCCTCTTAATCTT 748
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160
DB 749 GCTGAAGTCTCTATTNNAGTCTCCGATGTTGNTATNAGAAAGTAC----- 793
QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180
DB 794 -----AAGGTTCCAAAGCAA 808
QY 180 stleProGlyLeu---LysArgLysAlaAsp 189
DB 809 ACTCCCTGGAATCGCCCAAAAAAAGGCAGAA 839
RESULT 75
US-10-267-502-211
; Sequence 211, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 211
; LENGTH: 669
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-10-267-502-211
Alignment Scores:
Pred. No.: 2.05e-53 Length: 669
Score: 520.00 Matches: 94
Percent Similarity: 74.5% Conservative: 41
Best Local Similarity: 51.9% Mismatches: 46
Query Match: 56.2% Indels: 0
DB: 18 Gaps: 0
US-09-830-972-2_COPY_975_1163 (1-189) x US-10-267-502-211 (1-669)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
DB 76 GTGGAATCCCTTATCTACTGCGCGCATGTGAAGAAATCCGGCATTTGCTTCGGCGCTGC 135
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 136 CTGATCACACTGGCGGCATCTCCAGCTTCTCGGTGATCAGCGTGTTCGCCTACTTGTG 195
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 196 CTCCTCAACCTCTTCGCGCACCGTCGCTTCAGAACTCAAAATCTGTGACACAGCCGCTG 255
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 256 CAAAGACAAAGAGAGGTGACCCCTTTAAGGATTAACCTGGAGCTGGATCTGACGCTGTG 315
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
DB 316 CAGAAAGGTACAGAACATTCGCGCGTGGCTGTGGACATATCAATGGCTTCATCTCC 375
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 376 GAGCTGAGCGCTCTCTTCTTGTGAGGATATCATCGATTGATCAAGTTGCGGCTCAT 435
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
DB 436 CTGTGGGTCTTCACCTAGCTGGTGCCTGGTTCATATGCGATGACTCTGTCTATCTTGGCC 495
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
DB 496 TTTGTCTCGCTGTTTACCTTGCCCAAGGTCTACAGAGAACACACGAATCGATCGACACT 555
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
DB 556 CACTTGGATCTGGTGGCAGCAAAATTGACAGAAATCACCGACAAAGATCCGAGTGGCCATC 615
QY 182 Pro 182
DB 616 CCC 618
RESULT 76
US-09-809-391-102
; Sequence 102, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
```



```
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 794
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-809-391-102

Alignment Scores:
Pred. No.: 5,15e-52 Length: 794
Score: 509.50 Matches: 101
Percent Similarity: 76.3% Conservative: 38
Best Local Similarity: 55.4% Mismatches: 41
Query Match: 55.0% Indels: 3
DB: Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-809-391-102 (1-794)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
254 GCGGTGCACGATCTATTTCCTGGAGAGATGTGAAGAAGACTGGTTGTCTTGGAC-- 311
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerVal-ThrAlaTyrIl 40
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
312 ACGTGATCATGCTGCTTCCTCGCAGCTTCAGTGTCAATGCTGGTTCCTTAMCT 371
Qy 40 eAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAl 60
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
372 CATCTGGCTCTTCTCTCTGTCCACCATCACTTCAGGATCTACAAGTCGTCATCCAAGC 431
Qy 60 alLeGlnLysSerAspGluGlyHisProPhe-ArgAlaTyrLeuGluSerGluValAlaI 80
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
432 TGTWAGAAATCAGAAAGGCCATCCAAWTCCAAAGCCTACTCGAGCATGACATTACTC 491
Qy 80 LeSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrI 100
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
492 TGTCTCTCAGAGCTTCCATAATTACATGATGCTGCCATGTGCACATCAACAGGCC 551
Qy 100 LeLysGluLeuArgIlePheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
552 TGAACACTCAATTATTCCTCTCTCTGTGTAGAGATCTGTTGACTCTCTTGAAGCTGGCTG 611
Qy 120 alLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleL 140
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
612 TCTTCATGTGGCTGATGACCTATGTGTGTGTGTTTAAACGGAATCACCCCTTCTAATTC 671
Qy 140 euAlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleA 160
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
672 TTGCTGAAGTCTCATTTTCAGTGTCCCGATGCTGTATGAGAGTACAGACCCAGATTG 731
Qy 160 spHisTyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaL 180
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
732 ATCACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCCAAGCA 791
Qy 180 ys 180
Db : ||
792 AA 793

RESULT 77
US-09-882-171-102
; Sequence 102, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/043,671
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Qy	1	SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla	20
Db	254	CGCGTGCAGCATCTGATTTCTTGGAGAGATGGAGAAGACTGGGGTTCTCTTTGGAC--	311
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerVal-ThrAlaTyrI	40
Db	312	ACGCTGATCATGCTGCTTTCCCTGGCAGCTTTTCAGTGTTCATCATGTGGGGTTCTTAMCT	371
Qy	40	eAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAl	60
Db	372	CATCTGGCTCTTCTCTGTGCACCATCACTTCAGGATCTACAGTCCGTCATCCCAAG	431
Qy	60	alleGlnLysSerAspGluGlyHisProPhe-ArgAlaTyrIleuGluSerGluValAlaI	80
Db	432	TGTWCAGAAATCAGAAAGAAGCCATCCAAWTCCAAAGCCCTACTCGGACGTAGACATTACTC	491
Qy	80	leSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrI	100

Db 492 TGTCCTCAGAGCTTTCCATGAATATACATGAATGCTGCCATGCTGCACATCAACAGGCC 551  
Qy 100 lEysGluLeuArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
Db 552 TGAAGCTCATATATCGTCTCTTTCTGGTAGAGATCTGGTGACCTCTTGAAGCTGGCTG 611  
Qy 120 alLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuL 140  
Db 612 TCTTCATGTGGCTGATGACCTATGTGGTCTGTTTAAACGGAATCACCCCTTCTAAATTC 671  
Qy 140 euAlaLeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleA 160  
Db 672 TTGCTGAAGCTCTCATTTTCAGTGTCCGATTTGCTATGAGAAGTACAGACCCAGATTG 731  
Qy 160 spHisTyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaL 180  
Db 732 ATCACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATGTTGAAAAGATCCCAAGCA 791  
Qy 180 Ys 180  
Db 792 AA 793  
RESULT 78  
US-10-164-861-102  
; Sequence 102, Application US/10164861  
; Publication No. US20030225248A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: PZ002PI  
; CURRENT APPLICATION NUMBER: US/10/164,861  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: US/09/149,476  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: PCT/US98/04493  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 757  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 102  
; LENGTH: 794  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-164-861-102

Alignment Scores:  
Pred. No.: 5,15e-52 Length: 794  
Score: 509.50 Matches: 101  
Percent Similarity: 76.37% Conservative: 38  
Best Local Similarity: 55.49% Mismatches: 41  
Query Match: 55.08% Indels: 3  
DB: 17 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-164-861-102 (1-794)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 254 GCGGTGCAGATCTGATTTCTCGAGAGATGTGAAGAGATCGGTTGTTCTTTGGAC-- 311  
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerVal-ThrAlaTyrIle 40  
Db 312 ACGCTGATCATCTGCTTTCCGTCGACGCTTTCAGTGTTCATCATGTGGGTTTCTTAMCT 371  
Qy 40 eAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAl 60  
Db 372 CATCTGCTCTCTCTCTGTGCACCATCATCTTACAGGATCTACAGTCCGTCATCCCAAGC 431  
Qy 60 alLeuGlnLysSerAspGluGlyHisProPhe-ArgAlaTyrLeuGluSerGluValAlaI 80  
Db 432 TGTWCAGAAATCAGAAAGGCCATCCATTCAGAGCTTACCTGGACGTAGACATTACTC 491  
Qy 80 leSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrI 100  
Db 492 TGTCCTCAGAGCTTTCCATGAATATACATGAATGCTGCCATGCTGCACATCAACAGGCC 551

Qy 100 lEysGluLeuArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
Db 552 TGAAGCTCATATATCGTCTCTTTCTGGTAGAGATCTGGTGACCTCTTGAAGCTGGCTG 611  
Qy 120 alLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuL 140  
Db 612 TCTTCATGTGGCTGATGACCTATGTGGTCTGTTTAAACGGAATCACCCCTTCTAAATTC 671  
Qy 140 euAlaLeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleA 160  
Db 672 TTGCTGAAGCTCTCATTTTCAGTGTCCGATTTGCTATGAGAAGTACAGACCCAGATTG 731  
Qy 160 spHisTyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaL 180  
Db 732 ATCACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATGTTGAAAAGATCCCAAGCA 791  
Qy 180 Ys 180  
Db 792 AA 793  
RESULT 79  
US-10-424-599-57998  
; Sequence 57998, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 57998  
; LENGTH: 878  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_23384C.1  
US-10-424-599-57998

Alignment Scores:  
Pred. No.: 1.06e-51 Length: 878  
Score: 507.50 Matches: 95  
Percent Similarity: 75.00% Conservative: 46  
Best Local Similarity: 50.53% Mismatches: 46  
Query Match: 54.86% Indels: 1  
DB: 18 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-424-599-57998 (1-878)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 152 GTGGAGAGCTGATCTACTGCGCGGATTCCAAGAAATCCCGTCCAGTGTTCGGAGGAGTA 211  
Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 212 CTCGTCGTTCTACTCGCTTACATATTTCTCTTAATCAGTGTGTAGCTTACGTTTCA 271  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 272 CTCAATCCCTTGGCAATTAATTTAGACGTTTACAAAGTATTGTTCACAGCAGTT 331  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 332 CAAAAGACTGCGGATGACATCCATTCAGAAATATCTGGAACTCGATGTCTCTACCC 391  
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
Db 392 CAAGAAAAGTTAAACAAATCACAGAAAGTGGCGCTTGCACACATCAATGCCGCTATTGTG 451



US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-264-237-163 (1-668)

```
Qy 2 ValValAspLeuLeuTyTrpArgAspIleValSerThrGlyValValPheGlyAlaSer 21
Db 248 GTTGTGGACCTCTCTGAGAGACATTAAGAGACTGGAGTGGTGTGGTGCCAGC 307
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyRileAla 41
Db 308 CTATTCTCTGCTCTTTCATTGACAGTATTGACGATTGTGAGCGTAACAGCCTACATTGCC 367
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyRileGlyValIleGlnAlaIle 61
Db 368 TTGGCCCTGCTCTCTGACCATCATCTTTAGGATATACAAAGGGTGTGATCCAAAGTATC 427
Qy 62 GlnIysSerAspGluGlyHisProPheArgAlaTyRileuGluSerGluValAlaIleSer 81
Db 428 CAGAAATCAGATGAGGCCACCCATTGAGGATATCTGGAATCTGGAATGTGCTATATCT 487
Qy 82 GluGluLeuValGlnIleTySerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 488 GAGGAGTTGGTTTCAGAACTACAGTAATTTCTGCTCTTGTGTCATGTGCACTGCACGATAAG 547
Qy 102 -GluLeuArgArgLeuPheLeu 108
Db 548 GGAACCTCAGGCGCTCTTNCCT 569
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## RESULT 82

US-10-491-213-80

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; Sequence 80, Application US/10491213
; Publication No. US20050048490A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; AZIMZAI, Yalda;
; APPLICANT: BAUGHN, Mariah R.; BECHA, Shaurya D.;
; APPLICANT: BOROWSKY, Mark L.; CHAWLA, Navinder K.;
; APPLICANT: ELLIOTT, Vicki S.; EMERLING, Brooke M.;
; APPLICANT: GANDHI, Aneena R.; GIETZEN, Kimberly J.;
; APPLICANT: GORVAD, Ann E.; GRIFFIN, Jennifer A.;
; APPLICANT: HAPALIA, April J.A.; ISON, Craig H.;
; APPLICANT: KABLE, Amy E.; KALAEUS, Daniel P.;
; APPLICANT: LEHR-MASON, Patricia M.; LU, Dying Aina M.;
; APPLICANT: MARQUIS, Joseph P.; NGUYEN, Damiel B.;
; APPLICANT: RAMKUMAR, Jayalaxmi; RICHARDSON, Thomas W.;
; APPLICANT: KAREHT, Stephanie K.; SWARNAKAR, Anita;
; APPLICANT: TANG, Y. Tom; TRAN, Uyen K.;
; APPLICANT: WARREN, Bridget A.; XU, Yuming;
; APPLICANT: YAO, Monique G.; YUE, Huibin;
; APPLICANT: YUE, Henry
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
; FILE REFERENCE: PF-1213 USN
; CURRENT APPLICATION NUMBER: US/10/491,213
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: PCT/US02/31095
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/326,389
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/327,380
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/328,186
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/329,690
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/345,384
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/348,165
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/350,219
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US 60/344,518
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/345,143
; PRIOR FILING DATE: 2001-11-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 114
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; SOFTWARE: PERL Program

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; SEQ ID NO 80
; LENGTH: 2017
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7503970CB1
US-10-491-213-80
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## Alignment Scores:

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Pred. No.: 3.68e-47 Length: 2017
Score: 475.00 Matches: 92
Percent Similarity: 70.33% Conservative: 36
Best Local Similarity: 50.55% Mismatches: 54
Query Match: 51.35% Indels: 0
DB: 21 Gaps: 0
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US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-491-213-80 (1-2017)

```
Qy 2 ValValAspLeuLeuTyTrpArgAspIleValSerThrGlyValValPheGlyAlaSer 21
Db 954 GTGGCGGACCTCTGCTACTGGAAGCAGCAGGAGCGTCAGGAGTGGTCTTCACAGGCGCTG 1013
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyRileAla 41
Db 1014 ATGGTCTCCCTCTCTGCTCTGCTGCTTACGATCGTGTCCGTGGCGCGGCGCACTGGCT 1073
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyRileGlyValIleGlnAlaIle 61
Db 1074 CTGTTGTGCTCTGCTGCGGACCATCTCTCTCAGGGTTTACCGCAAGTGTCTGAGGCGCTG 1133
Qy 62 GlnIysSerAspGluGlyHisProPheArgAlaTyRileuGluSerGluValAlaIleSer 81
Db 1134 CACCGGGGGATGAGGCAACCCCTTTCAGGCGCTTACCTGGATGAGGACCTCACCTGACT 1193
Qy 82 GluGluLeuValGlnIleTySerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 1194 CGGGAGCAGACGGAACGTTTGTCTCCACCATCATCTCCCGCGTGGTCTCGGCGGCCAGG 1253
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 1254 CAGCTGGCGCACTTCTTCTGTTAGAAACCTCGTGGATTCCCTCAAGCTGGCGCTCTCTC 1313
Qy 122 MetTrpValPheThrTyRValGlyAlaLeuPheArgGlyLeuThrLeuLeuAla 141
Db 1314 TTCTACATCTTGACCTGCTGGGGGCCATCTTCAATGGTTTGACTCTTCTCATTTCTGGGA 1373
Qy 142 LeuIleSerLeuPheSerIleProValIleTyRValGluArgHisGlnValGlnIleAspHis 161
Db 1374 GTGATTGGTCTATTACCATCCCTCTGCTGACCGGAGCAGCAGGCTCAGATCGACCAA 1433
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValIleAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 1434 TATGTGGGGTTGTGACCAATCAGTTGAGCCACATCAAGCTAAGTCCGAGCTAAATC 1493
Qy 182 ProGly 183
Db 1494 CCAGGG 1499
```

## RESULT 83

US-10-723-860-3043

```
; Sequence 3043, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
```

; PRIOR APPLICATION NUMBER: 60/429,739  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 8393  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3043  
; LENGTH: 2190  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-723-860-3043

Alignment Scores:  
Pred. No.: 4 18e-47 Length: 2190  
Score: 475.00 Matches: 92  
Percent Similarity: 70.33% Conservative: 36  
Best Local Similarity: 50.55% Mismatches: 54  
Query Match: 51.35% Indels: 0  
DB: 20 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-723-860-3043 (1-2190)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
DB 1162 GTGGCGGACCTGCTGCTACTGGAAGACACGAGGAGCTCAGGAGTGGTCTTCACAGCCCTG 1221  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 1222 ATGGTCTCCCTCCTCGCTCTGCTGCTTACGATCGTGTGCGCGCGCAGCTTGGCT 1281  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 1282 CTGTGCTGCTGCGGACCACTCTCTCAGGGTTTACCGAAGTGTGCGAGCCGCTG 1341  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 1342 CACCGGGGGGATGGAGCAACCTTTCCAGGCTTACCTGGATGTGGACCTCACCTTGACT 1401  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 1402 CGGAGACAGACGGAAGCTTTGTCACACAGATCACCTCCCGCTGGTCTCGCGGCGCAG 1461  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 1462 CAGCTGCGGACCTTCTCTCTGTAGAGACCTCTGTGGATTCCTCAAGTGGCCCTCTCT 1521  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
DB 1522 TTCTACATCTTGACCTTCGTGGGTGCACTTTCAATGTTTGCATCTTCTCATTTCTGGGA 1581  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 1582 GTGATTGGTCTATTACCATCCCTCTGCTGTACCGGACGACACAGCTCAGATCGACCAA 1641  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 1642 TATGTGGGTGGTGACCAATCAGTTGAGCCACATCAAGCTAAGATCCGAGCTAAATC 1701  
QY 182 ProGly 183  
DB 1702 CCAGGG 1707

## RESULT 84

US-10-723-860-7073  
; Sequence 7073, Application US/10723860  
; Publication No. US20040253606A1  
; GENERAL INFORMATION:  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Gineburg, Wendy M.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators  
; FILE REFERENCE: 05892.0193.NPUS01  
; CURRENT APPLICATION NUMBER: US/10/723,860  
; CURRENT FILING DATE: 2003-11-26

; PRIOR APPLICATION NUMBER: 60/429,739  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 8393  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7073  
; LENGTH: 3044  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-723-860-7073

Alignment Scores:  
Pred. No.: 7e-47 Length: 3044  
Score: 475.00 Matches: 92  
Percent Similarity: 70.33% Conservative: 36  
Best Local Similarity: 50.55% Mismatches: 54  
Query Match: 51.35% Indels: 0  
DB: 20 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-723-860-7073 (1-3044)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
DB 872 GTGGCGGACCTGCTGCTACTGGAAGACACGAGGAGCTCAGGAGTGGTCTTCACAGCCCTG 931  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 932 ATGGTCTCCCTCCTCGCTCTGCTGCTTACGATCGTGTGCGCGCGCAGCTTGGCT 991  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 992 CTGTGCTGCTGCGGACCACTCTCTCAGGGTTTACCGAAGTGTGCGAGCCGCTG 1051  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 1052 CACCGGGGGGATGGAGCAACCTTTCCAGGCTTACCTGGATGTGGACCTCACCTTGACT 1111  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 1112 CGGAGACAGACGGAAGCTTTGTCACACAGATCACCTCCCGCTGGTCTCGCGGCGCAG 1171  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 1172 CAGCTGCGGACCTTCTCTCTGTAGAGACCTCTGTGGATTCCTCAAGTGGCCCTCTCT 1231  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
DB 1232 TTCTACATCTTGACCTTCGTGGGTGCACTTTCAATGTTTGCATCTTCTCATTTCTGGGA 1291  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 1292 GTGATTGGTCTATTACCATCCCTCTGCTGTACCGGACGACACAGCTCAGATCGACCAA 1351  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 1352 TATGTGGGTGGTGACCAATCAGTTGAGCCACATCAAGCTAAGATCCGAGCTAAATC 1411  
QY 182 ProGly 183  
DB 1412 CCAGGG 1417

## RESULT 85

US-10-424-599-51318  
; Sequence 51318, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599

; PRIOR APPLICATION NUMBER: US 60/271,955		
; PRIOR FILING DATE: 2001-02-28		
; NUMBER OF SEQ ID NOS: 58994		
; SOFTWARE: PatentIn version 3.2		
; SEQ ID NO 17576		
; LENGTH: 566		
; TYPE: DNA		
; ORGANISM: Human		
US-10-242-535A-17576		
Alignment Scores:		
Pred. No.:	6.33e-47	Length: 566
Score:	466.00	Matches: 97
Percent Similarity:	97.12%	Conservative: 4
Best Local Similarity:	93.27%	Mismatches: 3
Query Match:	50.38%	Indels: 1
DB:	17	Gaps: 0
US-09-830-972-2_COPY_975_1163 (1-189) x US-10-242-535A-17576 (1-566)		
Qy	86	GlnLysTyrSerAenSerAlaLeuGlyHisValAenSerThrIleLysGluLeuArgArg 105
Db	1	CAGAAGCACACAGTAATTCCTGCTCTGG-CATGTGAACCTGCACGATAAAGAACTCAGGCGC 59
Qy	106	LeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPhe 125
Db	60	CTCTTCCTAGTTGATGATTTAGTTGATTCCTCGAAGTTTGCAGTATTGATGTGGGTATTT 119
Qy	126	ThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeuLeuSerLeu 145
Db	120	ACCTATGTTGTGGCTTGTTTAAATGCTCGACACTACTGATTTTGGCTCTCATTTCCACTC 179
Qy	146	PheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeu 165
Db	180	TTCAGTGTTCTGTTATTATGAACGGGATCAGGCACAGATAGATCATTTCTAGGACTT 239
Qy	166	AlaAenLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 185
Db	240	GCAATAAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAAATCCCTGGATTGAAG 299
Qy	186	ArgLysAlaAsp 189
Db	300	CGCAAAAGCTGAA 311
RESULT 87		
US-10-085-783A-17576		
; Sequence 17576, Application US/10085783A		
; Publication No. US20040037841A1		
; GENERAL INFORMATION:		
; APPLICANT: ChondroGene Inc.		
; APPLICANT: Liaw, C.C.		
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis		
; FILE REFERENCE: 4231/2002		
; CURRENT APPLICATION NUMBER: US/10/085,783A		
; CURRENT FILING DATE: 2002-02-28		
; PRIOR APPLICATION NUMBER: US 60/305,340		
; PRIOR FILING DATE: 2001-07-13		
; PRIOR APPLICATION NUMBER: US 60/275,017		
; PRIOR FILING DATE: 2001-03-12		
; PRIOR APPLICATION NUMBER: US 60/271,955		
; PRIOR FILING DATE: 2001-02-28		
; NUMBER OF SEQ ID NOS: 58994		
; SOFTWARE: PatentIn version 3.2		
; SEQ ID NO 17576		
; LENGTH: 566		
; TYPE: DNA		
; ORGANISM: Human		
US-10-085-783A-17576		
Alignment Scores:		
Pred. No.:	6.33e-47	Length: 566
Score:	466.00	Matches: 97
Percent Similarity:	97.12%	Conservative: 4

Best Local Similarity: 93.27% Mismatches: 3  
Query Match: 50.38% Indels: 1  
DB: 18 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-085-783A-17576 (1-566)

QY 86 GlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArgArg 105  
DB 1 CAGAAGCACAGTAATTCCTCTTGG-CATGTCACTGCACGATAAAGGAATCAGGCGC 59  
QY 106 LeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPhe 125  
DB 60 CTCCTTCTAGTTGATGATTAGTTGATCTCTGAAGTTTGCAGATTGATGATGATTT 119  
QY 126 ThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuLeuSerLeu 145  
DB 120 ACTATGTTGGTGGCTTGTATTAATGCTGTGACACTACTGATTTGGCTCTCAATTCAC 179  
QY 146 PheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeu 165  
DB 180 TTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCATTTATAGGACT 239  
QY 166 AlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 185  
DB 240 GCATATGAAGTTTAAAGATGCTATGCTTAAATCCAGCAAAATCCCTGGATTGAAG 299  
QY 186 ArgLysAlaAsp 189  
DB 300 CGCAAGCTGAA 311

## RESULT 88

US-09-960-352-2205  
; Sequence 2205, Application US/09960352  
; Patent No. US20020137139A1  
; GENERAL INFORMATION:  
; APPLICANT: Warren, Wesley C.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Byatt, John C.  
; APPLICANT: Mathialagan, Nagappan  
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
; FILE REFERENCE: 16511.006/37-21 (10298)C  
; CURRENT APPLICATION NUMBER: US/09/960,352  
; CURRENT FILING DATE: 2001-09-24  
; NUMBER OF SEQ ID NOS: 15112  
; SEQ ID NO 2205  
; LENGTH: 431  
; TYPE: DNA  
; ORGANISM: Bos taurus  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (309)  
; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: Clone ID: 10-LIB3058-011-Q1-K1-C5  
US-09-960-352-2205

Alignment Scores:  
Pred. No.: 1,83e-42 Length: 431  
Score: 428.00 Matches: 89  
Percent Similarity: 98.89% Conservative: 0  
Best Local Similarity: 98.89% Mismatches: 1  
Query Match: 46.27% Indels: 0  
DB: 9 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-960-352-2205 (1-431)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
DB 161 GTTGTTGACCTCTCTACTGGAGAGACATTAAGAGACTGGAGTGTGTGTCGACG 220  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaVal 41  
DB 221 TTGTTCTGCTCTCTCGTGACAGTATTTCAGCATTTGAGTGTGTAACGGCTACATTGCC 280

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 281 TTGGCCCTGCTCTCTGTGACTATCATCTATAGGATATATAAGGGTGTGATCCAGGCTATC 340  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 341 CAGAAATCTGATGAAGGCCACCATTTCAGGGCATATTTGGAATCTGAAGTTCCTATATCT 400  
QY 82 GluGluLeuValGlnLysTyrSerAsnSer 91  
DB 401 GAGGAGTTGGTTCAGAGTACAGCAATCT 430

## RESULT 89

US-10-052-283-137  
; Sequence 137, Application US/10052283  
; Publication No. US20030064379A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND METHOD OF USE THEREOF  
; FILE REFERENCE: P2751R1C1  
; CURRENT APPLICATION NUMBER: US/10/052,283  
; CURRENT FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: PCT/US00/20006  
; PRIOR FILING DATE: 2000-07-21  
; PRIOR APPLICATION NUMBER: US 60/145,701  
; PRIOR FILING DATE: 1999-07-26  
; NUMBER OF SEQ ID NOS: 564  
; SEQ ID NO 137  
; LENGTH: 598  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-052-283-137

Alignment Scores:  
Pred. No.: 1.43e-38 Length: 598  
Score: 398.00 Matches: 74  
Percent Similarity: 80.83% Conservative: 23  
Best Local Similarity: 61.67% Mismatches: 23  
Query Match: 43.03% Indels: 0  
DB: 14 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-052-283-137 (1-598)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
DB 234 GCGGTGCAGATCTGATTTCTGGAGAGATGTGAAGAGACTGGTTCCTTGGCACC 293  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 294 ACGCTGATCATGCTGCTTCCCTGGCAGCTTTTCAGTGTCTCATCAGTGTGTTCTTACCTC 353  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
DB 354 ATCTGGGCTCTCTCTGTCCACATCAGCTTCAGATCTACAGTCCGTCATCCAGCT 413  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
DB 414 GTACAGAGTTCAGAGAGAGGCCATCCATTTCAAAGCCTACCTGGACGTAGACATTAATCTCTG 473  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
DB 474 TCCTCAGAAGCTTTCATAAATTACATGATGTGTCATGTGTCACATCAACAGGGCCCTG 533  
QY 101 LysGluLeuArgArgLeuLeuValValAspLeuValAspSerLeuLysPheAlaVal 120  
DB 534 AAACCTATTATTCGTCCTCTTCTGTTAGAGATCTGGTTGACTCTCTTGAAGCTGGCTGTC 593  
RESULT 90  
US-10-764-420-1065  
; Sequence 1065, Application US/10764420



Publication No. US20050084872A1

GENERAL INFORMATION:  
APPLICANT: Lum, Pek Yee  
APPLICANT: Tan, Yejun  
APPLICANT: Dai, Hongyue  
TITLE OF INVENTION: Methods For Determining Whether An Agent  
FILE REFERENCE: ROSA122057  
CURRENT APPLICATION NUMBER: US/10/764,420  
PRIORITY FILING DATE: 2004-01-23  
PRIORITY APPLICATION NUMBER: US 60/442,797  
PRIORITY FILING DATE: 2003-01-24  
PRIORITY APPLICATION NUMBER: US 60/474,413  
PRIORITY FILING DATE: 2003-05-30  
NUMBER OF SEQ ID NOS: 3683  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1065  
LENGTH: 682  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 267, 544, 623  
OTHER INFORMATION: n = A,T,C or G  
US-10-764-420-1065

Alignment Scores:  
Pred. No.: 6,81e-37 Length: 582  
Score: 385.00 Matches: 74  
Percent Similarity: 78.86% Conservative: 23  
Best Local Similarity: 60.16% Mismatches: 25  
Query Match: 41.62% Indels: 1  
DB: 21 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-764-420-1065 (1-682)

Qy 1 SerValValAspLeuLeuTyrTrp-ArgAspIleLysLysThrGlyValValPheGlyVal 20  
Db 316 GCGGTGCATGATCTGATTTCTTGGCGGAGATGCTGAAGAAGACTGGTGTGCTTGGCAC 375  
Qy 20 aSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 376 CACGCTGATCATGCTGCTCTCTGGCAGCTTTTCAGTGTATTCAGTGTGCTCTTACCT 435  
Qy 40 eAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAl 60  
Db 436 CATCTGGCTCTACTCTCTGTCACCATCAGCTTCAGAGCTACAGCTGTCATCCCAAGC 495  
Qy 60 aileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 496 TGTGCAAGTCAAGAGAGGACATCCATTCAAGCCCTACCTGGATGNGACATTACACT 555  
Qy 80 eSerGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
Db 556 GGCCTCAGAGCTTTCCACAGCTACATGAATGCTGCAATGGTGCATGTCACCAAGGCCCT 615  
Qy 100 eLysGluLeuArgGluPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
Db 616 CAATCTNTATTCTGCTCTTCTTGGTAGAAGACTTGGTTGACTCTTGAAGCTGGCTGT 675  
Qy 120 lLeuMet 122  
Db 676 CTTCA TG 682

RESULT 91

US-10-425-115-152719/c  
Sequence 152719, Application US/10425115  
Publication No. US20040214272A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants  
FILE REFERENCE: 38-21(53222)B  
CURRENT APPLICATION NUMBER: US/10/425,115  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 369326  
SEQ ID NO 152719  
LENGTH: 745  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: MFT4577\_70862C.1  
US-10-425-115-152719

Alignment Scores:  
Pred. No.: 1,31e-35 Length: 745  
Score: 375.00 Matches: 68  
Percent Similarity: 67.72% Conservative: 39  
Best Local Similarity: 43.04% Mismatches: 51  
Query Match: 40.54% Indels: 0  
DB: 20 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-425-115-152719 (1-745)

Qy 25 LeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu 44  
Db 705 TTGTTGTCGTCGCATATATGCTCACTGATTAGCGTAGTTGCTTATCTGGCTATGTTCTA 646  
Qy 45 LeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSer 64  
Db 645 CAATCTGGATGCAATCTTTTACGTCGTATATAAACTGCTCTACAGACAGTAATAAACT 586  
Qy 65 AspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeu 84  
Db 585 AATGAAGTCACTCCCAAGATATCTTCAAGCGCTTGGACATCAGCTACCAAGGAAAA 526  
Qy 85 ValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArg 104  
Db 525 GCTGAAGACTGACCAAAATTAGCTGTTGTGCACATCAATGCGGTATGTTGTAACCTTGT 466  
Qy 105 ArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrpVal 124  
Db 465 CGCTTGTACTTGTGTAAGACTTGTGTTGACTCTGCCAAATCTTTTGGTATTCTCTGGGTG 406  
Qy 125 PheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuLeuAlaLeuIleSer 144  
Db 405 TTGACATATGTTGGCGCTTGTTCACGCGCTTACACTCATAATTATTGGATTATTGCT 346  
Qy 145 LeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGly 164  
Db 345 CTGTTCACTTACCACCAAGTTTATGAGAACCAATAGACTCAATATGATCAAAATATTGAA 286  
Qy 165 LeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
Db 285 GTAGTTAGAACAGATTGCTGAATTGCAATTCAGTAACAAAGTTCGAGCAGCTATTCCA 232

RESULT 92

US-10-050-704-93  
Sequence 93, Application US/10050704  
Publication No. US20030050442A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: 62 Human Secreted Proteins  
FILE REFERENCE: P2039P1  
CURRENT APPLICATION NUMBER: US/10/050,704  
CURRENT FILING DATE: 2002-01-18  
PRIORITY APPLICATION NUMBER: 09/684,524  
PRIORITY FILING DATE: 2000-10-10  
PRIORITY APPLICATION NUMBER: PCT/US00/08979  
PRIORITY FILING DATE: 2000-04-06  
PRIORITY APPLICATION NUMBER: 60/128,693  
PRIORITY FILING DATE: 1999-04-09  
PRIORITY APPLICATION NUMBER: 60/130,991

```
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2317)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-050-704-93

Alignment Scores:
Pred. No.: 6.65e-33 Length: 2454
Score: 359.50 Matches: 65
Percent Similarity: 77.50% Conservatives: 28
Best Local Similarity: 54.17% Mismatches: 26
Query Match: 38.86% Indels: 1
DB: 19 Gaps: 1

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-050-704-93 (1-2454)
QY 71 ArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsn 90
   |||||.....:|||||
Db 59 AGAGCCTACCTGGACGTAGACATTACTCTGCTCCTCAGAAGCTTTCATAATTACATGAAT 118
   |||||.....:|||||
QY 91 SerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArgGluPheLeuValAsp 110
   |||||.....:|||||
Db 119 GCTGCCATGCTGCACATCAACAGGCGCTGAAACTCATTTCTCTCTCTGGTAGAA 178
   |||||.....:|||||
QY 111 AspLeuValAspSerLeuLysPheAlaValLeuMetTrrpValPheThrTyrValGlyAla 130
   |||||.....:|||||
Db 179 GATCTGGTTGACTCTTGAAGCTGGCTGCTTCATGTGGCTGATGACCTATGTGTGCT 238
   |||||.....:|||||
QY 131 LeuPheAsnGlyLeuThrLeuLeuLeuAlaLeuLeuSerLeuPheSerIleProVal 150
   |||||.....:|||||
Db 239 GTTTTAAAGGAATCACCCTTCTAATCTTGTGTAAGTCTCATTTTCAGTGTCCGATT 298
   |||||.....:|||||
QY 151 IleTyrGluArgHisGlnValGlnLeuLeuLeuLeuLeuLeuSerLeuPheSerIleProVal 170
   |||||.....:|||||
Db 299 GTCTATGAGAAGTACAGACCCAGATTGATCACTATGTTGGCATCGCCGAGATCAGACC 358
   |||||.....:|||||
QY 171 LysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeu---LysArgLysAlaAsp 189
   |||||.....:|||||
Db 359 AAGTCAATTGTTGAAAGATCCAGCAAAACTCCCTGGAATCGCCAAAAAAGGCAGAA 418
   |||||.....:|||||

RESULT 94
US-09-880-107-3484
; Sequence 3484, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3484
; LENGTH: 639
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(639)
; OTHER INFORMATION: n = a or c or g or t
US-09-880-107-3484

Alignment Scores:
Pred. No.: 2.06e-32 Length: 639
Score: 348.00 Matches: 83
Percent Similarity: 81.73% Conservatives: 2
Best Local Similarity: 79.81% Mismatches: 12
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; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2317)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-050-704-93

Alignment Scores:
Pred. No.: 6.65e-33 Length: 2454
Score: 359.50 Matches: 65
Percent Similarity: 77.50% Conservatives: 28
Best Local Similarity: 54.17% Mismatches: 26
Query Match: 38.86% Indels: 1
DB: 14 Gaps: 1

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-050-704-93 (1-2454)
QY 71 ArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsn 90
   |||||.....:|||||
Db 59 AGAGCCTACCTGGACGTAGACATTACTCTGCTCCTCAGAAGCTTTCATAATTACATGAAT 118
   |||||.....:|||||
QY 91 SerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArgGluPheLeuValAsp 110
   |||||.....:|||||
Db 119 GCTGCCATGCTGCACATCAACAGGCGCTGAAACTCATTTCTCTCTCTGGTAGAA 178
   |||||.....:|||||
QY 111 AspLeuValAspSerLeuLysPheAlaValLeuMetTrrpValPheThrTyrValGlyAla 130
   |||||.....:|||||
Db 179 GATCTGGTTGACTCTTGAAGCTGGCTGCTTCATGTGGCTGATGACCTATGTGTGCT 238
   |||||.....:|||||
QY 131 LeuPheAsnGlyLeuThrLeuLeuLeuAlaLeuLeuSerLeuPheSerIleProVal 150
   |||||.....:|||||
Db 239 GTTTTAAAGGAATCACCCTTCTAATCTTGTGTAAGTCTCATTTTCAGTGTCCGATT 298
   |||||.....:|||||
QY 151 IleTyrGluArgHisGlnValGlnLeuLeuLeuLeuLeuLeuSerLeuPheSerIleProVal 170
   |||||.....:|||||
Db 299 GTCTATGAGAAGTACAGACCCAGATTGATCACTATGTTGGCATCGCCGAGATCAGACC 358
   |||||.....:|||||
QY 171 LysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeu---LysArgLysAlaAsp 189
   |||||.....:|||||
Db 359 AAGTCAATTGTTGAAAGATCCAGCAAAACTCCCTGGAATCGCCAAAAAAGGCAGAA 418
   |||||.....:|||||

RESULT 93
US-10-798-512-93
; Sequence 93, Application US/10798512
; Publication No. US20040152164A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/10/798,512
; CURRENT FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US/09/684,524
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
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Query Match: 37.62% Indels: 8  
DB: 9 Gaps: 2  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-09-880-107-3484 (1-639)  
QY 2 ValValAspLeuLeuTyTTPArgAspLeuLysThrGlyValValPheGlyAlaSer 21  
DB 233 GTTGTGACCTCTCTGTACTGGAGACACATTAGAAGACTGGAGTGGTGTGGTCCAGC 292  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerLeuValSerValThrAlaTyRileAla 41  
DB 293 CTATTCTCTGCTCTCTGACATTTAGCATTTGAGGTGAACAGNCTACATTGCC 352  
QY 42 LeuAlaLeuLeuSerValThrPheSerPheArgLileTyLysGlyValLileGlnAlaIle 61  
DB 353 TTGGNCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAGCTATC 412  
QY 62 GlnLysSer-AspGluGlyHisProPheArgAlaTyRileuGluSerGluValAlaIle-- 80  
DB 413 CAGAAATCAAGATGAAGGCCACCCATTCAGGCATATCTGGNATCTGAAGTGNATTTCT 472  
QY 81 ---SerGluGluLeuValGlnLysTy-SerAsnSerAlaLeuGlyHisValAsnSerTh 99  
DB 473 TAGGAGTGGTCCANAAGTCAAGATCTGTCT-----GGGCANGTGAAGTGAAC 519  
QY 99 rileLysGlu 102  
DB 520 GATAAAGGAC 529  
RESULT 95  
US-10-633-423-9  
; Sequence 9, Application US/10633423  
; Publication No. US20040191240A1  
; GENERAL INFORMATION:  
; APPLICANT: Tohyama, Masaya  
; APPLICANT: Yamashita, Toshihide  
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION  
; FILE REFERENCE: 59150-8023.US900  
; CURRENT APPLICATION NUMBER: US/10/633,423  
; CURRENT FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: US 10/427,741  
; PRIOR FILING DATE: 2003-04-30  
; PRIOR APPLICATION NUMBER: JP 2003-92923  
; PRIOR FILING DATE: 2003-03-28  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-633-423-9  
Alignment Scores:  
Pred. No.: 1.85e-28 Length: 60615  
Score: 341.00 Matches: 70  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 36.86% Indels: 0  
DB: 19 Gaps: 0  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-633-423-9 (1-60615)  
QY 2 ValValAspLeuLeuTyTTPArgAspLeuLysThrGlyValValPheGlyAlaSer 21  
DB 45956 GTTGTGACCTCTCTGTACTGGAGACACATTAGAAGACTGGAGTGGTGTGGTCCAGC 46015  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerLeuValSerValThrAlaTyRileAla 41  
DB 46016 TTATTCTCTGCTCTCTGACATTTAGCATTTGAGGTGAACGCCCTACATTGCC 46075  
QY 42 LeuAlaLeuLeuSerValThrPheSerPheArgLileTyLysGlyValLileGlnAlaIle 61  
DB 46076 TTGGCCCTGCTCTCTGACATTTAGGATATACAAGGGTGTGATCCAGCTATC 46135  
QY 62 GlnLysSerAspGluGlyHisProPheArg 71  
DB 46136 CAGAAATCAGATGAAGGCCACCCATTTCAGG 46165  
RESULT 97  
US-09-918-995-5532  
; Sequence 5532, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5532  
; LENGTH: 497  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature

QY 62 GlnLysSerAspGluGlyHisProPheArg 71  
DB 46136 CAGAAATCAGATGAAGGCCACCCATTTCAGG 46165  
RESULT 96  
US-10-427-741-9  
; Sequence 9, Application US/10427741  
; Publication No. US20040191291A1  
; GENERAL INFORMATION:  
; APPLICANT: Tohyama, Masaya  
; APPLICANT: Yamashita, Toshihide  
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION  
; FILE REFERENCE: 59150-8023  
; CURRENT APPLICATION NUMBER: US/10/427,741  
; CURRENT FILING DATE: 2003-04-30  
; PRIOR APPLICATION NUMBER: JP 2003-92923  
; PRIOR FILING DATE: 2003-03-28  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 60615  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-427-741-9  
Alignment Scores:  
Pred. No.: 1.85e-28 Length: 60615  
Score: 341.00 Matches: 70  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 36.86% Indels: 0  
DB: 19 Gaps: 0  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x US-10-427-741-9 (1-60615)  
QY 2 ValValAspLeuLeuTyTTPArgAspLeuLysThrGlyValValPheGlyAlaSer 21  
DB 45956 GTTGTGACCTCTCTGTACTGGAGACACATTAGAAGACTGGAGTGGTGTGGTCCAGC 46015  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerLeuValSerValThrAlaTyRileAla 41  
DB 46016 TTATTCTCTGCTCTCTGACATTTAGCATTTGAGGTGAACGCCCTACATTGCC 46075  
QY 42 LeuAlaLeuLeuSerValThrPheSerPheArgLileTyLysGlyValLileGlnAlaIle 61  
DB 46076 TTGGCCCTGCTCTCTGACATTTAGGATATACAAGGGTGTGATCCAGCTATC 46135  
QY 62 GlnLysSerAspGluGlyHisProPheArg 71  
DB 46136 CAGAAATCAGATGAAGGCCACCCATTTCAGG 46165  
RESULT 97  
US-09-918-995-5532  
; Sequence 5532, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5532  
; LENGTH: 497  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature

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; LOCATION: (1)...(497)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-5532

Alignment Scores:
Pred. No.: 3,36e-30 Length: 497
Score: 328.50 Matches: 59
Percent Similarity: 81.55% Conservatives: 25
Best Local Similarity: 57.28% Mismatches: 18
Query Match: 35.51% Indels: 1
DB: 10 Gaps: 1

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-918-995-5532 (1-497)

QY 88 TyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArgLeuPhe 107
Db 57 TACATGAATGCTGCCATGCGCACATCAACAGCTCCCTGAAACTCAATTATTCGTCCTTT 116
QY 108 LeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyr 127
Db 117 CTGGTAGAAGATCTGGTTCACCTTGAAGCTGGCTGCTTCATGTGGCTGATGACCTAT 176
QY 128 ValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLysLeuAlaLeuLysSerLeuPhe 147
Db 177 GTTGGTCTGTTTAAACGAATCACCTTCTAATCTTCTGTAAGTCTCAATTTCACT 236
QY 148 IleProValIleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAla 167
Db 237 GTCCCGATTGCTATGAGAAGTACAGACCCAGATTGATCACTATGTGGCATGCCCGCA 296
QY 168 LysSerValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeu---Lys 186
Db 297 GATCAGACCAAGTCAATTGTTGAAAAGATCCAGCAAAACTCCCTGGAATGCCAAAAA 356
QY 187 LysAlaAsp 189
Db 357 AAGGCAGAA 365

RESULT 98
US-10-101-510-401
; Sequence 401, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 401
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-401

Alignment Scores:
Pred. No.: 4.84e-30 Length: 573
Score: 328.00 Matches: 59
Percent Similarity: 79.21% Conservatives: 21
Best Local Similarity: 58.42% Mismatches: 21
Query Match: 35.46% Indels: 0
DB: 15 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-101-510-401 (1-573)

QY 1 SerValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
Db 263 GCGGTGCAGCATCTGATTTCTCGAGAGATGTGAAGAAGACTGGGTGTTGCTTTGGCACC 322

; LOCATION: (1)...(561)
; OTHER INFORMATION: n = A,T,C or G
US-10-052-283-128

Alignment Scores:
Pred. No.: 2.54e-29 Length: 561
Score: 322.00 Matches: 64
Percent Similarity: 71.19% Conservatives: 20
Best Local Similarity: 54.24% Mismatches: 33
Query Match: 34.81% Indels: 1
DB: 14 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x US-10-052-283-128 (1-561)

QY 1 SerValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
Db 205 GCGGTGCAGCATNTGATTTNTGGAGAGATGTGAAGAAGACTGGGTGTTGTTTGGCACC 264
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 265 ACGCTGATCATGCTGCTTCCCTGGCAGCTTTTCAGTGTNATCAGTGTGGTTCTTACCTC 324
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 325 ATCTCGTGNNTTCTCTCTGTCCATCATCAGNTTCAGATTATACAGTCCGATNATCCAGCT 384
QY 61 IleGlnLysSerAspGlyHisProPheArgAlaTyrLeuGluSerGluVal-AlaIle 80
Db 385 GTACAGAAGTCAGAAGAAGGCCATTCATTCAAAGCCTACCTGGANGTAGACATTAATTNT 444
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QY      80  eSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrI1 100
Db      445  GTCCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGTCANATCAACAGGGCCCT 504
QY      100  eLysGluLeuArgArgGluPheLeuValAspLeuValAspSerLeuLys 117
Db      505  GAAATCATATTATTGTCTTTNTTGTGTAGAGATTGTTGGTTGANTCCTTGAAG 556

RESULT 100
US-09-758-140-19
; Sequence 19, Application US/09758140
; Patent No. US20020012965A1
; GENERAL INFORMATION:
; APPLICANT: Strittmatter, Stephen M.
; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth
; FILE REFERENCE: 44574-5073-US
; CURRENT APPLICATION NUMBER: US/09/758,140
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/175,707
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,378
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 198
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(198)
; OTHER INFORMATION: Full receptor binding region of No. US20020012965A1o gene
US-09-758-140-19

Alignment Scores:
Pred. No.:      6.57e-30      Length:      198
Score:          321.00      Matches:      65
Percent Similarity: 98.48%      Conservative: 0
Best Local Similarity: 98.48%      Mismatches: 1
Query Match:    34.70%      Indels:      0
DB:             9          Gaps:      0

US-09-830-972-2_COPY_975_1163 (1-189) x US-09-758-140-19 (1-198)

QY      51  PheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPhe 70
Db      1  TTTAGGATATACAGGGTGTGATCCAGCTATCCAGAAATCAGATGAAGGCCACCCATTC 60
QY      71  ArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsn 90
Db      61  AGGGCATATCTGGAATCTGAAGTGTCTATATCTGAGGAGTTGGTTTCAGAGTACAGTAAT 120
QY      91  SerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArgArgGluPheLeuValAsp 110
Db      121  TCTGCTCTTGGTCATGTGAAGTGCACGATAGAGAACTCAGGCGCTCTTCTTAGTTGAT 180
QY      111  AspLeuValAspSerLeu 116
Db      181  GATTTAGTTGATTCCTG 198
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Search completed: June 19, 2005, 07:08:18  
Job time : 511.5 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 19, 2005, 06:25:42 ; Search time 2558 Seconds  
(without alignments)

2812.411 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163

Perfect score: 925

Sequence: 1 SVVDLLYWRDIKTKGVVFGA.....VKDAMAKIQAKIPGLKPKAD 189

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 190322134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=100 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09830972.qcgn 1\_1\_6828 @runat\_16062005\_153945\_19031 -NCPU=6 -ICPU=3  
-NO MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_ges1:\*  
9: gb\_ges2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	925	100.0	779	7	CO401465
2	921	99.6	695	7	CV077130 AGENCOURT
3	921	99.6	791	7	CF977898 F26A06.04
4	913	98.7	600	9	AY404972 Mus muscu
5	913	98.7	679	4	B1149602 602848410
6	913	98.7	708	4	B1157842 602923001
7	907	98.1	794	1	AU080127
8	907	98.1	799	1	AU080133
9	904	97.7	598	7	CF118424 f8543.z1

10	904	97.7	600	9	AY404970
11	904	97.7	650	6	CB215381
12	904	97.7	667	7	CN429712
13	904	97.7	672	7	CK977984
14	904	97.7	682	6	CB162885
15	904	97.7	712	7	CK971318
16	904	97.7	743	6	CD102817
17	904	97.7	758	4	BG697436
18	904	97.7	788	1	AL533461
19	904	97.7	843	4	BG570231
20	904	97.7	849	7	CR765672
21	904	97.7	875	1	AL573494
22	904	97.7	1540	3	CR611869
23	904	97.7	1785	3	AF077050
24	903	97.6	781	4	BI079496
25	901	97.4	730	1	AU297347
26	898	97.1	634	6	CB067821
27	898	97.1	670	7	CV030029
28	898	97.1	960	7	CN646472
29	898	97.1	983	7	CN803408
30	898	97.1	1031	7	CN647521
31	898	97.1	3533	3	AK034902
32	895	96.8	990	4	BI691132
33	894	96.6	751	7	CK357937
34	893	96.5	718	1	AA986233
35	892	96.4	592	7	CN482802
36	892	96.4	805	7	CO735185
37	892	96.4	958	4	BM801698
38	891	96.3	749	4	BG296048
39	891	96.3	757	4	BG715173
40	890	96.2	924	5	B0845601
41	890	96.2	1042	7	CN805577
42	889	96.1	871	6	CD110203
43	887	95.9	921	5	BU503291
44	885	95.7	1013	7	CO048918
45	885	95.7	1018	7	CN801888

#### ALIGNMENTS

RESULT 1

CO401465

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CO401465 779 bp mRNA linear EST 01-JUL-2004  
AGENCOURT 26749547 NIH MGC 255 Rattus norvegicus cDNA clone  
IMAGE:7317070 5', mRNA sequence.

CO401465.1 GI:495833381

CO401465

EST.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 779)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: [csapba@mail.nih.gov](mailto:csapba@mail.nih.gov)

Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical

College of Wisconsin

cDNA Library Preparation: Express Genomics

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LHAM15373 row: 0 column: 20

High quality sequence start: 23

High quality sequence stop: 690.

**FEATURES**  
**SOURCE**

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Location/Qualifiers
1. .779
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon.10116"
/clone="IMAGE:7317070"
/sex="both"
/tissue_types="Brain - Pooled from several tissues from one
or more individuals"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_255"
/note="Organ: Brain/CNS; Vector: pExpress-1; Site_1:
ECorv; Site_2: Not; RNA obtained from brain tissue of 8
wk old animal. Tissues were snap-frozen and kept at -80C
before RNA extraction and purification (Tri-reagent
method). cDNA was primed using oligo-dT primer:
5'-pGACTGTTTACATCGCAGCGCGCCC(TT)25-3', and cloned into
the ECorv/NotI sites of pExpress-1. Size-selection >1.25kb
resulted in an average insert size of 1.7 kb. This primary
library is a normalized (primary library is NIH MGC_254)
and was constructed by Express Genomics (Frederick, MD).
Note: this is a NIH MGC library"

```

## ORIGIN

Alignment Scores:		
Pred. No.:	1.09e-103	77
Score:	925.00	18
Percent Similarity:	100.00%	Matches:
Best Local Similarity:	100.00%	Conservative:
Query Match:	100.00%	Mismatch:
DB:	7	Indels:
		Gaps:

US-09-830-972-2 COPY 975 1163 (1-189) X C0401465 (1-779)

Qy	1	SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla	20
Db	114	TCAGTTGTTGTCCTCTCTACTCGAGAGACATATTAGAAGACTCGAGTGGTGTGGTGCC	173
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	174	AGCTTAATCCTGCTGCTGCTCTGACAGTGTTTCAGCATTTGTCAGTGTAAAGCGCTACATT	233
Qy	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
Db	234	GCCTTGGCCCTGCTCTGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCT	293
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
Db	294	ATCCAGAAATCAGATGAAGGCCACCACCTTCAGGGCATATTTAGTAATCTGAAGTTGCTATA	353
Qy	81	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle	100
Db	354	TCAGAGGAATTGGTTTCAGAAATACAGTAATTTCTGCTCTTGGTCAITGTAACAGCACAAATA	413
Qy	101	LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal	120
Db	414	AANGAACTCAGGCGGCTTTCTTAGTGAATTTAGTTGATCCCTGAAGTTTGCAGTG	473
Qy	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
Db	474	TTGATGTGGGTGTTTACTTATGTTGGTGCTTGTTCATATGCTCTGACACTACTGATTTTA	533
Qy	141	AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp	160
Db	534	GCCTCATCTCACTCTTCAGTAATTCCTGTTATTATTAAGACGGCATTCAGGTGCGATAGAT	593
Qy	161	HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys	180
Db	594	CATTATCTAGGACTTGCAAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAAGCAAA	653
Qy	181	IleProGlyLeuLysArgLysAlaAsp	189
Db	654	ATCCCTGGATTGAAGCGCAAGACAGAT	680

## RESULT 2

CV077130	CV077130	695 bp	mRNA	linear	EST 25-AUG-2004
LOCUS	AGENCOURT31475102	NIH MCC_251	Rattus norvegicus	cDNA clone	
DEFINITION	IMAGE:7388978	5', mRNA sequence.			
ACCESSION	CV077130				
VERSION	CV077130.1	GI:51544161			
KEYWORDS	EST.				

RECORDS  
SOURCE  
ORGANISM

## CONCLUSIONS

## REFERENCE

## AUTHORS

**TITLE** National Institutes of Health, Mammali

**JOURNAL Unpublished (1999)**

CONTACT: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Drs. Joset Lazar  
College of Wisconsin

College of Wisconsin  
cDNA Library Preparation: Open Biocore

cDNA Library Preparation: Open Biosystems

DNA Sequencing by: Agencourt Bioscience Corporation  
I.M.A.G.E.: CONRAD LIBRARY Arrayed by: THE

DNA sequencing by: AgenaSource Bioscience Corp.  
Clone distribution: MGC clone distribution

found through the I.M.A.G.E. Consortium/LLNL  
 CRONE distribution; MCG CRONE distribution

found through the I.M.A.G.E. Consortium/ ENNA  
<http://image.llnl.gov>

accp://image.tntt.gov  
plate: LLAM15561 row: c column: 24

High quality sequence stop: 696.

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FEATURES
  source
    Location/Qualifiers
      1..695
        /organism="Rattus norvegicus"
        /mol_type="mRNA"
        /db_xref="taxon:10116"
        /clone="IMAGE:738978"
        /lab_host="DH10B TonA"
        /clone_lib="NIH_MGC_251"
        /note="Organ: Thymus; Vector: pExpress-1; Site 1: EcoRV;
        site 2: NotI; RNA obtained from testis tissue of 8 wk old
        animal. Tissues were snap-frozen and kept at -80C before
        RNA extraction and purification (Tri-reagent method). CDN
        was primed using oligo-dr primer:
        5'-pGAGTGTTCAGTTCGGAGCGCCGCC(T)25-3' and cloned into
        the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb
        resulted in an average insert size of 1.6 kb. This primary
        library is normalized (non-normalized primary library is
        NIH_MGC_250) and was constructed by Open Biosystems. Note
        this is a NIH_MGC library"

ORIGIN
Alignment Scores:
Pred. No.:      2,9e-103      Length:      695
Score:          921.00      Matches:      188
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      99.57%      Indels:      0
DB:              7      Gaps:      0

US-09-830-972-2_COPY_975_1163 (1-189) x CV077130 (1-695)

Qy      2      ValValAspLeuLeuTyTTPArgAspIleIysIysThrGlyValValPheGlyAlaSer 21
      |||
Db      126      GTTGTTCACCTCCTTACTCGGAGAGACATTAAAGAACTGGAGTGGTGTTCGTCGAGC 185
      |||

Qy      22      LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyIleAla 41
      |||
Db      186      TTATTCTCTGCTCTCTGACAGTGTTGACGATTGTTCAGTGTAAAGCGCTACATTGCC 245
      |||

Qy      42      LeuAlaLeuSerValThrIleSerPheArgIleTyIysGlyValIleGlnAlaIle 61

```



Db 246 TTGGCCCTGCTCGTGACTATCATAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATC 305  
 Qy 62 GlnlySerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 306 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAAATCTGAAGTTGCTATATCA 365  
 Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 366 GAGGAATTTGGTTTCAGAAATACAGTAATCTGCTCTTGGTTCATGTGAACAGCACATAAAA 425  
 Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 426 GAACGTAGCGCGCTTTCTTCTAGTGATGATTTAGTTGATTCCTCGAAGTTTGCAGTGTG 485  
 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAlaLeuGlyHisValLeuIleAla 141  
 Db 486 ATGGGGTGTCTTACTTATGTGGTCCCTGTGTTCAATGGTCTGACACTACTGATTTAGCT 545  
 Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 546 CTGATCTCACCTCTTCAGTATTCCTGTTATTTATGAACGCGCATCAGGTCAGATAGATCAT 605  
 Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 606 TATCTAGGACTTGCAACACAGAGTGTAAAGATGCGATGCGCAAAATCCAAAGCAAAATC 665  
 Qy 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 666 CCTGGATTGAAGCGCAAGCAGAT 689

RESULT 3  
 CF977898  
 LOCUS F28A06\_048.abl.R Rat retinal ganglion cell Rattus norvegicus cDNA, 791 bp mRNA linear EST 24-JUN-2004  
 DEFINITION mRNA sequence.

ACCESSION CF977898  
 VERSION CF977898.1 GI:49173356

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 791)  
 Farkas,R.H., Qian,J., Goldberg,J.L., Quigley,H.A. and Zack,D.J.  
 Authors Gene Expression Profiling of Highly Purified Rat Retinal Ganglion Cells

JOURNAL Unpublished (2003)  
 COMMENT Contact: Farkas RH  
 Department of Ophthalmology  
 Johns Hopkins University School of Medicine  
 600 North Wolfe Street, Baltimore, MD 21287, USA  
 Tel: 410 502 5230  
 Fax: 410 502 5382  
 Email: rfarkas@jhmi.edu.

FEATURES Location/Qualifiers

source 1..791  
 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /tissue\_type="Retinal Ganglion Cells"  
 /lab\_host="DH10B"  
 /clone\_lib="Rat retinal ganglion cell"  
 /note="Organ: Eye; Vector: pDNR-LIB; Site 1: Sfil; Site 2: Sfil; The library was constructed from purified rat retinal ganglion cells. The Creator SMART cDNA Library method (Clontech) was used. EST analysis was performed on the unamplified, non-normalized, non-subtracted library."

ORIGIN

Alignment Scores:

Pred. No.: 3.48e-103 Length: 791  
 Score: 921.00 Matches: 188  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.57% Indels: 0  
 DB: 7 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CF977898 (1-791)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 Db 167 GTTGTGGACCTCCCTCTACTGGAGAGACATTAAAGAGACTGGAGTGTGTTTGGTCCAGC 226  
 Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 227 TTATTCCTGCTGCTCTCTGACAGTGTTCAGCATTTGTCAGTGTAAAGCGCTACATTGCC 286  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 287 TTGGCCCTGCTCTCGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATC 346  
 Qy 62 GlnlySerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 347 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAAATCTGAAGTTGCTATATCA 406  
 Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 407 GAGGAATTTGGTTTCAGAAATACAGTAATCTGCTCTTGGTTCATGTGAACAGCACATAAAA 466  
 Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 467 GAACGTAGCGCGCTTTCTTCTAGTGATGATTTAGTTGATTCCTCGAAGTTTGCAGTGTG 526  
 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAlaLeuGlyHisValLeuIleAla 141  
 Db 527 ATGGGGTGTCTTACTTATGTGGTCCCTGTGTTCAATGGTCTGACACTACTGATTTAGCT 586  
 Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 587 CTGATCTCACCTCTTCAGTATTCCTGTTATTTATGAACGCGCATCAGGTCAGATAGATCAT 646  
 Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 647 TATCTAGGACTTGCAACACAGAGTGTAAAGATGCGATGCGCAAAATCCAAAGCAAAATC 706  
 Qy 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 707 CCTGGATTGAAGCGCAAGCAGAT 730

RESULT 4

AY404972

LOCUS

DEFINITION

Mus musculus RTM4 gene, VIRTUAL TRANSCRIPT, partial sequence, 600 bp DNA linear GSS 16-DEC-2003

ACCESSION AY404972

VERSION AY404972.1

KEYWORDS GI:39760946

SOURCE GSS.

ORGANISM Mus musculus (house mouse)

Mus musculus

REFERENCE 1 (bases 1 to 600)

AUTHORS

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 600)

AUTHORS

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.

FEATURES  
source  
1. .600  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
<1. .>600  
/gene="RTN4"  
/locus\_tag="HCM2068"

ORIGIN

Alignment Scores:  
Pred. No.: 2.3e-102 Length: 600  
Score: 913.00 Matches: 186  
Percent Similarity: 99.47% Conservative: 1  
Best Local Similarity: 98.94% Mismatches: 1  
Query Match: 98.70% Indels: 0  
DB: 9 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AY404972 (1-600)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 34 GTTGTGACCTCTGTACTGGAGACATTAAGAGACTGGAGTGGTGTGGTCCAGC 93

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 94 TTATTCCTGCTGCTCTGACAGTGTTCAGCAATTTGTCAGTGTAAACGGCTTACATGCC 153

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 154 TTGGCCCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGCTATC 213

QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 214 CAGAAATCAGATGAAGCCCACTTCAGGCAATATTTGGAATCTGAAGTTGCCATATCA 273

QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 274 GAGGAATGGTTCAGAAATATAGTAATCTGCTTGTGTCATGTGAACAGCACAAATAAA 333

QY 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 334 GAATTTAGGCGGTCTCTTCTAGTTGATGATTTAGTTGATTCCTGAAGTTTCAGTGTG 393

QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
DB 394 ATGTGGTATTTACTACGTGTGGTCTGTTGTTCAATGGTTTGACACTACTGATTTAGCC 453

QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 454 CTGATCTCACTCTCAGTATTCCTGTTATATATGAACGCATCAGCGGCAGATAGATCAT 513

QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaValIle 181  
DB 514 TATCTAGGACTTGCAAACAAAGCGTTAAGGATGCCATGGCCAAATCCNAGCAAAATC 573

QY 182 ProGlyLeuLysArgLysAlaAsp 189  
DB 574 CTGGATTGAAGCGCAACAGCA 597

RESULT 5  
BI149602  
LOCUS  
DEFINITION  
60284841.0F1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:5011899 5',  
mRNA sequence.  
ACCESSION BI149602

VERSION BI149602.1 GI:14609603  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 679)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: sgabbs-remail.nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM11062 row: c column: 04  
High quality sequence stop: 679.

FEATURES  
Location/Qualifiers  
1. .679  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="CZECH II"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5011899"  
/tissue\_type="spontaneous tumor, metastatic to mammary."  
Stem cell origin.  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_Lu29"  
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Library constructed by Life Technologies. Investigator  
providing samples: Gilbert Smith, NIH"

ORIGIN

Alignment Scores:  
Pred. No.: 2.74e-102 Length: 679  
Score: 913.00 Matches: 186  
Percent Similarity: 99.47% Conservative: 1  
Best Local Similarity: 98.94% Mismatches: 1  
Query Match: 98.70% Indels: 0  
DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BI149602 (1-679)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 37 GTTGTGACCTCTGTACTGGAGACATTAAGAGACTGGAGTGGTGTGGTCCAGC 96

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 97 TTATTCCTGCTGCTCTGACAGTGTTCAGCAATTTGTCAGTGTAAACGGCTTACATGCC 156

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 157 TTGGCCCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGCTATC 216

QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 217 CAGAAATCAGATGAAGCCCACTTCAGGCAATATTTGGAATCTGAAGTTGCCATATCA 276

QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 277 GAGGAATGGTTCAGAAATATAGTAATCTGCTTGTGTCATGTGAACAGCACAAATAAA 336

QY 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 337 GAATTTAGGCGGTCTCTCTTCTAGTTGATGATTTAGTTGATTCCTGAAGTTTCAGTGTG 396

QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141

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Db      397 ATGTGGGTATTACTTACCTGGTGGTCTGTTCATGCTTTGACACTACTGATTTAGCC 456
Qy      142 LeuileSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db      457 CTGATCTCACCTCTTCAGTATTCTCTGTTATATATGAACGGCATCAGCGCATAGATCAT 516
Qy      162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      517 TATCTAGGACTTGCAACACAGAGTGTAAAGATGCCATGCCCAAAATCCAGCAAAATC 576
Qy      182 ProGlyLeuLysArgLysAlaAsp 189
Db      577 CCTGATTGAAGCGCAAGCAGAA 600

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RESULT 6
LOCUS   BI157842              708 bp      mRNA      linear      EST 05-JUL-2001
DEFINITION 602923001F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5062944 5',
mRNA sequence.
ACCESSION BI157842
VERSION   BI157842.1 GI:14617843
KEYWORDS  EST.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 708)
TITLE     NIH-MGC http://mgs.nci.nih.gov/.
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M1170 row: b column: 01
High quality sequence stop: 708.
Location/Qualifiers
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/clone="IMAGE:5062944"
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/clone_lib="NCI_CGAP Mam3"

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/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sali;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
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## FEATURES

source

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1..708
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/tissue_type="tumor, gross tissue"
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/clone_lib="NCI_CGAP Mam3"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sali;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
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## ORIGIN

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Alignment Scores:
Pred. No.:      2,91e-102      Length:      708
Score:          913.00         Matches:    186
Percent Similarity: 99.47%      Conservative: 1
Best Local Similarity: 98.94%    Mismatches: 1
Query Match:     98.70%         Indels:     0
DB:              4             Gaps:       0
US-09-830-972-2_COPY_975_1163 (1-189) x BI157842 (1-708)

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Qy      2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21

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Db      59 GTTCTTGACCTCCTCTACTGCGAGACACATTAGAAGACTGGAGTGGTGTCTTTGGTCCAGC 118
Qy      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db      119 TTATTCCTGCTGCTGCTCTCTGACAGTGTTCAGCATTTGTTCAGTGAACGGCCTACATTC 178
Qy      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
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Qy      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
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Qy      82 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db      299 GAGGAATGGTTCAGAAATATAGTAATCTCTGCTCTTGGTCAATGTAACAGCACATAAAA 358
Qy      102 GluLeuArgArgLeuPheLeuValAspSerLeuValAspSerLeuLysPheAlaValLeu 121
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Qy      122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db      419 ATGTGGGTATTACTTACCTGTTGGTGGTCTTGTTCATGCTTGTGACACTACTGATTTAGCT 478
Qy      142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db      479 CTGATCTCACCTCTTCAGTATTCTCTGTTATATGAACGGCATCAGCGCATAGATCAT 538
Qy      162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      539 TATCTAGGACTTGCAACACAGAGGTTAAGATGCCATGCCCAAAATCCAGCAAAATC 598
Qy      182 ProGlyLeuLysArgLysAlaAsp 189
Db      599 CCTGATTGAAGCGCAAGCAGAA 622
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DEFINITION AU080127 Sugano mouse brain mncb Mus musculus cDNA clone MNCB-5261
5', mRNA sequence.
ACCESSION AU080127
VERSION   AU080127.1 GI:6084881
KEYWORDS  EST.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE 1 (bases 1 to 794)
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Hashimoto,K., Kusuda,J., Tanuma,R., Ito,A., Hirata,M., Toyoda,A.,
Suzuki,Y., Sasaki,M. and Sugano,S.
Isolation of full-length cDNA clones from a mouse brain cDNA
library made by oligo-capping method
Unpublished (1999)
Contact: Katsuyuki Hashimoto
Division of Genetic Resources
National Institute of Infectious Diseases
23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
Email: khashi@nih.go.jp
URL: http://www.nih.go.jp/yoken/genbank/.
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Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AY404970 (1-600)

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QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 94 CTATTCTCTGCTTTCATTGACAGTATTTCAGCATTTGTGAGCGTAACAGCCTACATTGCC 153  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 61  
DB 154 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAAAGTATC 213  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 214 CAGAAATCAGATGAAGCCACCATTTCAGGCATATCTGGAATCTGGAATCTGATATCT 273  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 274 GAGGAGTTGGTTCAGAAAGTACAGTAATCTGCTCTTGGTCATGTGAACCTGCACGATAAG 333  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 334 GAACCTCAGCGCGCTCTCTTAGTGTATGATTTAGTTGATTTCTGGAAGTTTCAGTGTG 393  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
DB 394 ATGTGGATATTACCTATGTTGGTGGCTTTGTTAATGGTCTGACACTACTGATTTGGCT 453  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 454 CTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATGATCAT 513  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 514 TATCTAGGACTTGCATAAATGAAGATGTAAAGATGCTATGGCTAAATCCAAAGAAATC 573  
QY 182 ProGlyLeuLysArgLysAlaAsp 189  
DB 574 CTGGATTGAAGCGCAAGCTGAA 597

RESULT 11  
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DEFINITION 5', mRNA sequence.

ACCESSION CB215381  
VERSION CB215381.1 GI:28263573  
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 650)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

## JOURNAL COMMENT

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov

cDNA Library Preparation:

cDNA Sequencing by: The I.M.A.G.E. Consortium/LLNL

Sequencing Center (NISC)

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

info@image.llnl.gov

Plate: LLAM13163 row: G column: 23

Seq primer: M13RPI reverse primer (ABI).

## FEATURES

source

Location/Qualifiers

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/clone="IMAGE:5937070"

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## ORIGIN

Alignment Scores: 3.35e-101 Length: 650  
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Score: 904.00  
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Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CB215381 (1-650)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
DB 19 GTTGTGACCTCTGTTACTGGAGACATTAAAGACTGGAGTGGTGTGGTCCAGC 78  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 79 CTATTCTCTGCTCTTTCATTGACAGTATTTCAGCATTTGTGAGCGTAACAGCCTACATTGCC 138  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 61  
DB 139 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAAAGTATC 198  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 199 CAGAAATCAGATGAAGCCACCATTTCAGGCATATCTGGAATCTGGAATCTGATATCT 258  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 259 GAGGAGTTGGTTCAGAAAGTACAGTAATTTCTGCTTGTGTCATGTGAACCTGCACGATAAG 318  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 319 GAACCTCAGCGCGCTCTTCTTAGTGTATGATTTAGTTGATTTCTGGAAGTTTCAGTGTG 378  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
DB 379 ATGTGGATATTACCTATGTTGGTGGCTTTGTTAATGGTCTGACACTACTGATTTGGCT 438  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 439 CTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATGATCAT 498

Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 499 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAATC 558

Qy 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 559 CCTGGATTGAAGCGCAAGCTGAA 582

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 LOCUS 17000600059220 GRN\_PRENU Homo sapiens cDNA 5', mRNA sequence.  
 DEFINITION CN429712  
 VERSION CN429712.1 GI:47417306  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 667)  
 Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,  
 Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M.S., Mandalam, R.,  
 Lebkowski, J. and Stanton, L.W.  
 Transcriptionome characterization elucidates signaling networks that  
 control human ES cell growth and differentiation  
 Nat. Biotechnol. 22 (6), 707-716 (2004)  
 Contact: Brandenberger R  
 Regenerative Medicine  
 Geron Corporation  
 230 Constitution Drive, Menlo Park, CA 94025, USA  
 Tel: 650 473 8658  
 Fax: 650 473 7760  
 Email: rbrandenberger@geron.com  
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 /db\_xref="taxon:9606"  
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ORIGIN  
 Alignment Scores:  
 Pred. No.: 3.47e-101 Length: 667  
 Score: 904.00 Matches: 183  
 Percent Similarity: 98.94% Conservative: 3  
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US-09-830-972-2\_COPY\_975\_1163 (1-189) x CN429712 (1-667)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
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Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 143 CTATTCCTGCTGCTTCATTGACAGTATTGACAGTGTGAGCGTAACAGCCTCATTTGCC 202

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 203 TTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 262

Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 263 CAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 322

Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 323 GAGGAGTTGGTTTCAGAGTACAGTAATCTGCTCTTGGTCATGTGACTGCACGATAAG 382

Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 383 GAACCTCAGGGCCCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTGCAGTGTG 442

Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
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Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
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Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
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Qy 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 623 CCTGGATTGAAGCGCAAGCTGAA 646

RESULT 13  
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 LOCUS 4109431 BARC 9BOV Bos taurus cDNA clone 9BOV37\_106 5', mRNA  
 DEFINITION CK977984  
 VERSION CK977984.1 GI:45495958  
 KEYWORDS EST.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 672)  
 Sonstegard, T.S., Van Tasell, C.P., Matukumalli, L.K., Harhay,  
 G.P., Bosak, S., Rubenfield, M. and Gaabbarre, L.C.  
 Production of EST from cDNA libraries derived from immunologically  
 activated bovine gut  
 Unpublished (2004)  
 Contact: Tad S. Sonstegard  
 Bovine Functional Genomics Laboratory  
 Animal and Natural Resources Institute  
 Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA  
 Tel: 3015048416  
 Fax: 3015048414  
 Email: tads@anri.barc.usda.gov  
 Single pass sequencing. Bases called and trimmed with phred  
 0.000925 using options -trim\_alt "-trim\_fasta. Vector identified  
 by cross match using options -minmatch 12 -minscore 18  
 Plate: 37 row: I column: 06  
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 Site 2: NotI; Equimolar amounts of mRNA extracted from  
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 Exposure to Ostertagia ostertagi was initiated at 15 weeks

of age, fundic and pyloric abomasum"

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ORIGIN
Alignment Scores:
Pred. No.: 3,51e-101 Length: 672
Score: 904.00 Matches: 183
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Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.73% Indels: 0
DB: 7 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x CK977984 (1-672)

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QY 22 LeuPheLeuLeuSerLeuThrValPheSerLeuValSerValThrAlaTyrLeuAla 41
Db 165 TTGTTCTGCTGCTCTGCTGACAGTATTCAGCATTTGAGTGTAAACGGCCTACATG 224
QY 42 LeuAlaLeuLeuSerValThrLeuSerPheArgGlyLeuLysGlyValLeuGlnAla 61
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Db 285 CAGAAATCTGATGAAGCCACCATTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT 344
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QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 405 GAACCTCAGACGCTCTCTCTAGTGTATGTTAGTTGATCTCTGAAGTTGCTGAGTTG 464
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
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DEFINITION 5', mRNA sequence.
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VERSION CB162885.1 GI:28149011
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 682)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center

```

Korea Research Institute of Bioscience & Biotechnology  
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 41 row: F column: 04  
High quality sequence stop: 682.  
Location/Qualifiers  
1. 682

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/note="Organ: Liver; Vector: pT7T3-Pac; Site 1: EcoRI;  
Site 2: NotI; The library was contributed by the Soares  
laboratory and it was constructed as described by Bonaldo,  
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research  
6(9): 791-806. RNA was prepared from harvested cell  
culture."

## ORIGIN

Alignment Scores: 3,58e-101 Length: 682  
Pred. No.: 904.00 Matches: 183  
Score: 98.94% Conservativeness: 3  
Percent Similarity: 98.94% Mismatches: 2  
Best Local Similarity: 97.34% Indels: 0  
Query Match: 97.73% Gaps: 0  
DB: 6

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CB162885 (1-682)

QY 2 ValValAspLeuLeuTyrTrpArgAspLeuLysThrGlyValValPheGlyAlaSer 21  
Db 115 GTTGTGACCTCTCTACTGGAGACATTAAGAGACTGGAGTGGTGTGGTCCACG 174  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerLeuValSerValThrAlaTyrLeuAla 41  
Db 175 CTATTCCTGCTGCTTTCATTCAGCATTTGAGCATTTGAGCGGTGATCCAGCTATC 234  
QY 42 LeuAlaLeuLeuSerValThrLeuSerPheArgGlyLeuLysGlyValLeuGlnAla 61  
Db 235 TTGGCCCTGCTCTCTGTCACCATCAGCTTTAGGATATATAAGGGTGTGATCCAGCTATC 294  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaLeuSer 81  
Db 295 CAGAAATCAGATGAAGCCACCATTCAGGGCATATCTGGAATCTGGAAGTTGCTATATCT 354  
QY 82 GluGluLeuValGlnLysTyrSerLeuSerAlaLeuGlyHisValAsnSerThrLeuLys 101  
Db 355 GAGGAGTTGGTTTCAAGATACAGTAAATTCCTGCTCTTGGTTCATGTGAACCTGCAGTAAAG 414  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
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QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
Db 475 ATGTGGGTATTTACCTATGTTGGTCTGTTTAAATGTTGCTGACACTACTGATTTTGGCT 534  
QY 142 LeuLeuSerLeuPheSerLeuProValLeuTyrGluArgHisGlnValGlnLeuAspHis 161  
Db 535 CTCAATTCACCTCTTCAGTGTCTCTGTTATTATGAACGGCATCAGCGCAATATAGATCAT 594  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysileGlnAlaLysile 181  
Db 595 TATCTAGGACTTGCATAAATAAGAAATGTTAAAGATGCTATGGCTAAATCCAGCAAAATC 654  
QY 182 ProGlyLeuLysArgLysAlaAsp 189  
Db 655 CCTGGATTGAAGCGCAAAAGCTGAA 678



```

RESULT 15
CK971318
LOCUS
DEFINITION 4087182 BARC 9BOV Bos taurus cDNA clone 9BOV3_J07 5', mRNA
sequence.
ACCESSION CK971318
VERSION CK971318.1 GI:45489292
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 712)
AUTHORS Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay,
G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
TITLE Production of EST from cDNA libraries derived from immunologically
activated bovine gut
JOURNAL Unpublished (2004)
COMMENT Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
Tel: 3015048416
Fax: 3015048414
Email: tads@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim alt -trim fasta. Vector identified
by cross match using options -minmatch 12 -minscore 12
Plate: 3 - row: J column: 07
Seq primer: CCCAGTCACGACGTTGTAAACG
High quality sequence stop: 712.
FEATURES
Location/Qualifiers
1..712
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone="9BOV3_J07"
/sex="Male"
/tissue_type="Pooled"
/dev_stage="Multiple"
/lab_host="DH10B T1 phage resistant"
/clone_lib="BARC 9BOV"
/notes="Organ: Abomasum; Vector: pAgen-1; Site: 1: EcoRV;
Site 2: NotI; Equimolar amounts of mRNA extracted from
fundic and pyloric abomasums of 18 and 21 week old steers.
Exposure to Osteragia osteragi was initiated at 15 weeks
of age. fundic and pyloric abomasum"
ORIGIN
Alignment Scores:
Pred. No.: 3.81e-101 Length: 712
Score: 904.00 Matches: 183
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.34% Mismatches: 2
Query Match: 97.73% Indels: 0
DB: 7 Gaps: 0
US-09-830-972-2_COPY_975_1163 (1-189) x CK971318 (1-712)
Qy 2 ValValAspLeuLeuTyrrTtrPArgAspIleIysIysThrGlyValValPheGlyAlaSer 21
Db 18 GTTGTGTGACCTCCTACTCTGAGAGACATTAAAGACTGGAGTGGTGTGGTGCCAGC 77
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrrIleAla 41
Db 78 TTGTTCTCTGCTCTCCTGACAGTATTAGCATTTGAGTGTACGGCTCATATTGCC 137
Qy 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrrIysGlyValIleGlnAlaIle 61
Db 138 TTGGCCCTGCTCTCTGTGACTATCATCAGCTTTTAGGATATATAAGGGTGTGATCCAGGCTATC 197

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Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrrLeuGluSerGluValAlaIleSer 81
Db 198 CAGAAATCTGATGAGGCCACCCATTAGGGCATTTTGGAAATCTGAAGTTGCTATATCT 257
Qy 82 GluGluLeuValGlnLysTyrrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 258 GAGGAGTTGGTTTCAAGAGTACAGCAATCTCTCTTGGTTCATGTTAACGACACATAAAA 317
Qy 102 GluLeuArgGluLeuPheLeuValAspIleValAspSerLeuLysPheAlaValLeu 121
Db 318 GAATCTAGAGCCCTCTTCTTAGTTGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 377
Qy 122 MetTrpValPheThrTyrrValGlyValAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
Db 378 ATGTGGGTATTACTATGTTGGTTCCTTGTCAATGGTCTGACACTACTAATTTGGCT 437
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrrGluArgHisGlnValGlnIleAspHis 161
Db 438 CTGATTTTCACTCTTCAGTGTCTCTGTTATTATTATGAACGGCATCAGGCGCAATAGATCAT 497
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 498 TATCTGGGACTTGCAATAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAATC 557
Qy 182 ProGlyLeuLysArgLysAlaAsp 189
Db 558 CCTGGATTGAAGCGTAAAGCTGAA 581
RESULT 16
CK102817
LOCUS
DEFINITION AGENCOURT 14009211 NIH MGC_186 Homo sapiens cDNA clone
sequence.
ACCESSION CK102817
VERSION CK102817.1 GI:30755991
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 743)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM166 row: m column: 24
High quality sequence stop: 617.
FEATURES
Location/Qualifiers
1..743
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30373271"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_186"
/notes="Organ: Pooled-Skin; Vector: pDNR-LIB; Site: 1: SfiI
(ggcatattggcc); Site 2: SfiI (ggcgcctggcc); Library is
oligo-dT primed and directionally cloned. cDNA was
prepared from a pooled samples of tissues from Skin,
meninges, duramater, pia matter and choroid plexus.
5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGCGCATTTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGGCGGCGGCGCATG-dt(30)BN-3'
(where B = A, C, G, or T). Average

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insert size 1.47 kb (range 0.50-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library"

## ORIGIN

Alignment Scores:  
 Pred. No.: 4,05e-101 Length: 743  
 Score: 904.00 Matches: 183  
 Percent Similarity: 98.94% Conservative: 3  
 Best Local Similarity: 97.34% Mismatches: 2  
 Query Match: 97.73% Indels: 0  
 DB: 6 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CD102817 (1-743)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 151 GTTGTGACCTCTGTTACTGGAGAGACATTAGAGACTGGAGTGGTGGTGGTGGCAGC 210  
 Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 211 CTATTCTCTGCTTCTTCAATGACAGTATTGACGATTTGAGCGTAAACAGCTACATTGCC 270  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 271 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTTGTGATCCAGCTATC 330  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 331 CAGAAATCAGATGAGGCCACCCATTCAGGGATATCTGGATCTGAAGTTGCAATCTATCT 390  
 Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 391 GAGGAGTTGTTTTCAGAAATGACAGTAAATCTGCTCTTGGTTCATCTGAACTGCAGATAAG 450  
 Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 451 GAACTCAGCGCGCTCTCTTGTAGTATGATGATTTAGTTGATCTCTGAAAGTTTCAGGTGG 510  
 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
 Db 511 ATGTGGTATTACCTATGTTGGTGGTCTGTTTAAATGCTCAGACACTACTGATTTGGCT 570  
 Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 571 CTCAATTCACCTCTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 630  
 Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 631 TATCTAGGACTTGCATAATGAAGATGTTAAAGATGCTATGCTGCTAAATCCAGCAAAATC 690  
 Qy 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 691 CTGGATTGAGCGCAAAAGCTGAA 714

## RESULT 17

BG697436 758 bp mRNA linear EST 07-MAY-2001  
 LOCUS 602660623P1 NCI\_CGAP\_Skn3 Homo sapiens cDNA clone IMAGE:4804012 5',  
 DEFINITION mRNA sequence.

ACCESSION BG697436

VERSION BG697436.1 GI:13963656

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 758)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@mail.nih.gov  
 Tissue Procurement: James Cleaver, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA  
 Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM10700 row: m column: 05  
 High quality sequence stop: 756.

## FEATURES

## source

1..758

Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4804012"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_lib="NCI CGAP Skn3"

/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.5kb. Library constructed by Life

Technologies. Note: this is a NCI\_CGAP Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 4,17e-101 Length: 758  
 Score: 904.00 Matches: 183  
 Percent Similarity: 98.94% Conservative: 3  
 Best Local Similarity: 97.34% Mismatches: 2  
 Query Match: 97.73% Indels: 0  
 DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BG697436 (1-758)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 132 GTTGTGACCTCTGTTACTGGAGAGACATTAGAGACTGGAGTGGTGGTGGTGGCAGC 191  
 Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 192 CTATTCTCTGCTTCTTCAATGACAGTATTGACGATTTGAGCGTAAACAGCTACATTGCC 251  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 252 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTTGTATCCAGCTATC 311  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 312 CAGAAATCAGATGAGGCCACCCATTCAGGGCATATCTGGAATCTGAAAGTTGCTATATCT 371  
 Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 372 GAGGAGTTGGTTTCAGAGTACAGTAAATCTGCTCTTGGTTCATGTAAGTGCAGATAAG 431  
 Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 432 GAACTCAGCGCGCTCTCTTGTAGTATGATTTAGTTGATCTCTGAAAGTTTCAGTGTGG 491  
 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
 Db 492 ATGTGGTATTACCTATGTTGGTGGCTTTTAAATGTTCTGACACTACTGATTTGGCT 551  
 Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 552 CTCAATTCACCTCTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 611  
 Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 612 TATCTAGGACTTGCATAATGAAGATGTTAAAGATGCTATGCTGCTAAATCCAGCAAAATC 671  
 Qy 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 182 ProGlyLeuLysArgLysAlaAsp 189

Db 672 CCTGGATTGAAGCGCAAAAGCTGAA 695

RESULT 18  
AL533461 788 bp mRNA linear EST 24-MAR-2004  
LOCUS  
DEFINITION AL533461 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone  
CSODN004YJ08 5-PRIME, mRNA sequence.  
ACCESSION  
VERSION AL533461.3 GI:45708351  
KEYWORDS  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 788)  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT On Feb 13, 2001 this sequence version replaced gi:31260542.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
was not normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
This sequence belongs to sequence cluster 1423.r  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?s=CSODN004DE04QP1&c=1423.r.

FEATURES  
Location/Qualifiers  
source  
1..788  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CSODN004YJ08"  
/tissue\_type="ADULT BRAIN"  
/dev\_stage="adult"  
/clone\_lib="Homo sapiens ADULT BRAIN"  
/note="Organ: brain; Vector: pCMVSPORT\_6; 1st strand cDNA  
was primed with a NotI-oligo(dT) primer. Five prime end  
enriched, double-strand cDNA was digested with Not I and  
cloned into the Not I and EcoRV sites of the pCMVSPORT 6  
vector. Library was not normalized."

## ORIGIN

Alignment Scores:  
Pred. NO.: 4.4e-101 Length: 788  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: 1 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AL533461 (1-788)

Qy 2 ValValAspLeuLeuThrValPheSerIleValSerValThrAlaValAlaSer 21  
Db 156 GTTGTGACCTCCGTACTGGAGAGACATTAAAGACTGGAGTGGTGGCCAGC 215  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValAla 41  
Db 216 CTATCTCTGCTGCTTTCATTGACAGTATTACGATTGTGAGCGTAACAGCTACATTGCC 275  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAla 61  
Db 276 TTGGCCCTGCTCTGTGACCATCATGCTTTAGGATATACAGGGTGTGATCCAGGTATC 335  
Qy 62 GlnIysSerAspGluGlyHisPropGheArgIleValThrLeuGluSerGluValAlaIleSer 81  
Db 336 CAGAAATCAGATGAAGGCCACCCCATTCAGGCGCATATCTGGAATCTGAAGTTGTATATCT 395

Qy 82 GluGluLeuValGlnIlystYrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
Db 396 GAGGAGTTGGTTCAGAAAGTACAGTAATCTGCTCTTGGTCAATGTAACGATGAAG 455  
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 456 GAATCTAGGCGCCTCTTCTTAGTTGATGATTAGTTAGTTCTCTGAAGTTGCGATGTTG 515  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
Db 516 ATGGGGTATTACCTATGTTGGTCTTGTATGCTGACACTACTGATTTGGCT 575  
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
Db 576 CTCAATTCCTCTTCACTGTTCTCTGTTATTATGACCGCATCAGGCACAGATGATCAT 635  
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaValLeu 181  
Db 636 TATCTAGGACTTGCAATAAGAATGTTAAAGATCTATGCTAAATCCAGCAAAATC 695  
Qy 182 ProGlyLeuLysArgLysAlaAsp 189  
Db 696 CCTGGATTGAAGCCAAAGCTGAA 719

RESULT 19  
BG570231 843 bp mRNA linear EST 10-APR-2001  
LOCUS  
DEFINITION BG570231 NIH\_MGC\_77 Homo sapiens cDNA clone IMAGE:4717662 5',  
mRNA sequence.  
ACCESSION BG570231  
VERSION BG570231.1 GI:13577884  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 843)  
TITLE NIH-MGC http://mgc.nci.nih.gov/  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs@mail.nih.gov  
Tissue Procurement: CLONTECH Laboratories, Inc.  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LUCM1567 row: o column: 07  
High quality sequence stop: 801.  
Location/Qualifiers  
source  
1..843  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4717662"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_77"  
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site\_1:  
SfiI (ggccattggcc); Site\_2: SfiI (ggccattggcc); 5' and  
3' adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CAGCGCATATGGCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCCGCGGCGGACATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.9  
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

ORIGIN  
Alignment Scores:  
Pred. No.: 4.85e-101 Length: 843



```

DEFINITION  AL573494 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
              clone CSODI051YB11 3-PRIME, mRNA sequence.
ACCESSION   AL573494
VERSION     AL573494.3 GI:46246666
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 875)
            Li W.B., Gruber C., Jesse J., and Polayes D.
            Full-length cDNA libraries and normalization
            Unpublished (2001)
            On Feb 16, 2001 this sequence version replaced gi:31294840.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            1423.r
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CSODI051CA06NPL&c=1423.r.
FEATURES             Location/Qualifiers
     source           1..875
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CSODI051YB11"
                     /tissue type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA
                     digested with Not I and EcoR V sites of the pCMVSPORT 6
                     vector. Library was normalized."
ORIGIN
Alignment Scores:  5.11e-101      Length:      875
Pred. No.:        904.00         Matches:    183
Score:            98.94%         Conservative: 3
Percent Similarity: 97.34%      Mismatches:  2
Best Local Similarity: 97.34%   Indels:     0
Query Match:      97.73%       Gaps:      0
DB:               1

US-09-830-972-2_COPY_975_1163 (1-189) x AL573494 (1-875)

Qy      2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db      875 GTTGTGGACCTCTCTGTACTGGAGACATTAAAGACTGGAGTGGTGGTGGTGGCCAGC 816
Qy      22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db      815 CTATTCTCTGCTGCTTTTCATTACAGTATTTCAGCATTTGACGGTAACAGCCTACATTGCC 756
Qy      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db      755 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAAAGCTATC 696
Qy      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db      695 CAGAAATCAGATGAAGGCCACCCATTACGGGCATATCTGGAATCTGAAGTTGCTATATCT 636
Qy      82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db      635 GAGGAGTTGGTTTCAGAGTACAGTAATCTCTCTTGTGTCATGTGAAGTCGACCATTAAG 576
Qy      102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db      575 GAACTCAGCGCCCTCTCTTCTAGTTGATGATTTAGTTGATTTCTCTGAAAGTTTGCAAGTGTG 516

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Qy      122 MetTrpValPheThrTyrValGlyValAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db      515 ATGTGGGTATTACTATGTGGTGGCTTGTATTATGGTCTGACACTACTGATTTGGCT 456
Qy      142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db      455 CTCATTTCACTCTTCAGTGTCTCTGTATTATTAAGCGCATCAGGCACAGATAGATCAT 396
Qy      162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      395 TATCTAGACTTGCAATAAGATGTTAAAGATCTATGGCTAAATCCAAGCAAAATC 336
Qy      182 ProGlyLeuLysArgLysAlaAsp 189
Db      335 CCTGATTGAAGCCCAAGCTGAA 312

RESULT 22
CR611869
LOCUS
DEFINITION full-length cDNA clone CSODN004VJ08 of Adult brain of Homo sapiens
              (human).
ACCESSION   CR611869
VERSION     CR611869.1 GI:50492676
KEYWORDS    HTC; CNSLT cDNA.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1540)
            Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
            Full-length cDNA libraries and normalization
            Unpublished
            Contact: Peng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
            Faraday Avenue
            Redwood City, CA 94061
            Genoscope.
            Direct Submission
            Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr)
            - Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source           1..1540
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CSODN004VJ08"
                     /tissue type="Adult brain"
                     /plasmid="pCMVSPORT_6"
ORIGIN
Alignment Scores:  1.14e-100      Length:      1540
Pred. No.:        904.00         Matches:    183
Score:            98.94%         Conservative: 3
Percent Similarity: 97.34%      Mismatches:  2
Best Local Similarity: 97.73%   Indels:     0
Query Match:      97.73%       Gaps:      0
DB:               3

US-09-830-972-2_COPY_975_1163 (1-189) x CR611869 (1-1540)

Qy      2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db      156 GTTGTGGACCTCTCTGTACTGGAGACATTAAAGACTGGAGTGGTGGTGGTGGCCAGC 215
Qy      22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

```

Db 216 CTATTCCTGCTCTTCATTGACAGTATTCAGCATTTGTCAGCGTAACAGCCTACATGGCC 275  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 276 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATATCAAGGGTGTGATCCAAGCTATC 335  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 336 CAGAAATCAGATGAAGGCCACCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 395  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
Db 396 GAGGAGTTGGTTCAGAGTACAGTAATCTCTGCTTGTGTCATGTCGACGATGAAG 455  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 456 GAACCTCAGCGCGCTCTCTTAGTGTATGATTTAGTTGATTTCTCTGAAGTTGTCAGTGTG 515  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
Db 516 ATGTGGGTATTTACCTATGTTGGTCTTGTATTAATGGTCTGACACTACTGATTTGGCT 575  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
Db 576 CTATTCACCTCTTCAGTGTCTCTGTTATTAAGCGCATCAGGCACAGATAGATCAT 635  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 636 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAGCAAAATC 695  
QY 182 ProGlyLeuLysArgLysAlaAsp 189  
Db 696 CCTGGATTGAAGCGCAAGCTGAA 719

RESULT 23  
AF077050 1785 bp mRNA linear HTC 21-NOV-2002  
LOCUS Homo sapiens neuroendocrine-specific protein C homolog mRNA,  
DEFINITION complete cds.  
ACCESSION AF077050  
VERSION AF077050.1 GI:4689147  
KEYWORDS HTC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 1785)  
AUTHORS Song, H., Peng, Y., Zhou, J., Huang, Q., Dai, M., Mao, Y., Yu, Y., Xu, X.,  
Luo, B., Hu, R., and Chen, J.  
TITLE Human neuroendocrine-specific protein C (NSP) homolog gene  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1785)  
AUTHORS Song, H.  
JOURNAL Direct Submission  
TITLE Submitted (10-JUL-1998) Rui-Jin Hospital, Shanghai Institute of  
JOURNAL Endocrinology, Molecular Medical Center, 197 Rui-Jin Road II,  
Shanghai 200025, P.R. China  
FEATURES  
1..1785  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="pituitary"  
214..813  
/codon\_start=1  
/product="neuroendocrine-specific protein C homolog"  
/protein\_id="AAD27783.1"  
/db\_xref="GI:4689148"  
- /translation="MDGQKNWKKVLLYWRDIKKTKVVGASFLLLSLTVPSIV  
SVTAYIALALSVLTISFRYKGVIAIQKSDGHPFRAYLESEVAISBELVKYNSA  
LGHVACTIKELRLFLVDLDFKFAVLMVFTYVGFALFNLGLILLILSLFSPVP  
IYERHQAQIDHYLGLANKNVKDMAKIQAKIPGLKRKA"

FEATURES  
source

CDS

ORIGIN

# Alignment Scores:

Pred. No.: 1.41e-100 Length: 1785  
Score: 904.00 Matches: 183  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.34% Mismatches: 2  
Query Match: 97.73% Indels: 0  
DB: 3 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AF077050 (1-1785)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 247 GTTGTGGACCTCTCTGCTGAGACATTAAGAGACTGGAGTGGTGTGGTCCACG 306  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 307 CTATTCCTGCTGCTTTTCATTGACAGTATTCAGCATTTGTGAGCGTAACAGCCTACATTGCC 366  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 367 TTGGCCCTGCTCTCTGTCACCATCAGCTTTTAGGATATATCAAGGGTGTGATCCAAGCTATC 426  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 427 CAGAAATCAGATGAAGGCCACCATTCAGGCATATCTGGAATCTGAAGTTGCTATATCT 486  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
Db 487 GAGGAGTTGGTTCAGAACTACAGTAATCTCTGCTTGTGTCATGTGAAGCTGACGATAAAG 546  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 547 GAACCTCAGCGCGCTCTCTTAGTGTATGATTTAGTTGATTTCTGGAAGTTGTCAGTGTG 606  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
Db 607 ATGTGGGTATTTACCTATGTTGGTGGCTTGTATTAATGGTCTGACACTACTGATTTGGCT 666  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
Db 667 CTCATTTCACTCTTCAGTGTCTCTGTTATTAAGAGTGTAAAGATGCTATGGCTAAATCCAAGCAAAATC 726  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 727 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAGCAAAATC 786  
QY 182 ProGlyLeuLysArgLysAlaAsp 189  
Db 787 CCTGGATTGAAGCGCAAGCTGAA 810

RESULT 24

Bi079496

LOCUS

DEFINITION

Bi079496

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Bi079496 781 bp mRNA linear EST 20-JUN-2001  
602876306F1 NCI\_CGAP\_Mam2 Mus musculus cDNA clone IMAGE:5008248 5',  
mRNA sequence.

Bi079496

Bi079496.1 GI:14497826

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.

1 (bases 1 to 781)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)

DNA Sequencing by: Incyte Genomics, Inc.



QY 122 MetTrrpValPheThrTyrValGlyAlaLeuPheAseGlyLeuThrLeuLeuLeuAla 141  
 |||||  
 Db 522 ATGTGGGTATTACCTATGTTGGTCTGTTTAAATGGTCTGACACTACTGATTTGGCT 581  
 |||||  
 QY 142 LeuLeuSerLeuPheSerileProValleTyrGluAtrGHisGlnValGlnleAseHis 161  
 |||||  
 Db 582 CTCATTCACTCTTCACTGTTCTCTGTTATTATGAACGGCATCAGCACAGATAGATCAT 641  
 |||||  
 QY 162 TyrLeuGlyLeuAlaAseNlySerValLysAsePalaMetAlaLysleGlnAlaLysle 181  
 |||||  
 Db 642 TATCAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGCTTAAATCCACGGAATC 701  
 |||||  
 QY 182 ProGlyLeuLysArgLysAlaAse 189  
 |||||  
 Db 702 CCTGGATTGAAGCGCAAGCTGAA 725  
 |||||

## RESULT 26

CB067821 634 bp mRNA linear EST 21-JAN-2003  
 LOCUS iq38a06.y1 HR85 islet Homo sapiens cDNA clone IMAGE: 5, similar to  
 DEFINITION TR:Q9Y293 Q9Y293 FOOCEN-S. [1], mRNA sequence.

ACCESSION CB067821  
 VERSION  
 KEYWORDS

SOURCE EST.  
 CB067821.1 GI:27812341

ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## AUTHORS

1. (bases 1 to 634)  
 Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K.,  
 Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,  
 Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,  
 Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,  
 Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarishvili, R.,  
 Williams, T., Jackson, Y., and Bowers, Y.  
 Endocrine Pancreas Consortium  
 Unpublished (2000)

## TITLE

Other ESTs: iq38a06.x1  
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium  
 Harvard University, Howard Hughes Medical Institute  
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
 MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:

Washington University Genome Sequencing Center For information on  
 obtaining a clone please contact: Dr. Hiroshi Inoue  
 (hinoue@im.wustl.edu)

Seq primer: -40UP from Gibco

High quality sequence stop: 460.

Location/Qualifiers

## FEATURES

source

1. .634  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:"  
 /tissue\_type="Purified pancreatic islet"  
 /lab\_host="DH10B"  
 /clone\_lib="HR85 islet"

/note="Organ: Pancreas; Vector: pBluescript SK(-); Site 1:  
 Not1; Site 2: XhoI; cDNA made by oligo-dT priming.  
 Size-selected on agarose gel. Average insert size ~1kb. 5'  
 XhoI site was destroyed after directional cloning.  
 Amplified once. Contact information: Hiroshi Inoue, MD,  
 Metabolism Div. (Alan Permut Lab), Washington University  
 School of Medicine, Box 8127, 660 South Euclid Ave., St.  
 Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:  
 314-362-1916, Fax: 314-747-2692."

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.79e-100 Length: 634  
 Score: 898.00 Matches: 182  
 Percent Similarity: 98.40% Conservative: 3  
 Best Local Similarity: 96.81% Mismatches: 3  
 Query Match: 97.08% Indels: 0  
 DB: 6 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CB067821 (1-634)

QY 2 ValValAspLeuLeuTyrTriArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
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 Db 71 GTTGTGGACCTCTGCTGACCATCAGCTTAAAGAGACTGGAGTGGTGTGTTGGTCCAGC 130  
 |||||  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerileValSerValThrAlaTyrleAla 41  
 |||||  
 Db 131 CTATTCTGCTGCTTTCATTGACATATTGAGCATTTGAGCATTAACAGCCTACATTTGCC 190  
 |||||  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValleGlnAlaIle 61  
 |||||  
 Db 191 TTGGCCCTGCTCTCTGTCACCATCAGCTTAAAGATATACAAGGGTGTGATCCAAAGCTATC 250  
 |||||  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 |||||  
 Db 251 CAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGATCTGAAGTTGCTATATCT 310  
 |||||  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 |||||  
 Db 311 GAGGAGTTGGTTCAAGATACAGTAATTTCTGCTCTTGGTCATGTGAACCTGCACGATAAAG 370  
 |||||  
 QY 102 GluLeuArgArgLeuPheIleuValAspIleuValAspSerLeuLysPheAlaValleu 121  
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 Db 371 GAACATCAGCGCCCTCTCTTATGATGATTTAGTTAGTATCTCTGAAGTTTGCATGTTG 430  
 |||||  
 QY 122 MetTrrpValPheThrTyrValGlyAlaLeuPheAseGlyLeuThrLeuLeuLeuAla 141  
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 Db 431 ATGTGGGTATTACCTATGTTGGTCCCTGTTTAAATGGTCTGACACTACTGATTTGGCT 490  
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 QY 142 LeuLeuSerLeuPheSerileProValleTyrGluArgHisGlnValGlnleAseHis 161  
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 Db 491 CTCATTTCACTCTTCACTGTTCTCTGTTTATGAACGGCATCAGGCACAGATAGATCAT 550  
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 QY 162 TyrLeuGlyLeuAlaAseNlySerValLysAsePalaMetAlaLysleGlnAlaLysle 181  
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 Db 551 TATCTAGGACTTGCAAATGAAGATGTTAAAGATGCTATGGCTTAAATCCACGAANATC 610  
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 QY 182 ProGlyLeuLysArgLysAlaAse 189  
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 Db 611 CCTGGATTGAAGCGCAAGCTGAA 634  
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## RESULT 27

CV030029

LOCUS

DEFINITION

CV030029

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 670)

Rual, J.F., Hirozane-Kishikawa, T., Hao, T., Bertin, N., Li, S.,

Driscoll, A., Li, N., Rosenberg, J., Lamesch, P., Vidalain, P.O.,

Clintcot, A., Hartley, J.L., Esposito, D., Cheo, D., Moore, T.,

Simmons, B., Sequerra, R., Bosak, S., Doucette-Stamm, L., Le Peuch, C.,

Vandenhaeghe, J., Cusick, M.E., Albaladejo, J.S., Hill, D.E., and Vidal, M.

Human ORFome Version 1.1: a Platform for Reverse Proteomics

Genome Res. (2004) In press

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

TITLE

JOURNAL

COMMENT

CV030029 670 bp mRNA linear EST 20-AUG-2004  
 9024 Full Length cDNA from the Mammalian Gene Collection Homo  
 sapiens cDNA 5' similar to BC014366, mRNA sequence.



1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA  
Tel: 617 632 5180  
Fax: 617 632 5739

Email: Marc\_Vidal@fci.harvard.edu

ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF results from a PCR reaction using an MGC full-length cDNA as template DNA and ORF specific primers

PCR Primers

FORWARD: ATGGACGGTCAAGAGAAATTTGG

BACKWARD: CATTACGCTTGGCTTCATC

Insert Length: 670 Std Error: 66.00

Plate: 11045 row: 02 column: B

Seq primer: ACTGCGCTGCTTTTACAACTGCTGACTGGGAAAC

High quality sequence start: 101

High quality sequence stop: 669

POLYA-No.

Location/Qualifiers

1. .670

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/tissue\_type="mixed"

/clone\_lib="Full length cDNA from the Mammalian Gene

Collection"

/note="Vector: mixed; The ORFs were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway cloning into pDONR223 Donor vector. Reference: MGC (Mammalian Gene Collection) Program Team, Generation and Initial Analysis of more than 15,000 Full-Length Human and Mouse cDNA Sequences. PNAS, 2002, 99(26), 16899-16903"

# FEATURES

source

## ORIGIN

Alignment Scores:  
Pred. No.: 1.93e-100 Length: 670  
Score: 898.00 Matches: 182  
Percent Similarity: 98.40% Conservative: 3  
Best Local Similarity: 96.81% Mismatches: 3  
Query Match: 97.08% Indels: 0  
DB: 7 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CV030029 (1-670)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 34 GTTGTGACCTCTGTTACTGGAGACATTAAGAGACTGGAGTGGTGGTGGCCAGC 93  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 94 CTATTCCTGCTGCTTTCATTGACAGATTTCAGCATTGTGAGCGTAACAGCCTACATTGCC 153  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 154 TTGGCCCTGCTCTCTGTGACCATCAGCTTTTAGGATATACAAAGGTGTGATCAAGCTATC 213  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 214 CAGAAATCAGATGAAGGCCACCCATTACGGGCATATCTGGAAATCTGAAGTTGCTATATCT 273  
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
Db 274 GAGGAGTTGGTTTCAGAACTACAGTAATTCCTCTGTGTCATGTGAACTGCACGATAAG 333  
Qy 102 GluLeuArgArgLeuPheLeuValAspIleValAspSerLeuLysPheAlaValLeu 121  
Db 334 GAACTCAGCGCCTCTCTTATAGTTGATGATTAGTTGATTCTCTGAAGTTTGCAGTGTG 393  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheArgGlyLeuThrLeuLeuIleAla 141  
Db 394 ATGTGGGTATTACCTATGTTGGTCCCTGTTTATGTGCTGACACTACTGATTTGGCT 453  
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161

Db 454 CTCATTTCACTCTTCAGTGTCTCTGTTATTATTAAGCGCATCAGGCACAGATGATCAT 513  
Qy 162 TrrLeuGlyLeuAlaAenLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 514 TATCTAGACTTGCATAAATAAGAAATGTTAAAGATGCTATGCTAAATCCAAGCAAAATC 573  
Qy 182 ProGlyLeuLysArgLysAlaAsp 189  
Db 574 CCTGATTGAAGCGCANAGCTGAA 597  
RESULT 28  
CN646472  
LOCUS  
DEFINITION  
CN646472 960 bp mRNA linear EST 13-MAY-2004  
ILLUMIGEN MCQ 26335 Katze MBR Macaca mulatta cDNA clone IBTUM-8548  
5' similar to bases 129 to 958 highly similar to human RTN4  
(Hs.436349), mRNA sequence.  
ACCSSION  
CN646472 GI:47159915  
VERSION  
EST.  
KEYWORDS  
SOURCE  
ORGANISM  
Macaca mulatta (rhesus monkey)  
Macaca mulatta  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
Cercopithecoidea; Macaca.  
REFERENCE  
1 (bases 1 to 960)  
Katze M.G., Thomas M., Korth M., Iadonato S.P. and Magness C.L.  
Large-scale Rhesus Macaque cDNA Sequencing  
Unpublished (2003)  
JOURNAL  
COMMENT  
Contact: C. Magness  
Illumigen Biosciences Inc.  
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA  
Tel: 2063780400  
Fax: 2063780408  
Email: cmagness@illumigen.com  
Sequenced on 2004.03.09. 743 Q20 bases.  
PCR Primers  
FORWARD: CCCTCACTAAAGGGAACAAAA  
BACKWARD: CACTATAGGCGGAATTGGGTA  
Insert Length: 960 Std Error: 0.00  
Plate: CL000173 row: H column: 11  
Seq primer: CCCTCACTAAAGGGAACAAAA  
POLYA-No.

## FEATURES

source

Location/Qualifiers

1. .960

/organism="Macaca mulatta"

/mol\_type="mRNA"

/strain="Indian"

/db\_xref="taxon:9544"

/clones="IBTUM:8548"

/sex="female"

/dev stage="adult"

/lab\_host="E. coli SOLR"

/clone\_lib="Katze\_MBR"

/note="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;  
Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis  
kit (Catalog #200400) and ZAP-cDNA Gigapack III Gold  
Cloning Kit (Catalog #200450)"

## ORIGIN

Alignment Scores:

Pred. No.: 3.22e-100 Length: 960  
Score: 898.00 Matches: 181  
Percent Similarity: 98.94% Conservative: 5  
Best Local Similarity: 96.28% Mismatches: 2  
Query Match: 97.08% Indels: 0  
DB: 7 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CN646472 (1-960)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 129 GTTGTGACCTCTCTCTACTGAGAGACATGAAGAAGACTGGAGTGGTGGTGGCCAGC 188

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 |||||  
 Db 189 CTATTCCCTGCTCTTCAATGACAGTATTGACGATTTGAGTGTAAACAGCCTACATTCGCC 248  
 |||||  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 |||||  
 Db 249 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCTATC 308  
 |||||  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 |||||  
 Db 309 CAGAAATCAGATGAAAGCCACCATTCAGGGCATATCTGGAATCTGAACTTCGATATCT 368  
 |||||  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
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 Db 369 GAGGAGTTGGTTTTCAGAAATGACATGATCTGCTTGTGTCATGTGAACCTGCACGATAAG 428  
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 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 |||||  
 Db 429 GAATCAGCGCGCTCTCTTAGTTGATGATTTAGTTGATCTCTGAAGTTTCAGTGTG 488  
 |||||  
 QY 122 MetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 |||||  
 Db 489 ATGTGGGTATTTACCTATGTTGGTGCCTTGTGTTTAAATGGTCTCAGCGTACTGATTTGGCT 548  
 |||||  
 QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 |||||  
 Db 549 CTCATTTCACTCTTCAGTGTCTCTTATTTATGAACGGCATCAGGCGACAGATGATCAT 608  
 |||||  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 |||||  
 Db 609 TATCTAGGACTTGCAATTAAGAAATGTTAAAGATGCTATGGCTAAATCCAGCGAAATC 668  
 |||||  
 QY 182 ProGlyLeuLysArgLysAlaAsp 189  
 |||||  
 Db 669 CCTGGATTGAAGCGCAAGCTGAA 692  
 |||||

## RESULT 29

CN803408 983 bp mRNA linear EST 26-MAY-2004  
 ILLUMIGEN MCQ 32945 Katze MMR Macaca mulatta cDNA clone  
 IBIUW:11396 5' similar to Bases 136 to 983 highly similar to human

RTN4 (Hs.436349), mRNA sequence.  
 CN803408 GI:47699384

## ACCESSION

VERSION CN803408.1

## KEYWORDS

SOURCE Macaca mulatta (rhesus monkey)

## ORGANISM

Macaca mulatta  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
 Cercopithecinae; Macaca.

## REFERENCE

1 (bases 1 to 983)

## AUTHORS

Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L.

## TITLE

Large-scale Rhesus Macaque cDNA Sequencing

## JOURNAL

Unpublished (2003)

## COMMENT

Contact: C. Magness  
 Illumigen Biosciences Inc.  
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA  
 Tel: 2063780400  
 Fax: 2063780408  
 Email: cmagness@illumigen.com

Sequenced on 2004.04.03. 731 Q20 bases.

## PCR Primers

FORWARD: CCTCACTAAAGGGAACAAA

BACKWARD: CACTATAGGCGAATTGGGTA

Insert Length: 983 Std Error: 0.00

Plate: CL000275 row: C column: 03

Seq primer: CCTCACTAAAGGGAACAAA

## POLYA=No.

## Location/Qualifiers

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 /organism="Macaca mulatta"  
 /mol\_type="mRNA"  
 /strain="Indian"

## FEATURES

## source

/db\_xref="taxon:9544"

/clone="IBIUW:11396"

/sex="female"

/dev\_stage="adult"

/lab\_host="E. coli SOLR"

/clone\_lib="Katze MMR"

/note="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;  
 Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis  
 kit (Catalog #200400) and ZAP-CDNA Gigapack III Gold  
 Cloning Kit (Catalog #200450)"

## ORIGIN

Alignment Scores:  
 Pred. No.: 3.33e-100 Length: 983  
 Score: 898.00 Matches: 181  
 Percent Similarity: 98.94% Conservative: 5  
 Best Local Similarity: 96.28% Mismatches: 2  
 Query Match: 97.08% Indels: 0  
 Db: 7 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CN803408 (1-983)

QY 2 ValValAspLeuLeuTyrTyrArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 |||||  
 Db 136 GTTGTGGTACCTCCCTACTGAGAGACATGAGAGACTGGAGTGGTGTGGTCCAGC 195  
 |||||  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 |||||  
 Db 196 CTATTCCCTGCTCTTTCATTCACAGTATTCAGCATTGTGAGTGTAAACAGCCTACATTCGC 255  
 |||||  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 |||||  
 Db 256 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCTATC 315  
 |||||  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 |||||  
 Db 316 CAGAAATCAGATGAAGCGCACCCATTGAGGCATATCTGGAATCTGAAGTTGCGATATCT 375  
 |||||  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 |||||  
 Db 376 GAGGAGTTGGTTTTCAGAAATGACATGATCTGCTTGTGTCATGTGAACCTGCACGATAAG 435  
 |||||  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 |||||  
 Db 436 GAATCAGCGCGCTCTCTTAGTTGATGATTTAGTTGATCTCTGAAGTTTCAGTGTG 495  
 |||||  
 QY 122 MetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 |||||  
 Db 496 ATGTGGGTATTTACCTATGTTGGTGCCTTGTGTTTAAATGGTCTGACGCTACTGATTTGGCT 555  
 |||||  
 QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 |||||  
 Db 556 CTCATTTCACTCTTCAGTGTCTCTGTTTATGAACGGCATCAGGCGACAGATGATCAT 615  
 |||||  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 |||||  
 Db 616 TATCTAGGACTTGCAATTAAGAAATGTTAAAGATGCTATGGCTAAATCCAGCGAAATC 675  
 |||||  
 QY 182 ProGlyLeuLysArgLysAlaAsp 189  
 |||||  
 Db 676 CCTGGATTGAAGCGCAAGCTGAA 699  
 |||||

## RESULT 30

## LOCUS

CN647521

## DEFINITION

ILLUMIGEN MCQ 28658 Katze MMR Macaca mulatta cDNA clone IBIUW:7529  
 5' similar to Bases 129 to 1018 highly similar to human RTN4  
 (Hs.436349), mRNA sequence.

## ACCESSION

CN647521

## VERSION

CN647521.1 GI:47160964

## KEYWORDS

Macaca mulatta (rhesus monkey)

## SOURCE

Macaca mulatta

## ORGANISM

Macaca mulatta

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
Cercopitheciinae; Macaca.

1 (bases 1 to 1031)  
Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.  
Large-scale Rhesus Macaque cDNA Sequencing  
Unpublished (2003)  
Contact: C. Magness  
Illumigen Biosciences Inc.  
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA  
Tel: 2063780400  
Fax: 2063780408  
Email: cmagness@illumigen.com  
Sequenced on 2004.03.24. 773 Q20 bases.  
PCR Primers

FORWARD: CCCTCACTAAAGGGAACAAA  
BACKWARD: CACTATAGGCGAATGGGTA  
Insert Length: 1031 Std Error: 0.00  
Plate: CU000187 row: G column: 05  
Seq primer: CCCTCACTAAAGGGAACAAA  
POLYA=No.

Location/Qualifiers

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/mol\_type="mRNA"  
/strain="Indian"  
/db\_xref="taxon:9544"  
/clone="IBIUM.7529"  
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/dev\_stage="adult"  
/lab\_host="E. coli SOLR"  
/clone\_lib="Katze MMRB"  
/note="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;  
Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis  
kit (catalog #200400) and ZAP-cDNA Gigapack III Gold  
Cloning Kit (Catalog #200450)"

FEATURES  
source

#### ORIGIN

Alignment Scores:  
Pred. No.: 3.57e-100 Length: 1031  
Score: 998.00 Matches: 181  
Percent Similarity: 98.94% Conservative: 5  
Best Local Similarity: 96.28% Mismatches: 2  
Query Match: 97.08% Indels: 0  
DB: 7 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CM647521 (1-1031)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 129 GTTGTGACCTCTCTACTCGAGAGACATGAAGAAGACTGGAGTGGTGTGGTGGCCAGC 188  
Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 189 CTATTCTCTGCTGCTTTCATTGACAGTATTGACGATTGTGAGTGTGAACAGCCCTACATTGCC 248  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 249 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAAGCTATC 308  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 309 CAGAAATCAGATGAAGCCACCCATTGAGGCATATCTGGAATCTGAAGTTGGCATATCT 368  
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
Db 369 GAGGAGTTGGTTCAGAGTACAGTAATCTCTCTCTGTCATGTCAACCTGCACGATAAAG 428  
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 429 GAATCTAGGCCCTCTCTCTTAGTTGATGATTTAGTTGATCTCTGAAAGTTTGCAGTGTG 488  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141

Db 489 ATGTGGGTATTACTATGTTGGTGCCTGTTTAAATGCTCTGACGCTACTGATTTGGCT 548  
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
Db 549 CTCAATTCACCTTCCTGCTGTTCTGTTATTATGAACGGCATCAGGCACATAGATCAT 608  
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 609 TATCTAGGACTTGCATATAGAATGTTAAAGATCTATGGCTAAATCCAGCGGAATC 668  
Qy 182 ProGlyLeuLysArgLysAlaAsp 189  
Db 669 CCTGGATTGAAGCGCAAAAGCTGAA 692

#### RESULT 31

AK034902.

LOCUS

DEFINITION

AK034902.1 GI:26084268

HTC; CAP trapper.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 Carninci,P. and Hayashizaki,Y.

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

2

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

3

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

4

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

5

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

6

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

7

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

3533 bp mRNA linear HTC 03-APR-2004  
Mus musculus 12 days embryo embryonic body between diaphragm region  
and neck cDNA, RIKEN full-length enriched library, clone:9430059L06  
product:RETICULON 4 (NEURITE OUTGROWTH INHIBITOR) (NOCO PROTEIN)  
(POOCEN) (GLUT4 VESICLE 20 KDA PROTEIN) homolog [Rattus  
norvegicus], full insert sequence.  
AK034902  
AK034902.1 GI:26084268  
HTC; CAP trapper.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 Carninci,P. and Hayashizaki,Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
9279253  
10349636  
2  
3  
Shibata,K., Itoh,M., Aizawa,K., Nagaoaka,S., Sasaki,N., Carninci,P.,  
Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,  
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,  
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,  
Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,  
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,  
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861  
4  
5  
The RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)  
6  
The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
7  
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,  
Kukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,  
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,  
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,













/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally; oligo-dt primed.  
Average insert size 3.3 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
Pred. No.: 1.67e-99 Length: 749  
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Percent Similarity: 98.39% Conservativeness: 0  
Best Local Similarity: 98.39% Mismatches: 3  
Query Match: 96.32% Indels: 0  
DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BG296048 (1-749)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 125 GTTGTGACCTCTCTACTGAGAGACATTAAAGACTGGAGTGGTGTGGTCCAGC 184  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 185 TTATTCCTGCTGCTCTCTGACAGTGTTCAGCATTTGTCAGTGAACGGCTACATTGCC 244  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 245 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAGGGTGTGATCCAGCATC 304  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 305 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCCATATCA 364  
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
Db 365 GAGGAATTTGGTTCAGAAATATAGTAATCTCTCTGTGTCATGTGAACAGCACATAAAA 424  
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 425 GAATTTAGGCGCTCTCTTCTTAGTGTGATTTAGTTGATTCCTTCCCTGAAGTTGCGAGTTG 484  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAlaIle 141  
Db 485 ATGTGGGTATTTACTTACGTTGGTGGCTTGTTCATGTTGACACTACTGATTTAGCT 544  
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
Db 545 CTGATCTCACCTTTCAGTATTCCTGTTATATATGACGGCATCAGCGCGCAGATAGATCAT 604  
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 605 TATCTAGGACTTGCACACAGAGCGTTAAGATGCCATGGCCAAATCCAAAGCAAAATCC 664  
Qy 182 ProGlyLeuLysArgLys 187  
Db 665 CTTGGATTGAAGCGCAAG 682

## RESULT 39

BG715173 757 bp mRNA linear EST 08-MAY-2001  
LOCUS 602675631P1 NIH\_MGC\_96 Homo sapiens cDNA clone IMAGE:4798279 5',  
DEFINITION mRNA sequence.

ACCESSION BG715173

VERSION BG715173.1 GI:13994106

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 757)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

## REFERENCE

AUTHORS

TITLE

JOURNAL

## COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: ccapbs-remail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LHAM10685 row: n column: 08  
High quality sequence stop: 757.

## FEATURES

Location/Qualifiers

source

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/mol\_type="mRNA"  
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/clone\_lib="NIH\_MGC\_96"  
/note="Organ: brain; Vector: pBluescriptR (modified  
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(gtcag); Oligo-dt primed using primer  
5'-TTTTTTTTTTTTTTVN-3', size-selected for average  
insert size 2.3 kb and normalized to ROT 5. This is a  
primary library enriched for full-length clones and  
constructed using the Cap-trapper method (Carninci, in  
preparation). Library constructed by M. Brownstein  
(NIH/NHGRI, National Institutes of Health). Note: this is  
a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
Pred. No.: 1.69e-99 Length: 757  
Score: 891.00 Matches: 181  
Percent Similarity: 97.87% Conservativeness: 3  
Best Local Similarity: 96.28% Mismatches: 4  
Query Match: 96.32% Indels: 0  
DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BG715173 (1-757)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 179 GTTGTGACCTCTCTACTGAGAGACATTAAAGACTGGAGTGGTGTGGTCCAGC 238  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 239 CTATTCCTGCTCTCTCTGACCATTCAGCATTTGACGCTTACAGCGTACAGCTACATTGCC 298  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 299 TTGGCCCTGCTCTCTGTGACCATTCAGCTTTAGGATATATAGGGTGTGATCCAGCATC 358  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 359 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 418  
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
Db 419 GGGGAGTTGGTTCAGAAAGTACAGTAATCTCTCTTGTCTCATGTGAAGTCCCGATAAAG 478  
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 479 GAACTCAGGGCGCTCTCTTCTTAGTGTGATTTAGTTGATTTCTCTGAAAGTTTGCAGTGTG 538  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAlaIle 141  
Db 539 ATGTGGGTATTTACTTACGTTGGTGGCTTGTATGATGGTCTGACACTACTGATTTGGCT 598  
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161

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Db      599 CTCATTTCAGTCTTCTGCTGTTATTTATGAAGCATCAGGCACAGATAGATCAT 658
Qy      162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      659 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATAATCCAGCAAAATC 718
Qy      182 ProGlyLeuLysArgLysAlaAsp 189
Db      719 CCTGGATTGAAGCGCAAAAGCTGAA 742

RESULT 40
BU845601
LOCUS   BU845601
DEFINITION   AGENCOURT_10414454 NIH_MGC_109 Homo sapiens cDNA clone
IMAGE: 6579264 5', mRNA sequence.
ACCESSION   BU845601
VERSION     BU845601.1 GI:24030042
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 924)
AUTHORS    NIH-MGC http://mgi.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgabbs-r@mail.nih.gov
           Tissue Procurement: ATCC
           cDNA Library Preparation: Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone Distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: L16W2782 row: e column: 24
           High quality sequence stop: 696.

FEATURES             source
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             /clone_lib="NIH_MGC_109"
             /note="Organ: ovary; Vector: pOTB7; Site 1: EcoRI; Site 2:
             XhoI; cDNA made by oligo-dT priming. Directionally cloned
             into EcoRI/XhoI sites using the following 5' adaptor:
             GGCACGAG(G). Library constructed by Ling Hong in the
             laboratory of Gerald M. Rubin (University of California,
             Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
             Superscript II RT (Life Technologies). Note: this is a
             NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.:      2,99e-99      Length:      924
Score:          890.00      Matches:    180
Percent Similarity: 97.87%      Conservative: 4
Best Local Similarity: 95.74%      Mismatches: 0
Query Match:    96.22%      Indels:     0
DB:             5           Gaps:         0

US-09-830-972-2_COPY_975_1163 (1-189) x BU845601 (1-924)

Qy      2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyValAsp 21
Db      244 GTTGTTGACCTCTCTACTGAGAGACATTAAAGACATGGAGTGGTGTGGTCCAGC 303
Qy      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db      304 CTATTCTCTGCTGCTTTCATTGACAGTATTACGACATTGTGAGCGTAACAGCCTACATTGCC 363

```

```

Qy      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db      364 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 423
Qy      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db      424 CAGAAATCAGATGAAGGCCACCCATTAGGGCATATCTGGAAATCTGAAGTTGCTATATCT 483
Qy      82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db      484 GAGGAGTTGGTTCAGAGTACAGTAATCTCTCTTGGTCATGTGAACTGCACGATAAG 543
Qy      102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db      544 GAACTCAGGCGCCTCTTCTTAGTTGATGATTAGTTAGTTGATTCTCTGAAGTTTGCAGTGTG 603
Qy      122 MetTrpValPheThrTyrValGlyAlaLeuPheGlnGlyLeuThrLeuLeuIleAla 141
Db      604 ATGTGGGTATTACTATGTTGGTGCCTGTTTAAATGGTCTGACACTACTGATTTGGCT 663
Qy      142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db      664 CTCAATTCACCTCTTCAGTGTTCCTGTTATTATGAACGGCATCAGGCACAGATAGATCAT 723
Qy      162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      724 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAANATCCAGCAAAATC 783
Qy      182 ProGlyLeuLysArgLysAlaAsp 189
Db      784 CCTGGATGAAGCGCAAAAGCTGAA 807

RESULT 41
BU805577
LOCUS   BU805577
DEFINITION   ILLUMIGEN MQC_36873 Katze_MBR Macaca mulatta cDNA clone
IBIUF:12670 5' similar to Bases 138 to 1022 highly similar to human
RTN4 (Hs.436349), mRNA sequence.
ACCESSION   BU805577
VERSION     BU805577.1 GI:47701553
KEYWORDS    EST.
SOURCE      Macaca mulatta (rhesus monkey)
ORGANISM    Macaca mulatta
REFERENCE   1 (bases 1 to 1042)
AUTHORS    Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L.
TITLE      Large-scale Rhesus Macaque cDNA Sequencing
JOURNAL    Unpublished (2003)
COMMENT    Contact: C. Magness
           Illumigen Biosciences Inc.
           2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
           Tel: 2063780400
           Fax: 2063780408
           Email: cmagness@illumigen.com
           Sequenced on 2004.05.12. 633 Q20 bases.
           PCR Primers
           FORWARD: CCCTCACTAAAGGGAACAAAA
           BACKWARD: CACTATAGGCGGAATTGGGTA
           Insert Length: 1042 Std Error: 0.00
           Plate: CL000243 row: C column: 03
           Seq primer: CCCTCACTAAAGGGAACAAAA
           POLYA=Yes.

FEATURES             Location/Qualifiers
     1..1042
         /organism="Macaca mulatta"
         /mol_type="mRNA"
         /strain="Indian"
         /db_xref="taxon:9544"
         /clone="IBIUF:12670"
         /sex="female"

```

```

/dev stage="adult"
/lab host="E. coli SOLR"
/clone lib="Katze.MMR"
/notes="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;
Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis
Kit (catalog #200400) and ZAP-cDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"

```

## ORIGIN

```

Alignment Scores:
Pred. No.: 3.54e-99 Length: 1042
Score: 890.00 Matches: 180
Percent Similarity: 98.40% Conservative: 5
Best Local Similarity: 95.74% Mismatches: 3
Query Match: 96.22% Indels: 0
DB: 7 Gaps: 0

```

```

US-09-830-972-2_COPY_975_1163 (1-189) x CN805577 (1-1042)

```

```

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 138 GTTGTGACCTCCTCTACTGAGAGACATGAAGAGACTGGAGTGGTGTGGTGGCCAGC 197
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 198 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTTGTGAGTGTAAACAGCCTACATTGCC 257
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 258 TTGGCCCTGCTCTCTGTGACCATCAGCTTTTAGGATATACAGGGGTGTGATCAAGCTATC 317
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 318 CAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAAATCTGAAGTTGCATATCT 377
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 378 GAGGAGTGGTTCAGAGTACAGTAATCTCTCTCTGTCATGTGAACTGCACGATAAAG 437
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 438 GAATCAGGCCCTCTCTCTAGTTGATGATTTAGTTAGTTCTCTGAAAGTTTGCAGTGTG 497
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 498 ATGTGGGTATTTACTATGTTGGTGGCTTTGTTTAAATGCTCTGACGCTACTGATTTGGCT 557
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 558 CTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 617
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaIleAla 181
Db 618 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGTAAATCCAAAGCGAAATC 677
Qy 182 ProGlyLeuLysArgLysAlaAsp 189
Db 678 CTGGATTGAAGCGCATAGCTGAA 701

```

```

RESULT 42
CD110203
LOCUS CD110203 871 bp mRNA linear EST 15-MAY-2003
DEFINITION AGENCOURT 13994940 NIH_MGC_148 Homo sapiens cDNA clone
IMAGE:30331865 5', mRNA sequence.
ACCESSION CD110203
VERSION CD110203.1 GI:30754412
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 871)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/

```

TITLE  
JOURNAL  
COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: csapbs-remail.nih.gov  
 Tissue Procurement: Dr. Stefan Hansson  
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help  
 and advice from Piero Carninci (RIKEN)  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: NDAM347 row: p column: 18  
 High quality sequence stop: 630.

## FEATURES

source

```

1..871
Location/Qualifiers
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clones="IMAGE:30331865"
  /tissue_type="pre-eclamptic placenta"
  /lab_host="DH10B Tora"
  /clone_lib="NIH_MGC_148"
  /notes="Organ: placenta; Vector: pBluescriptR; Site 1:
  all-XhoI; Site 2: BamH; Library is oligo-dT primed and
  directionally cloned using primer
  5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert
  size 2.3 kb and normalized to ROT 5. This is a primary
  library enriched for full-length clones and constructed
  using the Cap-trapper method (Carninci, in preparation).
  Library constructed by M. Brownstein (NIH/NHGRI,
  National Institutes of Health). Note: this is a NIH_MGC
  Library."

```

## ORIGIN

```

Alignment Scores:
Pred. No.: 3.65e-99 Length: 871
Score: 889.00 Matches: 182
Percent Similarity: 98.41% Conservative: 4
Best Local Similarity: 96.30% Mismatches: 2
Query Match: 96.11% Indels: 1
DB: 6 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x CD110203 (1-871)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 187 GTTGTGACCTCCTCTACTGAGAGACATTAAGAGACTGGAGTGGTGTGGTGGCCAGC 246
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 247 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTTGTGAGCTTAACAGCCTACATTGCC 306
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 307 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 366
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 367 CAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGAAGTTGCTATATCT 426
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 427 GAGGAGTGGTTCAGAGTACAGTAATCTGCTCTTGGTCAATGTAAGTGCACGATAAAG 486
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 487 GAATCAGGCCCTCTCTCTAGTTGATGATTTAGTTAGTTCTCTGAAAGTTTGCAGTGTG 546
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 547 ATGTGGGTATTTACTATGTTGGTGGCTTTGTTTAAATGCTCTGACACTACTGATTTGGCT 606

```

```

QY 142 LeuileSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 607 CTCATTTCCTCTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 666

QY 162 TyrLeuGlyLeuAlaAsnLysSerValIysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 667 TATCTAGGACTTGCAATTAAGATGTTAAAGATGCTATGGCTAAATCCACGCAAAATC 726

QY 182 ProGlyLeu-LysArgLysAlaAsp 189
Db 727 CCTGGAATCAAAAGCGCAAGCTGAA 751

RESULT 43
BU503291
LOCUS AGENCOURT_8933519 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6490526
DEFINITION 5', mRNA sequence.
ACCESSION BU503291
VERSION BU503291.1 GI:22809480
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 921)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: LLAM14040 row: h column: 15
High quality sequence stop: 627.
Location/Qualifiers
1..921
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6490526"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 6,99e-99 Length: 921
Score: 887.00 Matches: 183
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 97.34% Mismatches: 1
Query Match: 95.89% Indels: 1
DB: 5 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x BU503291 (1-921)

QY 2 ValValAspLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 156 GTTGTGACCTCTGCTGACAGACATTAAGACATGAGTGGTGTGGTGGCCAGC 215

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 216 TTATTCTGCTGCTGCTGACAGTGTTCAGCATTTGTCAGTGTGAACGGCCTACATTC 275

```

```

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 276 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAAGCTATC 335

QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 336 CAGAANTCAGATGAAGGCCACCCATTCAGGCAATATTTGGAAATCTGAAGTTCCTCCATATCA 395

QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 396 GAGGAATTTGGTTTCAGAAATATAGTAATTTCTGCTCTTGTGTCATGTGAACAGACAAATAAA 455

QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 456 GAAATTGAGCGCGTCTCTTCTTAGTTAGTATTTAGTTGATTCCTCGAAGTTTGCAGTGTG 515

QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 516 ATGTGGGTATTTACTTACGTGGTGGTCCCTTGTCAATGGTTTGACACTACTGATTTAGCT 575

QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 576 CTGATCTCAGTCTTTCAGTATTTCTGTTATATATGAACGGCATCAGGCGCAGATAGATCAT 635

QY 162 TyrLeuGlyLeuAlaAsnLysSerValIysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 636 TATCTAGGACTTGCAACACAGAGCGTTAAGATGCCATGGCCCAATCCAGCAAAATC 695

QY 182 Pro-GlyLeuLysArgLysAla 188
Db 696 CCTGGATGAGGCCCAAGC 717

CO048918 1013 bp mRNA linear EST 14-JUN-2004
ILLUMIGEN MCO 38898 Katze.MBR Macaca mulatta cDNA clone
BTUW:16203 57 similar to Bases 112 to 991 highly similar to human
RTN4 (Hs.436349), mRNA sequence.
ACCESSION CO048918
VERSION CO048918.1 GI:48688540
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
TITLE Cercopithecoidea; Macaca.
JOURNAL 1 (bases 1 to 1013)
COMMENT Katze.M.G., Thomas.M., Korth.M., Iadonato.S.P. and Magness,C.L.
Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)
Contact: C. Magness
ILLUMIGEN Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.05.13. 609 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
ILLUMIGEN Biosciences Inc. For further information, see
http://www.macaque.org
PCR Primers
FORWARD: CCTCCTACTAAAGGGAACAAA
BACKWARD: CACTATAGGCGGAATGGGTA
Insert Length: 1013 Std Error: 0.00
Plate: CL000160 row: G column: 08
Seq primer: CCCTCACTAAAGGGAACAAA
POLYA=Yes.
Location/Qualifiers
1..1013
/organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"
FEATURES
source

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/clone="IBIUM:16203"
/sex="female"
/dev stage="adult"
/lab_host="E. coli SOLR"
/clone_lib="Katze_MBR"
/notes="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;
Site 2: Xho I; Created from Stratagene ZAP-CDNA Synthesis
kit (catalog #200400) and ZAP-CDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"

```

## ORIGIN

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Alignment Scores:
Pred. No.: 1,41e-98 Length: 1013
Score: 885.00 Matches: 181
Percent Similarity: 98.41% Conservativeness: 5
Best Local Similarity: 95.77% Mismatches: 2
Query Match: 95.68% Indels: 1
DB: 7 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x C0048918 (1-1013)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 112 GTTGTGACCTCTCTACTCGAGAGACATGAAGAAGACTGGAGTGGTGTGGTCCAGC 171
Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 172 CTATTCCTGCTGCTTTCATGACAGTATTCAGCAATTTGAGTGTGAACAGCTACATTGCC 231
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 232 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCTATC 291
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 292 CAGAAATCAGATGAAGGCCACCCATTCAGGCATATCTGGAATCTGGAATTTGCGATATCT 351
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 352 GAGAGTGGTTCAGAGTACAGTAATCTGCTTTGTCATGTGAATGACGACGATTAAG 411
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 412 GAACCTCAGGCCCTCTCTTCTAGTTGATGATTTAGTTGATTTCTGAAAGTTTGCAGTGTG 471
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 472 ATGTGGGTATTTACCTATGTTGGTCCCTGTTTAATGCTCTGACGCTACTGATTTGGCT 531
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 532 CTATTTCTCTTCAGTGTTCCTGTTATTTATGAAGGCATCAGGCACAGATGATCAT 591
Qy 162 TyrLeuGlyLeuAlaAsnLysSer-ValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 592 TATCTAGGACTTGCAATAAGATGGTTAAAGATGCTATGCTAAATCCAAAGCGAAT 651
Qy 181 eProGlyLeuLysArgLysAlaAsp 189
Db 652 CCCTGGATTTGAAGCGCAAGCTGAA 676

```

## RESULT 45

```

CN801888 1018 bp mRNA linear EST 26-MAY-2004
LOCUS ILLUMIGEN MCQ 37222 Katze_MBR Macaca mulatta cDNA clone
DEFINITION IBIUM:16016 5' similar to Bases 146 to 1018 highly similar to human
RTN4 (Hs.436349), mRNA sequence.
ACCESSION CN801888
VERSION CN801888.1 GI:47697864
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

REFERENCE
AUTHORS Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
TITLE Large-scale Rhesus Macaque cDNA Sequencing
JOURNAL Unpublished (2003)
COMMENT Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.05.14. 594 Q20 bases.
PCR Primers
FORWARD: CCCTCACTAAAGGGACACAAA
BACKWARD: CACTATAGGCGGAATGGGTA
Insert Length: 1018 Std Error: 0.00
Plate: CL000272 row: E column: 10
Seq primer: CCCTCACTAAAGGGACACAAA
POLYA=No.

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## FEATURES

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source
1..1018
/organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"
/clone="IBIUM:16016"
/sex="female"
/dev stage="adult"
/lab_host="E. coli SOLR"
/clone_lib="Katze_MBR"
/notes="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;
Site 2: Xho I; Created from Stratagene ZAP-CDNA Synthesis
kit (Catalog #200400) and ZAP-CDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"

```

## ORIGIN

```

Alignment Scores:
Pred. No.: 1,42e-98 Length: 1018
Score: 885.00 Matches: 181
Percent Similarity: 98.41% Conservativeness: 5
Best Local Similarity: 95.77% Mismatches: 2
Query Match: 95.68% Indels: 1
DB: 7 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x CN801888 (1-1018)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 146 GTTGTGACCTCTCTACTCGAGAGACATGAAGAAGACTGGAGTGGTGTGGTCCAGC 205
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 206 CTATTCCTGCTGCTTTCATTCAGCAGTATTCAGCATTTGAGTGTGAACAGCTACATTGCC 265
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 266 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCTATC 325
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 326 CAGAAATCAGATGAAGGCCACCCATTCAGGCATATCTGGAATCTGGAATTTGCGATATCT 385
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 386 GAGGAGTGGTTCAGAGTACAGTAATCTGCTCTTGGTTCATGTGAACGACGATTAAG 445
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 446 GAACCTCAGGCCCTCTCTTCTAGTTGATGATTTAGTTGATTTCTGAAAGTTTGCAGTGTG 505
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141

```

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

Db 506 ATGTGGTATTTACCTATGTTGGTGGCTTTGTTAATGCTGCTGACGCTACTGATTTGGCT 565  
 QY 142 LeuileSerLeuPheSerileProValileTyrgluArgHisGlnValGlnleAspHis 161  
 Db 566 CTATTTCACTCTCAGTGTCTCTGTTATTTATGAAGCGCATCAGGCACAGATAGATCAT 625  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAla-LysII 181  
 Db 626 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAGCCGAAAT 685  
 QY 181 eProGlyLeuLysArgLysAlaAsp 189  
 Db 686 CCTGGATTGAAGCGCAAGCTGAA 710

## RESULT 46

LOCUS BG623462 747 bp mRNA linear EST 18-APR-2001  
 DEFINITION 602648520F1 NIH\_MGC\_79 Homo sapiens cDNA clone IMAGE:4770077 5',  
 mRNA sequence.

ACCESSION BG623462.1 GI:13674833

VERSION EST.

KEYWORDS

SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

## JOURNAL

Contact: Robert Strausberg, Ph.D.

Email: c9apbs-remail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Prepared by: The I.M.A.G.E. Consortium, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCW1636 row: g column: 06

High quality sequence stop: 742.

## FEATURES

source

1..747

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4770077"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_lib="NIH MGC 79"

/note="Organ: placenta; Vector: pDNR-LIB (Clontech);

Site 1: SfII (ggccgctcgcc); Site 2: SfiI

(ggccattatggcc); 5' and 3' adaptors were used in cloning

as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'

and 3' adaptor sequence:

5'-ATTCTAGCGCGAGCGCGGCACATG-dT(30)BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.3

kb (range 0.5-4.0 kb). 15/15 colonies contained inserts

by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto,

CA). Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:

Pred. No.: 1..626-98 Length: 747

Score: 883.00 Matches: 179

Percent Similarity: 96.81% Conservative: 3

Best Local Similarity: 95.21% Mismatches: 6

Query Match: 95.46% Indels: 0

DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BG623462 (1-747)

QY 2 ValValAspLeuTyTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21

Db 133 GTTGTGACCTCCTGCTACTGGAGACATTAAAGAGCTGGAGTGGTGTGGTCCAGC 192  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerileValSerValThrAlaTyrlleAla 41  
 Db 193 CTATTCTCTGCTGCTTTCATTGACAGTATTCAGCATTTGAGCGTAAACGCTACATGGC 252  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrlLysGlyValIleGlnAla 61  
 Db 253 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 312  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrlLeuGluSerGluValAlaIleSer 81  
 Db 313 CAGAAATCAGATGAAGGCCACCCATTACGGGATATCTGGAAATCTGAAGTTGCTATATCT 372  
 QY 82 GluGluLeuValGlnLysTySerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 373 GAGGAGTTGGTTTCAGAGTACAGTAATCTCTCTTGTGTCATGTGAACCTGCACGATAAG 432  
 QY 102 GluLeuArgArgLeuPheLeuValAspSerLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 433 GAACCTCAGCGCCTCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 492  
 QY 122 MetTrpValPheThrTyrlValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
 Db 493 ATGTGGGTATTTACCTATGTTGGGCCCTGTTTATGTTCTGACACTACTGATTTTGGCT 552  
 QY 142 LeuileSerLeuPheSerileProValileTyrgluArgHisGlnValIleAspHis 161  
 Db 553 CTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAAGCGCATCAGGCACAGATAGATCAT 612  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 613 TATCTAGGACTTGCAAAATGAAGATGTTTACAGATGCTTATGGTAAATCCAGCAAAATC 672  
 QY 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 673 CCTGGATTGAAGCGCAAGTGAAT 696

## RESULT 47

LOCUS BG740561

DEFINITION 602633075F1 NCI\_CGAP\_Skn3 Homo sapiens cDNA clone IMAGE:4778131 5',  
 mRNA sequence.

ACCESSION BG740561

VERSION BG740561.1 GI:14051214

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: c9apbs-remail.nih.gov

Tissue Procurement: James Cleaver, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA

Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10633 row: f column: 20

High quality sequence stop: 743.

Location/Qualifiers

1..758

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4778131"

/lab\_host="DH10B (T1 phage-resistant)"

/clone.lib="NCI\_CGAP\_Skn3"  
 /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.5kb. Library constructed by Life  
 Technologies. Note: this is a NCI\_CGAP Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 2.93e-98 Length: 758  
 Score: 881.00 Matches: 181  
 Percent Similarity: 97.35% Conservative: 3  
 Best Local Similarity: 95.77% Mismatches: 4  
 Query Match: 95.24% Indels: 1  
 DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BG740561 (1-758)

```

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 130 GTTGTGACCTCTCTGACGACATTAAGAAGACTGGAGTGGTGTGGTGGCCAGC 189
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 190 CTATTCCTGCTCTTTCATTCACAGTATTCAGCATTTGAGCGTAACAGCCTACATTGCC 249
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 250 TTGCGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 309
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 310 CAGAAATCAGATGAAGGCCACCCATTCAGGCATATCTGGAATCTGAAGTTGCTATATCT 369
Qy 82 GluLeuLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 370 GAGGAGTNGGTTTCAGAGTACAGTAATCTGCTCTTGCTCATGTGAACCTGCACGATAAG 429
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 430 GAATCAGCGCCCTCTTCTAGTGTGATTTAGTTGATTTCTGGAAGTTTGCAGTGTG 489
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
Db 490 ATGTGGGTATTTACTATGTGGTGGCTTGTGTTAATGCTCTGACACTACTGATTTGGCT 549
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 550 CTCATTTTCACTCTTTCAGTGTCTCTGTTATTTATGAACGGCATTCAGGCAGATGATCAT 609
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLys-AspAlaMetAlaLysIleGlnAlaLysIle 181
Db 610 TATCTAGACTTGCATATAGAAATGTTAACAAGATGCTATGCTAATATCCAGCAAAAT 669
Qy 181 eProGlyLeuLysArgLysAlaAsp 189
Db 670 CCCTGGATTGAAGCGCAAGCTGAA 694

```

## RESULT 48

CN641703 1081 bp mRNA linear EST 12-MAY-2004  
 LOCUS ILLUMIGEN MCQ 5216 Katze.MBR Macaca mulatta cDNA clone IBIUM:6014  
 DEFINITION 5' similar to Bases 156 to 1013 highly similar to human RTN4  
 (Hs.436349), mRNA sequence.

CN641703 GI:47152713

## ACCESSION

VERSION CN641703.1

## KEYWORDS

SOURCE EST.

## ORGANISM

Macaca mulatta (rhesus monkey)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

Cercopithecinae; Macaca.

## REFERENCE

1 (bases 1 to 1081)  
 Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.

## TITLE Large-scale Rhesus Macaque cDNA Sequencing

## JOURNAL

## COMMENT

Unpublished (2003)  
 Contact: C. Magness  
 Illumigen Biosciences Inc.  
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA  
 Tel: 2063780400  
 Fax: 2063780408  
 Email: cmagness@illumigen.com  
 Sequenced on 2003.12.04. 735 Q20 bases.  
 PCR Primers  
 FORWARD: CCCTCACTAAAGGAACAAAA  
 BACKWARD: CACTATAGGGCGAATTTGGGTA  
 Insert Length: 1081 Std Error: 0.00  
 Plate: CL000043 row: H column: 10  
 Seq primer: CCCTCACTAAAGGAACAAAA  
 POLYA-Yes.

## FEATURES

## source

1..1081  
 /organism="Macaca mulatta"  
 /mol\_type="mRNA"  
 /strain="Indian"  
 /db\_xref="taxon:9544"  
 /clone="IBIUM:6014"  
 /sex="female"  
 /dev\_stage="adult"  
 /lab\_host="E. coli SOLR"  
 /clone\_lib="Katze MBR"  
 /note="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;  
 Site 2: Xho I; Created from Stratagene ZAP-CDNA Synthesis  
 kit (catalog #200400) and ZAP-CDNA Gigapack III Gold  
 Cloning Kit (Catalog #200450)"

## ORIGIN

Alignment Scores:  
 Pred. No.: 4.85e-98 Length: 1081  
 Score: 881.00 Matches: 180  
 Percent Similarity: 97.88% Conservative: 5  
 Best Local Similarity: 95.24% Mismatches: 3  
 Query Match: 95.24% Indels: 1  
 DB: 7 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CN641703 (1-1081)

```

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 156 GTTGTGACCTCTCTACTGAGAGACATGAGAGACTGGAGTGGTGTGGTGGCCAGC 215
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 216 CTATTCCTGCTCTTTCATTCACAGTATTCAGCATTTGAGTGTAAACAGCCTACATTGCC 275
Qy 42 LeuAlaLeuLeuSerValThrIle-SerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 276 TTGCGCCCTGCTCTCTGTGACCATCANGCTTTTAGGATATACAGGGGTGTGATCCAGCTAT 335
Qy 61 eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 81
Db 336 CCAGAAATCAGATGAAGGCCACCCATTCAGGCATATCTGGAAATCTGAGTTGGATATC 395
Qy 81 rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLY 101
Db 396 TGAGGAGTTGGTTTCAGAAAGTACAGTAATTCCTGCTCTGGTTCATGTGAACATGCACGATAA 455
Qy 101 sGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLe 121
Db 456 GGAATCTCAGCGGCTCTCTTGTAGTGTGATGATTTAGTTGATTTCTGAAAGTTTGAGTGT 515
Qy 121 uMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAl 141
Db 516 GATGTGGGTATTTACCTATGTTGGTGGCTTGTGTTTAAATGGTCTGACGCTACTGATTTTGGC 575
Qy 141 aLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHi 161

```

Db 576 TCTATTCTCCTTCAGTCTCTGTTATTTATGAACGGCATCAGGCACACATAGATCA 635  
 Qy 161 sTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 636 TTATCTAGGACTTGCATAAATAAGATGTTAAAGATGCTATGGCTAAATCCAGCGAAAAT 695  
 Qy 181 eProGlyLeuLysArgLysAlaAsp 189  
 Db 696 CCTGGATTGAAGCGCAAGCTGAA 720

RESULT 49  
 CO259245  
 LOCUS 4130644 BARC 8BOV Bos taurus mRNA linear EST 23-JUN-2004  
 DEFINITION 4130644 BARC 8BOV Bos taurus cDNA clone 8BOV\_51K20 5', mRNA

ACCESSION CO259245  
 VERSION CO259245.1 GI:49144047  
 KEYWORDS EST.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 585)  
 AUTHORS Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassel,C.P. and Matukumalli,L.K.  
 TITLE Construction and Analysis of a cDNA Library Generated From Intestinal Muscle and Epithelial Tissues of Holstein Cattle

JOURNAL Unpublished (2004)  
 COMMENT Contact: Richard G. Baumann  
 Bovine Functional Genomics Lab  
 ANRI

BLDG 162: BARC-EAST, Beltsville, MD 20705, USA

Tel: 3015048604  
 Fax: 3015048744

Email: rbaumann@nri.barc.usda.gov

Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim\_alt '- -trim\_fasta. Vector identified by cross\_match using options -mismatch 12 -minscore 12

Plate: 51 row: K column: 20

Seq primer: CCTATTAGTGACACTATAGAAC

High quality sequence stop: 585.

Location/Qualifiers

FEATURES

1..585

/organism="Bos taurus"

/mol\_type="mRNA"

/strain="Holstein"

/db\_xref="taxon:9913"

/clone="8BOV\_51K20"

/sex="Female"

/tissue\_type="Epithelial, Muscle"

/dev\_stage="Lactating, Neonatal"

/lab\_host="DH10B Tona"

/clone\_lib="BARC 8BOV"

/note="Organ: Intestine; Vector: pCMVSPORT6.1; Site\_1:

Noti; Site\_2: EcoRI; Normalized cow cDNA intestinal

library in pCMVSPORT6.1, constructed from equimolar mRNA

pools derived from 5 sources, 4 lactating intestinal, 1

neonatal intestinal 4/5 Lactating, Proximal Duodenum,

Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal

Duodenum, Jejunum, Distal Ileum"

ORIGIN

Alignment Scores:

Pred. No.: 2,69e-98 Length: 585

Score: 880.00 Matches: 179

Percent Similarity: 98.37% Conservative: 2

Best Local Similarity: 97.28% Mismatches: 3

Query Match: 95.14% Indels: 0

DB: 7 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CO259245 (1-585)

Qy 2 ValValAspLeuLeuTyrTTPArgAspIleIysLysThrGlyValValPheGlyAlaSer 21  
 Db 32 GTTGTGTACCTCCCTCTACTCGAGAGACATTAAAGAACTGGAGTGGTGTCCGGTCCACG 91  
 Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 92 TTGTTCTCTGCTGCTCTCGCTGACAGTATTACGATTGTGAGTGTAAACGGCCTACATTGCC 151  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 152 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGGTGTGATCCAGGCTATC 211  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 212 CAGAAATCTGATGAAGGCCACCCATTACGGGCATATTTGGAATCTGAAGTTGCTATATCT 271  
 Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 272 GAGGAGTTGGTTTCAGAGTACAGCAATCTCTGCTCTTGGTCATGTTAACTGCACATAAAA 331  
 Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspLeuPheAlaValLeu 121  
 Db 332 GAATCAGACGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAGTTTGCAGTGTG 391  
 Qy 122 MetTTPValPheThrTyrValGlyAlaLeuPheGlnGlyLeuThrLeuLeuIleLeuAla 141  
 Db 392 ATGTGGGTATTTACCTATGTTGGTGCCTTGTCAATGGTCTGACACTACTAATTTTGGCT 451  
 Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 452 CTGATTTCACCTTCCTGAGTTCCTGTTATTATGAACGCATCAGGCCCAATAGATCAT 511  
 Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 512 TATCTGGACTTGCAATAAGATGTTAAAGATGCTATGGCTAAATCAAAGCAAAAATC 571  
 Qy 182 ProGlyLeuLys 185  
 Db 572 CCTGGATTGAAG 583

RESULT 50

BI838242

LOCUS BI838242

DEFINITION 603083162F1 NIH\_MGC\_120 Homo sapiens cDNA clone IMAGE:5222534 5',

BI838242

ACCESSION BI838242

VERSION BI838242.1 GI:15949792

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 742)

NIH-MGC http://mgi.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

Email: cgsbbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

plate: L1AM11559 row: k column: 15

High quality sequence stop: 734.

Location/Qualifiers

1..742

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5222534"

FEATURES

source



```

/lab host="DH10B"
/clone lib="NIH MGC 120"
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH MGC Library."

```

## ORIGIN

Alignment Scores: 3.78e-98 Length: 742

Pred. No.: 880.00 Matches: 181  
 Score: 97.35% Conservativeness: 3  
 Percent Similarity: 95.77% Mismatches: 4  
 Best Local Similarity: 95.14% Indels: 1  
 Query Match: 4 Gaps: 0  
 DB:

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BF838242 (1-742)

```

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleValysThrGlyValValPhe-GlyAlaSe 21
Db 135 GTTGTGACCTCTCTGACCATCAGTTTAGATATACAGGGTGTGATCCAGCTAT 314
Qy 21 rLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAl 41
Db 195 CCTATTCCTGCTCTTTCATTCAGACAGTATTCAGCAATGTGAGCGTAACAGCTACATTGC 254
Qy 41 aLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAlaI 61
Db 255 CTGGCCCTGCTCTCTGACCATCAGTTTAGATATACAGGGTGTGATCCAGCTAT 314
Qy 61 eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 81
Db 315 CCAGAAATCAGATGAAGCCACCCATTTCAGGCGATATCTGGAATCTGAAGTTGCTATATC 374
Qy 81 rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLy 101
Db 375 TGAGGAGTTGTTTTCAGAAAGTACAGTAATCTGCTCTGCTCTGATGAACTGCACGATAA 434
Qy 101 sGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLe 121
Db 435 GGAATCAGGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTGAGTGT 494
Qy 121 uMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAl 141
Db 495 GATGGGTATTTACCTATGTTGGTCTTGTGTTTAAATGCTGACACTTACTGATTTTGGC 554
Qy 141 aLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHi 161
Db 555 TCTCATTTTCATCTCTCAGTGTCTCTGTTTATTTATGAACGGATCAGGCACAGATAGATCA 614
Qy 161 sTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysI 181
Db 615 TTATCTAGGACTTTCGAAATAGATGTTTAAAGATGCTATGCTAAATCCAGCAAAAT 674
Qy 181 eProGlyLeuLysArgLysAlaAsp 189
Db 675 CCCTGGATTGAAGCGCAAGTGAAT 699

```

## RESULT 51

```

CN219472 821 bp mRNA linear EST 08-APR-2004
LOCUS WLA006H01.ab1 Wtbrain Gallus gallus cdna 5', mRNA sequence.
DEFINITION CN219472
ACCESSION CN219472
VERSION CN219472.1 GI:46298814
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 821)
Savolainen,P., Fitzsimmons,C.J., Arvestad,L., Andersson,L. and
Lundeberg,J.
EST analysis of brain and testis cDNA libraries from White leghorn
and Red Jungle Fowl
Unpublished (2004)
Contact: Peter Savolainen
Department of Biotechnology
Royal Institute of Technology, KTH
SE-106 91 Stockholm, SWEDEN
Tel: +46 (0)8 5537 8481
Fax: +46 (0)8 5537 8335
Email: Peter.Savolainen@biotech.kth.se
Seq primer: M13 reverse primer.
FEATURES
    source
        1..821
            /organism="Gallus gallus"
            /mol_type="mRNA"
            /strain="White Leghorn"
            /db_xref="taxon:9031"
            /sex="female"
            /lab_host="ElectroMAX DH10B (Invitrogen)"
            /clone_lib="Wtbrain"
            /note="Organ: brain; Vector: pSPORT-1; Site 1: Hind III;
            Site 2: EcoRI; The cDNA libraries were created with the
            Superscript Plasmid System (Invitrogen)."
```

## ORIGIN

Alignment Scores: 3.21e-97 Length: 821

Pred. No.: 873.00 Matches: 173  
 Score: 97.31% Conservativeness: 8  
 Percent Similarity: 93.01% Mismatches: 5  
 Best Local Similarity: 93.01% Indels: 0  
 Query Match: 94.38% Gaps: 0  
 DB:

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CN219472 (1-821)

```

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleValysThrGlyValValPheGlyAlaSer 21
Db 177 GTTGTGACCTCTCTTACTGCGAGACATTAAGAAGACAGAGTGGTGTGGTGCCAGC 236
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 237 TTGTTCCTGCTGCTCTCATTAACAGTGTTCAGCATCGTGACGCGTACATCTACATGCC 296
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAlaIle 61
Db 297 TTGGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAGGAGTATCCAGGCAATC 356
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 357 CAAAAGTCCGATGAAGCCATCCATTTAGGCGCTTACTTGGAGTCTGTAGTGTGTGTCT 416
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 417 GAAGAGCTGATTCAGAAATACAGAGTGTGTGCTGCTACATCAACGGCACAGTCAAG 476
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 477 GAGCTGAGACGCCCTCTTCCCTCGTTGATGACTTGGTTGATTCTCTGAAGTTTGAGTGTG 536
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
Db 537 ATGTGGGTGTTTCACTTACCTGTTGGTCTGTTTAAATGCTCTGACATTTACTGTGCT 596
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 597 TTGATTTTCGCTGTTCAGTGTTCCTGTTATTTATGAGAGACATCAGGCCCGCCAGCAT 656
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

```

```

|||||
657 TATTGGGACTAGTACAGACAGCTCAAGATGCGATGGCAAGATCCAGCAAGATC 716
|||||
182 ProGlyLeuLeuArgLys 187
|||||
717 CCTGGGCTGAAGCGCAA 734

RESULT 52
BG699748          784 bp      mRNA      linear      EST 07-MAY-2001
LOCUS             602681431F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4814382 5',
DEFINITION        mRNA sequence.
ACCESSION         BG699748
VERSION           BG699748.1 GI:13968365
KEYWORDS           EST.
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 784)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM10709 row: m column: 07
High quality sequence stop: 747.
FEATURES
Location/Qualifiers
1..784
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4814382"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_95"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtccag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.5 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this
is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 4e-97 Length: 784
Score: 872.00 Matches: 182
Percent Similarity: 97.88% Conservative: 3
Best Local Similarity: 96.30% Mismatches: 2
Query Match: 94.27% Indels: 2
DB: 4 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x BG699748 (1-784)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 169 GTTGTGACCTCTGCTACTGGAGACATTAGAGACTGGAGTGGTGTGGTGGCCAGC 228
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 229 CTATTCTGCTGCTTTCTATTGACAGTATTTCAGCATTTGAGCGTAAACAGCCTACATTGCC 288

```

```

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 289 TTGGCCCTGCTCTCTGTGACCATCAGCTTTTAGGATATACAAAGGGTGTGATCCAAAGCTATC 348
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 349 CAGAAATCAGATGAGGCCACCCATTACGGCATATCTGGAAATCTGAAGTTGCTATATCT 408
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 409 GAGGAGTTGGTTTCAGAAAGTACAGTAATCTGCTCTTGGTCATGTGAACCTGCACGATAAAG 468
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 469 GAATCAGCGCCCTCTTCTTAGTTGATGATTAGTTGATTCTCTGAAGTTGTCAGTTG 528
Qy 122 MetTrpValPheThrTyrValGlyAla-LeuPheAsnGlyLeuThrLeuLeuAla 141
Db 529 ATGTGGGTATTTACCTAATGTTGGTCCCTTTGTTTAATGTCGTGACACTACTGATTTTGGC 588
Qy 141 aLeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHi 161
Db 589 TCTCATTTCACTCTTCTAGTGTTCCTGTTATTATTGAACGGCATCAGGCACAGATAGATCA 648
Qy 161 sTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 181
Db 649 TTATCTAGGACTTGCAATTAAGAAATGTTCAAGATGCTATGGCTAAATATCCAAAGCAAAAT 708
Qy 181 eProGly-LeuLysArgLysAla 188
Db 709 CCTGGATTGAAGCGCAAGCT 731

RESULT 53
CA322433          817 bp      mRNA      linear      EST 09-JUL-2003
LOCUS             UI-M-FX0-cck-n-21-0-UI.r1 NIH_BMAP_FX0 Mus musculus cDNA clone
DEFINITION        IMAGE:6820918 5', mRNA sequence.
ACCESSION         CA322433
VERSION           CA322433.1 GI:24540531
KEYWORDS           EST.
SOURCE            Mus musculus (house mouse)
ORGANISM          Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 817)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5.
Location/Qualifiers
1..817
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6820918"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpb"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FX0"
/note="Organ: Brain; Vector: pYX- Asc; Site 1: EcoR I;

```

Site 2: Not 1; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

## ORIGIN

Alignment Scores:  
 Pred. No.: 4.24e-97 Length: 817  
 Score: 872.00 Matches: 186  
 Percent Similarity: 97.40% Conservative: 1  
 Best Local Similarity: 96.88% Mismatches: 2  
 Query Match: 94.27% Indels: 3  
 DB: 6 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CA322433 (1-817)

```

Qy 1 SerValValAspLeuLeu-TyrTrp-ArgAspIleLysThrGlyValValPheGlyA 20
Db 41 TCAGTTGTGACCTCTCTGGTACTGGGAGACATTAAGACCTGGAGTGGTGGTG 100
Qy 20 laSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrI 40
Db 101 CCAGCTATTCTCTGCTGCTCTCTGACAGTGTTCAGCATTTGTTCAGTGAAGCCATCA 160
Qy 40 leAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIlyGlyValIleGlnA 60
Db 161 TTGGCTTTGGCCCTCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAAG 220
Qy 60 laIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaI 80
Db 221 CTATCCAGAAATCAGATGAAGCCACCATTACAGGCATATTTCGAATCTGAAGTTGCCA 280
Qy 80 leSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrI 100
Db 281 TATCAGAGGAATTGGTTCCAGAAATATAGTATTCTGCTCTTGGTCATGTGAACAGCACAA 340
Qy 100 leLysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlav 120
Db 341 TAAAGAAATTGAGCGCTCTCTCTTAGTTGATGATTTAGTTGATTCCTGGAAGTTTGACG 400
Qy 120 alLeuMetTrrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleL 140
Db 401 TGTGATGTGGGATTTACTTACGTGTGGTGGTCTTGTTCATGATGGTTGACACTACTGATTT 460
Qy 140 euAlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleA 160
Db 461 TAGCTCTGATCTCACTCTTCAGTATTCTCTGTATATATATGAACCGCATCAGCGCAGATAG 520
Qy 160 spHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaL 180
Db 521 ATCATATTATAGGACTTGCACAAACAGAGCGTTAAGGATGCCATGCCCAAAATCCAAAGCA 580
Qy 180 ysIlePro-GlyLeuLysArgGlyAlaAsp 189
Db 581 AAATCCCTGGGATTTGAAGCCGANAGCAGAA 610

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RESULT 54  
 BI872386  
 LOCUS BI872386 857 bp mRNA linear EST 11-OCT-2001  
 DEFINITION 603397035F1 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:5400584 5',  
 mRNA sequence.  
 ACCESSION BI872386  
 VERSION BI872386.1 GI:16046048

## KEYWORDS

SOURCE EST.  
 ORGANISM Mus musculus (house mouse)

REFERENCE  
 1 (bases 1 to 857)  
 NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-remail.nih.gov

Tissue Procurement: The Cepko Laboratory  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov

Plate: LLAM12021 row: f column: 09

High quality sequence stop: 754.

FEATURES  
 Location/Qualifiers

1..857  
 /organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="IMAGE:5400584"

/tissue\_type="retina"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_94"

/notes="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 3.3 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:

Pred. No.: 4.53e-97 Length: 857  
 Score: 872.00 Matches: 186  
 Percent Similarity: 97.89% Conservative: 0  
 Best Local Similarity: 97.89% Mismatches: 1  
 Query Match: 94.27% Indels: 3  
 DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BI872386 (1-857)

```

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 130 GTTGTTCACCTCTCTGACTACTGAGAGACATTAAGAAGACTGGAGTGGTGGTGGCCAGC 189
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 190 TTATTCCTGCTGCTGCTCTGACAGATGTTGACAGATTCAGTGTGAACGGCTCATTTGCC 249
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 250 TTGGCCCTGCTCTCTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGCATATC 309
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 310 CAGAAATCAGATGAAGCCACCCATTTCAGGCGCATTTTGAATCTGAAGTTGCCATATCA 369
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 370 GAGGAATTTGGTTTCAAAAATATAGTAAATCTGCTCTTGGTCATGTGAACAGCACAAATAA 429
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 430 GAATTGAGGGGCTCTCTCTTAGTTGATGATTTAGTTAGTTCCCTGAAGTTTGCAGTGTG 489
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 490 ATGTGGGTATTTACTTACGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 549

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QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 550 CTGATCTCACTCTTCAGTATTCTCTGTATATATGAACGGCATCAGCGCGAGATAGATCAT 609  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValIlyAspAlaMetAla-LysIleGlnAla-LysI 181  
 Db 610 TATCTAGGACTTGCAAAACAGAGCGTTAAGGATGCCATGGCCAAATAATCCAGCAAAAA 669  
 QY 181 leProGlyLeu-LysArgIlyeAla 188  
 Db 670 TCCCTGGATTGGAAGCGCAAGCA 693

RESULT 55  
 COS04431  
 LOCUS  
 DEFINITION GGEZCB1023A09.g chicken breast muscle - CB1 Gallus gallus cdna  
 clone GGEZCB1023A09, mRNA sequence.

ACCESSION COS04431  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM Gallus gallus (chicken)

Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 647)  
 AUTHORS Alves,H.J., Jorge,E.C., Marchesin,M.L., Monteiro-Vitorello,C.B.,  
 Patricio,M., Ledur,M.C. and Coutinho,L.L.  
 TITLE Discovery of new genes expressed in the chicken breast muscle  
 JOURNAL Unpublished (2004)

COMMENT Contact: Helena J. Alves  
 Laboratory of Animal Biotechnology, Dep. of Animal Production  
 ESALQ - University of Sao Paulo  
 Av. Padua Dias, 11, Piracicaba, SP, 13418-900, Brazil  
 Tel: 55 19 3429 4434  
 Fax: 55 19 3429 4285  
 Email: hjalves@esalq.usp.br and llcoutin@esalq.usp.br  
 PCR Primers  
 BACKWARD: T7.

FEATURES  
 source

Location/Qualifiers  
 1..647  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9031"  
 /clone="GGEZCB1023A09"  
 /tissue\_type="breast muscle"  
 /dev\_stage="1 and 21 days old"  
 /lab\_host="DH5 alpha"  
 /clone\_lib="chicken breast muscle - CB1"

/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; This  
 cDNA library was constructed with the SuperScript plasmid  
 System with Gateway Technology kit (Invitrogen), following  
 manufacture's protocols. Plasmid DNA was purified using a  
 modified alkaline lysis method. Sequencing reactions were  
 conducted using the DYNAMIC Cycle Sequencing Kit for  
 MegabACE (Amersham Biosciences) according to the  
 manufacturer's recommendations. Clones were sequenced by  
 the 5' end with T7 primer. Sequencing reactions were  
 analyzed on MegabACE1000 DNA Sequencer (Amersham  
 Biosciences). The quality and clustering of the ESTs were  
 analyzed using the softwares Phred/capi. Only EST  
 sequences with Phred quality greater than 20 and at least  
 150 bp were considered for clustering."

ORIGIN

Alignment Scores:  
 Pred. No.: 4,048-97 Length: 647  
 Score: 871.00 Matches: 172  
 Percent Similarity: 96.81% Conservative: 10  
 Best Local Similarity: 91.49% Mismatches: 6  
 Query Match: 94.16% Indels: 0  
 DB: 7 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x COS04431 (1-647)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 54 GTTGTGGACCTCCCTTACTGCGGAGACATTAAAGAAGACAGAGTGGTGTGGTCCAGC 113  
 QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 114 TTGTTCTCTGCTCTCTCATTAACAGTGTTCAGCATCGTGAGCGTGACAGCTTACATTGCC 173  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 174 TTGGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAAGGGAGTTATCCAGGCAATC 233  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 234 CAAAAGTCCGATGAAGGCCATCCATTTAGGGCTTACTTTGGAGTCTGTAGTGTAGCTGTCT 293  
 QY 82 GluGlnLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 294 GAAGAGCTGATTTCAGAAATACAGCAGTGTGTGCTTGGTTCACATCAACGGCACAGTCAAG 353  
 QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 354 GAGCTGAGACGCCCTCTCTCGTTGATGACTTGGTTGATTCTCTGAAAGTTTGCAGTGTG 413  
 QY 122 MetTrpValPheThrTyrValGlyValAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 Db 414 ATGTGGGTGTTCACTTACGTGGTGGCTTGTATTAATGGTCTGACATTACTGATCTGGCT 473  
 QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 474 TTGATTTTCGCTGTTTCAGTGTTCCTGTTATTTATGAGAGACATCAGGCCACATCGACCAT 533  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValIlyAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 534 TATTTGGGACTAGTGAACAGACGTCAAGATCGGATGCGCAAGATCCAAAGCAAAAGATC 593  
 QY 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 594 CTGGGCTGAAGCGCAAACTGAG 617

RESULT 56  
 BG699274

LOCUS  
 DEFINITION 602678946F1 NIH\_MGC\_95 Homo sapiens cDNA clone IMAGE:4811674 5',  
 mRNA sequence.

ACCESSION BG699274  
 VERSION BG699274.1 GI:13967408

KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 774)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
 Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1AM10702 row: 1 column: 11

High quality sequence stop: 774.

FEATURES

Location/Qualifiers  
 1..774

SOURCE

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4811674"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_95"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtccag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTNN-3', size-selected for average
insert size 2.5 kb and normalized to 10^5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this
is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 6.94e-97 Length: 774
Score: 870.00 Matches: 181
Percent Similarity: 97.37% Conservative: 4
Best Local Similarity: 95.26% Mismatches: 3
Query Match: 94.05% Indels: 2
DB: 4 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x BG699274 (1-774)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleValysThrGlyValValPheGlyAlaSer 21
Db 169 GTTGTGACCTCCTGTAATGAGACATTAAGAAGACTGAGTGGTGTGGTGGCCAGC 228

Qy 22 LeupheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 229 CTATTCTCGCTGCTTCAATGACAGTATTGACGATTGTGACGCTGAACAGCCCTACATTGCC 288

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 289 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 348

Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 349 CAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGGAATCTGATATCT 408

Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 409 GAGGAGNTGGTTGAGAAGTACAGTAATCTCTGCTCTGTGCTCATGTGAACCTGACGATAAG 468

Qy 102 GluLeuArgArgLeuPheLeu-LeuValAspLeuValAspSerLeuLysPheAlaValLe 121
Db 469 GAACCTCAGCCGCTCTTCTTAGCTTGATTTAGTTAGTTGATTTCTGGAAGTTGAGTGT 528

Qy 121 uMetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAl 141
Db 529 GATGTGGGTATTTACCTATGTTGGTGGCTCTGTTAATGCTGTGACACTACTGATTTTGGC 588

Qy 141 aLeuIleSerLeuPheSer-IleProValIleTyrGluArgHisGlnValGlnIleAspH 161
Db 589 TCTCATTTCACTCTTCAGTTGTTCTGTTATTTATGAACGGCATCAGGCACAGATAGATC 648

Qy 161 isTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysI 181
Db 649 ATTATCTAGGACTTGCAATAGAAATGTTAAGATGCTATGGCTTAATCCAGCAAAA 708

Qy 181 leProGlyLeuLysArgLysAlaAsp 189
Db 709 TCCCTGGATTGAAGCGCAAGCTGAA 734

RESULT 57
CK305449
LOCUS
DEFINITION SB02029A2B02.f1 normalized Keck-Tagu Library SB02 Taeniopygia
```

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guttata cDNA clone SB02029A2B02.f1 5, mRNA sequence.
ACCESSION CK305449
VERSION CK305449.1 GI:44815023
KEYWORDS EST.
SOURCE Taeniopygia guttata
ORGANISM Taeniopygia guttata
REFERENCE 1 (bases 1 to 736)
AUTHORS Clayton,D.F., Arnold,A.P., Ball,G.F., Brenowitz,E., George,J.M.,
Mello,C.V., Wade,J., Replogle,K., Lewin,H., Band,M., Hernandez,A.
and Liu,L.
TITLE The Songbird Neurogenomics Initiative: An Evolving Public Resource
for Study of Genes, Brain, and Behavior
JOURNAL Unpublished (2004)
COMMENT Contact: David F. Clayton
University of Illinois
B107 CLSL, 601 S. Goodwin, Urbana, IL 61801, USA
Tel: 217 244 3668
Fax: 217 244 1648
Email: dclayton@uiuc.edu
Base Calling/Quality Scores: PHRED from Washington University
Genome Center.
Vector Trimming: Cross match from Washington University Genome
Center PHRAP suite. Low quality bases (Phred score < 20) were
trimmed from both ends of the sequence by an in-house script.
This sequence is vector free and at least 200 bp in length. Funded
by PHS grant # RO1 NS045264, 'Songbird Neurogenomics Initiative.'
PCR Primers
FORWARD: TAATACGACTCCTACTAGGG(T7)
BACKWARD: TAATACGCTCAGTAAAG(T3)
Insert Length: 736 Std Error: 0.00
Plate: SB02029A2 row: B column: 02
Seq primer: TAATACGACTCCTACTAGGG (T7)
High quality sequence stop: 736.
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1..736
/organism="Taeniopygia guttata"
/mol_type="mRNA"
/db_xref="taxon:59729"
/clone="SB02029A2B02.f1"
/tissue_type="brain"
/dev_stage="late embryo, post-hatch days 1, 10, 20, 45,
and adult (pooled)"
/lab_host="DH10B"
/clone_lib="normalized Keck-Tagu Library SB02"
/note="Organ: brain; Vector: pBS II SK(+); Site 1:
EcoRI(5' side of insert); Site 2: NotI (3' side of
insert); The library was constructed and normalized as
described by Bonaldo, M.F., Lennon, G. and Soares, M.B.
(1996), Genome Research 6(9): 791-806. An identifying tag
was added at the 3'during cDNA synthesis:
insertAAAAAAAAAAAAAAAAAATGCCA."
ORIGIN
Alignment Scores:
Pred. No.: 2.02e-96 Length: 736
Score: 866.00 Matches: 171
Percent Similarity: 96.28% Conservative: 10
Best Local Similarity: 90.96% Mismatches: 7
Query Match: 93.62% Indels: 0
DB: 7 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x CK305449 (1-736)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleValysThrGlyValValPheGlyAlaSer 21
Db 125 GTTGTGACCTCCTTTCTGCGGAGACATTAAGAAGACCGGGTGGTGTGGACCGC 184

Qy 22 LeupheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 185 TTGTTCTCGTCTCTCATTAACAGTCTTCAGCATCGTGTGAGTGTGCACAGCCTACATTGCC 244
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```

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaLe 61
Db 245 CTGGCCCTGCTCTCTGTACCATCAGCTTTAGGATATACAGGGAGTTATCCAGGCAATC 304
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 305 CAGAAGTCTGATGAGGGCCACCCCTTACAGGGCTTACCTGGATCGGATGTCGCGTGTG 364
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 365 GAGGAGCTCATCCAGAGTACAGCAACGTCGCTGGGCCAGCTGAACGGCACCTCCGG 424
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 425 GAGCTGGCGGCGCTCTTCTCGTCGATGACCTGGTGGATTCCTCAAGTTCGAGTATTG 484
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
Db 485 ATGTGGTCTTTCACCTTACGTCGTGGTCTGCTTCAATGGTCTGACATTACTGATCTGGCT 544
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 545 TTGATTTCGCTCTTCTCAGTGTCTCTGTTATTATGAGACATCAGGCCCAATCGACCAT 604
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 605 TACCTGGGACTTGTGTAACAAGAACCTCAAGATGCCATGGCAAGATCCAAAGCAAGATC 664
QY 182 ProGlyLeuLysArgLysAlaAsp 189
Db 665 CCTGGGTGAAGCGCAAACTGAA 688

RESULT 58
CK303615
LOCUS SB02018A1G04.f1 765 bp mRNA linear EST 01-MAR-2004
DEFINITION guttata cDNA clone SB02018A1G04.f1 5, mRNA sequence.
ACCESSION CK303615
VERSION CK303615.1 GI:44813189
KEYWORDS EST.
SOURCE Taeniopygia guttata
ORGANISM Taeniopygia guttata
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Estrilidae;
Estrildinae; Taeniopygia.
REFERENCE 1 (bases 1 to 765)
AUTHORS Clayton,D.F., Arnold,A.P., Ball,G.F., Brenowitz,E., George,J.M.,
Mello,C.V., Wade,J., Replogle,K., Lewin,H., Band,M., Hernandez,A.
and Liu,L.
TITLE The Songbird Neurogenomics Initiative: An Evolving Public Resource
JOURNAL for Study of Genes, Brain, and Behavior
COMMENT Unpublished (2004)
Contact: David F. Clayton
University of Illinois
Bi07 CUSL, 601 S. Goodwin, Urbana, IL 61801, USA
Tel: 217 244 3668
Fax: 217 244 1648
Email: dclayton@uiuc.edu
Base Calling/Quality Scores: PHRED from Washington University
Genome Center.
Vector Trimming: Cross_match from Washington University Genome
Center PHRAP suite. Low quality bases (Phred score < 20) were
trimmed from both ends of the sequence by an in-house script.
This sequence is vector free and at least 200 bp in length. Funded
by PHS grant # RO1 NS045264, 'Songbird Neurogenomics Initiative.'
PCR Primers
FORWARD: TAATACGACTCACTATAGG(T7)
BACKWARD: ATTAACCTCTACTAAG(T3)
Insert Length: 765 Std Error: 0.00
Plate: SB02018A1 row: G column: 04
Seq primer: TAATACGACTCACTATAGG (T7)
High quality sequence stop: 765.

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## FEATURES

source

## Location/Qualifiers

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1..765
/organism="Taeniopygia guttata"
/mol_type="mRNA"
/db_xref="taxon:59729"
/clone="SB02018A1G04.f1"
/tissue_type="brain"
/dev_stages="late embryo, post-hatch days 1, 10, 20, 45,
and adult (pooled)"
/lab_host="DH10B"
/clone_lib="normalized Keck-Tagu Library SB02"
/note="Organ: brain; Vector: pBS II SK(+); Site 1:
EcoRI(5' side of insert); Site 2: NotI (3' side of
insert); The library was constructed and normalized as
described by Bonaldo, M.F., Lennon, G. and Soares, M.B.
(1996), Genome Research 6(9): 791-806. An identifying tag
was added at the 3' during cDNA synthesis:
insertAAAAAAAAAAAAAAAAATGCGA."

```

## ORIGIN

## Alignment Scores:

```

Pred. No.: 2.13e-96 Length: 765
Score: 866.00 Matches: 171
Percent Similarity: 96.28% Conservative: 10
Best Local Similarity: 90.96% Mismatches: 7
Query Match: 93.62% Indels: 0
DB: 7 Gaps: 0

```

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CK303615 (1-765)

```

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysIleLysThrGlyValValPheGlyAlaSer 21
Db 119 GTTGTTCACCTCTCTTCTGCGGAGACATTAAAGACCCGGGGTGTGTTGGAGCCAGC 178
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 179 TTGTTCTTCGCTGCTCTCAATTACAGTGTTCAGCATCGTGTGAGTGTTCACAGCTTACATGCC 238
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaLe 61
Db 239 CTGGCCCTGCTCTCTGTCCATCAGCTTTAGGATATACAGGGAGTTATCCAGGCAATC 298
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 299 CAGAAGTCTGATGAGGGCCACCCCTTACGGGCTTACCTGGACTCGGATGTGGCCGTGTGCG 358
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 359 GAGGAGCTCATCCAGAGTACAGCAACGTCGCTGGGCCAGCTGAACGGCACCTCCGG 418
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 419 GAGCTGGCGGCGCTCTTCTCGTCGATGACCTGGTGGATTCCTCAAGTTCGAGTATTG 478
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
Db 479 ATGTGGTCTTTCACCTTACGTTGGTGGCTGTGTTCAATGGTCTGACATTACTGATCTGGCT 538
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 539 TTGATTTCGCTCTTCTCAGTGTCTCTGTTATTATGAGACATCAGGCCCAATCGACCAT 598
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 599 TACCTGGGACTTGTGTAACAAGAACCTCAAGATGCCATGGCAAGATCCAAAGCAAGATC 658
QY 182 ProGlyLeuLysArgLysAlaAsp 189
Db 659 CCTGGGTGAAGCGCAAACTGAA 682

RESULT 59
CK306874
LOCUS CK306874 793 bp mRNA linear EST 01-MAR-2004

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DEFINITION SB02042A1A11.f1 normalized Keck-Tagu Library SB02 Taeniopygia
guttata cDNA clone SB02042A1A11.f1 5, mRNA sequence.
ACCESSION CK306874
VERSION CK306874.1 GI:44816448
KEYWORDS EST.
SOURCE Taeniopygia guttata
ORGANISM Taeniopygia guttata
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archoosauria; Aves; Neognathae; Passeriformes; Estrildidae;
Estrildinae; Taeniopygia.
REFERENCE 1 (bases 1 to 793)
AUTHORS Clayton,D.F., Arnold,A.P., Ball,G.F., Brenowitz,E., George,J.M.,
Mello,C.V., Wade,J., Replogle,K., Lewin,H., Band,M., Hernandez,A.
and Liu,L.
TITLE The Songbird Neurogenomics Initiative: An Evolving Public Resource
for Study of Genes, Brain, and Behavior
JOURNAL Unpublished (2004)
COMMENT Contact: David F. Clayton
University of Illinois
B107 CLSL, 601 S. Goodwin, Urbana, IL 61801, USA
Tel: 217 244 3668
Fax: 217 244 1648
Email: dclayton@uiuc.edu
Base Calling/Quality Scores: PHRED from Washington University
Genome Center.
Vector Trimming: Cross match from Washington University Genome
Center PHRAP suite. Low quality bases (Phred score < 20) were
trimmed from both ends of the sequence by an in-house script.
This sequence is vector free and at least 200 bp in length. Funded
by PHS grant # RO1 NS045264, 'Songbird Neurogenomics Initiative.'
PCR Primers
FORWARD: TAATACGACTCCTATAGGG(T7)
BACKWARD: ATTAACCTCCTCAATAAG(T3)
Insert Length: 793 Std Error: 0.00
Plate: SB02042A1 row: A column: 11
Seq primer: TAATACGACTCCTATAGGG (T7)
High quality sequence stop: 793.
FEATURES
source
1..793
/organism="Taeniopygia guttata"
/mol_type="mRNA"
/db_xref="taxon:59729"
/clone="SB02042A1A11.f1"
/tissue_type="brain"
/dev_stage="late embryo, post-hatch days 1, 10, 20, 45,
and adult (pooled)"
/lab_host="DH10B"
/clone_lib="normalized Keck-Tagu Library SB02"
/note="Organ: brain; Vector: pBS II SK(+); Site 1:
EcoRI(5' side of insert); Site 2: NotI (3' side of
insert); The library was constructed and normalized as
described by Bonaldo, M.F., Lennon, G. and Soares, M.B.
(1996), Genome Research 6(9): 791-806. An identifying tag
was added at the 3' during cDNA synthesis:
insertAAAAAAAAAAAAAAAAATGCCA."
ORIGIN
Alignment Scores:
Pred. No.: 2.25e-96 Length: 793
Score: 866.00 Matches: 171
Percent Similarity: 96.28% Conservative: 10
Best Local Similarity: 90.96% Mismatches: 7
Query Match: 93.62% Indels: 0
DB: 7 Gaps: 0
US-09-830-972-2_COPY_975_1163 (1-189) x CK306874 (1-793)
Qy 2 ValValAepLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 89 GTTGTGACCTCCCTTCTTCTGCGAGACATTAGAGACCGGGGTGTGTGGACGAGC 148
Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValAlaTyrIleAla 41

```

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Db 149 TTGTTCTCGTCTCTCATTAACAGAGTGTTCAGCATCGTAGTGTACAGCCCTACATTGCC 208
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 209 CTGGCCCTGCTCTCTGTCCACCATCAGCTTTAGGATATACAGGGAGTATCCAGCAATC 268
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 269 CAGAAGTCTGATGAGGCCACCCCTTCAGGGCTTACCTGGACTCGGATGTGGCGTGTGCG 328
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 329 GAGGAGCTCATCCAGAAAGTACAGCAACGTCGTGTCGGGCCACAGTCGTAACGGCAGCGTCCGG 388
Qy 102 GluLeuArgLeuPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 389 GAGCTGGCGGCGCTCTTCCTCGTCGATGACCTGGTGGATTCCCTCAAGTTCGAGTATGTG 448
Qy 122 MetTrpValPheThrTyrValGlyValAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 449 ATGTGGTGTTCCTACTTACGTGGTGGCTTGTTCATGTCTGACATTACTGATCTGGCT 508
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 509 TTGATTTTCGCTCTTCAGTGTTCCTGTTATTATGAGAGACATCAGGGCCCAATCGACCAT 568
Qy 162 TyrLeuGlyLeuAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 569 TACCTGGGACTTGTGAACAAGAGCTCAAGATGCCATGCCAAGATCCAAAGATCCAAAGCAAGATC 628
Qy 182 ProGlyLeuLysArgLysAlaLeu 189
Db 629 CCTGGGTGAAGCCCAAACTGAA 652
RESULT 60
CK304164 852 bp mRNA linear EST 01-MAR-2004
DEFINITION SB02022B2C10.f1 normalized Keck-Tagu Library SB02 Taeniopygia
guttata cDNA clone SB02022B2C10.f1 5, mRNA sequence.
ACCESSION CK304164
VERSION CK304164.1 GI:44813738
KEYWORDS EST.
SOURCE Taeniopygia guttata
ORGANISM Taeniopygia guttata
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archoosauria; Aves; Neognathae; Passeriformes; Estrildidae;
Estrildinae; Taeniopygia.
REFERENCE 1 (bases 1 to 852)
AUTHORS Clayton,D.F., Arnold,A.P., Ball,G.F., Brenowitz,E., George,J.M.,
Mello,C.V., Wade,J., Replogle,K., Lewin,H., Band,M., Hernandez,A.
and Liu,L.
TITLE The Songbird Neurogenomics Initiative: An Evolving Public Resource
for Study of Genes, Brain, and Behavior
JOURNAL Unpublished (2004)
COMMENT Contact: David F. Clayton
University of Illinois
B107 CLSL, 601 S. Goodwin, Urbana, IL 61801, USA
Tel: 217 244 3668
Fax: 217 244 1648
Email: dclayton@uiuc.edu
Base Calling/Quality Scores: PHRED from Washington University
Genome Center.
Vector Trimming: Cross match from Washington University Genome
Center PHRAP suite. Low quality bases (Phred score < 20) were
trimmed from both ends of the sequence by an in-house script.
This sequence is vector free and at least 200 bp in length. Funded
by PHS grant # RO1 NS045264, 'Songbird Neurogenomics Initiative.'
PCR Primers
FORWARD: TAATACGACTCCTATAGGG(T7)
BACKWARD: ATTAACCTCCTCAATAAG(T3)
Insert Length: 852 Std Error: 0.00
Plate: SB02022B2 row: C column: 10
Seq primer: TAATACGACTCCTATAGGG (T7)
High quality sequence stop: 852.
Seq primer: TAATACGACTCCTATAGGG (T7)

```

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High quality sequence stop: 852.
Location/Qualifiers
1. .852
/organism="Taeniopygia guttata"
/mol_type="mRNA"
/db_xref="taxon:59729"
/clone="SB02022B2C10.f1"
/tissue_type="brain"
/dev_stage="late embryo, post-hatch days 1, 10, 20, 45, and adult (pooled)"
/lab_host="DH10B"
/clone_lib="normalized keck-tagu library SB02"
/note="Organ: brain; Vector: pBS II SK(+); Site_1: EcoRI(5' side of insert); Site_2: NotI (3' side of insert); The library was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. An identifying tag was added at the 3' during cDNA synthesis: insertAAAAAAAAAAAAAAAAAATGCGA."

ORIGIN
Alignment Scores:
Pred. No.: 2,49e-96 Length: 852
Score: 866.00 Matches: 171
Percent Similarity: 96.2% Conservative: 10
Best Local Similarity: 90.9% Mismatches: 7
Query Match: 93.6% Indels: 0
DB: 7 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x CK304164 (1-852)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 109 GTTGTGACCTCTTCTGTCGACCATGCTTACGATATACAGGGAGTTATCCAGGCAATC 168
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 169 TTGTTCTCTGCTCTCTATTAACAGTTTCAGATCGTGGAGTGTACAGCCTACATTGCC 228
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 229 CTGGCCCTGCTCTCTGTCCACCATGCTTACGATATACAGGGAGTTATCCAGGCAATC 288
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 289 CAGAAAGTCTGATGAGGGCCACCCCTTCAGGGCTTACCTGGACTCGGATGTGGCCGTGCG 348
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 349 GAGGAGCTCATCAGAGTACAGCAACGTCGTCGTCGGCCACGTCGACGGCAGCTCCGG 408
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 409 GAGTGGCGGCGCTCTTCTCGTCGATGACCTGGTGGATTCCCTCAAGTTGCGAGTATTG 468
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuAla 141
Db 469 ATGTGGTGTTCCTCACTACCTGCTGCTGTTCAATGGTCTGACATTACTGATCTCGCT 528
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 529 TTGATTCGCTCTTCAGTGTCTCTGTTATTATGAGACATCAGGCCCAATTCAGCAT 588
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 589 TACCTGGGACTTGTGAACAAGACGTCGAAGATGCCATGGCAAAGATCCAGCAAAGATC 648
QY 182 ProGlyLeuLysArgLysAlaAsp 189
Db 649 CTGGGTGAGCGCAAACTGAA 672

RESULT 61
CR548792
LOCUS
DEFINITION
DKFZp469H1132_r1 469 (synonym: pkidl) Pongo pygmaeus CDNA clone
DKFZp469H1132 5', mRNA sequence.
ACCESSION
CR548792
VERSION
CR548792.1 GI:50242416
KEYWORDS
EST.
SOURCE
Pongo pygmaeus (orangutan)
ORGANISM
Pongo pygmaeus
REFERENCE
1 (bases 1 to 683)
Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
Pongo, G., Han, M. and Wiemann, S.
Pongo pygmaeus mRNA (Bahr, A., Lauber, J., Mewes, H.W., et al.)
JOURNAL
Unpublished (2004)
COMMENT
Contact: MIPS
MIPS
Incoltaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen
(Hilden/Germany) within the cDNA sequencing consortium of the
German Genome Project. This clone (DKFZp469H1132) is available at
the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum,
Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email:
clone@rzpd.de Further information about the clone and the
sequencing project is available at
http://mips.gsf.de/projects/cdna/.
FEATURES
Location/Qualifiers
1. 683
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp469H1132"
/tissue_type="kidney"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="469 (synonym: pkidl)"
/note="vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIb"

ORIGIN
Alignment Scores:
Pred. No.: 2,41e-96 Length: 683
Score: 865.00 Matches: 176
Percent Similarity: 97.7% Conservative: 1
Best Local Similarity: 97.24% Mismatches: 4
Query Match: 93.51% Indels: 0
DB: 7 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x CR548792 (1-683)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 140 GTTGTGACCTCTCTCTGAGAGACATTAAGAGACTGGAGTGTGTTGGTCCAGC 199
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 200 CTATTCTTCGCTGCTTTCATTGACAGTATTCAGAGTGTGAGTGAACAGCCTACATTGCC 259
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 260 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 319
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 320 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGGAATGTGCTATATCT 379
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 380 GAGGAGTGTGGTTTCAGAAATACAGTAATTTCTGCTCTTGTGTCATGTGAATCTGCAATGAA 439
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121

```



Db 440 GAACCTAGCGGCTCTTCTTAGTGTGATTTAGTGTGATTTCTCTGAAGTTTGCAGTGTG 499

Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuLeuAla 141

Db 500 ATGTGGTATTACCTATTGTTGGTCCCTGTTTATGATGCTGACGCTACTGATTTGGCT 559

Qy 142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161

Db 560 CTCATTTTCACTCTTTCAGTGTCTCTCTTATTTATGAACGGCATCAGGCACAGATGATCAT 619

Qy 162 TyrLeuGlyLeuAlaAenLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

Db 620 TATCTAGGACTTGCAATGAAGATGTTAAAGATGCTATGGCTAAATTCGAAGCGAAATC 679

Qy 182 Pro 182

Db 680 CCT 682

RESULT 62

CO503803

LOCUS

DEFINITION GGEZCB1022G02.g chicken breast muscle - CB1 Gallus gallus cdna

ACCESSION CO503803

VERSION CO503803.1 GI:50273989

KEYWORDS EST.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

REFERENCE

AUTHORS Alves,H.J., Jorge,E.C., Marchesin,M.L., Monteiro-Vitorello,C.B.,

TITLE Discovery of new genes expressed in the chicken breast muscle

JOURNAL Unpublished (2004)

COMMENT Contact: Helena J. Alves

Laboratory of Animal Biotechnology, Dep. of Animal Production

ESALQ - University of Sao Paulo

Av. Pádua Dias, 11, Piracicaba, SP, 13418-900, Brazil

Tel: 55 19 3429 4434

Fax: 55 19 3429 4285

Email: hjalves@esalq.usp.br and llcoutin@esalq.usp.br

PCR Primers

BACKWARD: T7.

FEATURES

source

Location/Qualifiers

1..685

/organism="Gallus gallus"

/mol\_type="mRNA"

/db\_xref="taxon:9031"

/clone="GGEZCB1022G02"

/tissue\_type="breast muscle"

/dev\_stage="1 and 21 days old"

/lab\_host="DH5 alpha"

/clone\_lib="chicken breast muscle - CB1"

/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; This

cdna library was constructed with the SuperScript plasmid

System with Gateway Technology kit (Invitrogen), following

manufacturer's protocols. Plasmid DNA was purified using a

modified alkaline lysis method. Sequencing reactions were

conducted using the DYEnamic Cycle Sequencing Kit for

MegaBACE (Amersham biosciences) according to the

manufacturer's recommendations. Clones were sequenced by

the 5' end with T7 primer. Sequencing reactions were

analyzed on MegaBACE1000 DNA Sequencer (Amersham

bio sciences). The quality and clustering of the ESTs were

analyzed using the softwares Phred/Cap3. Only EST

sequences with Phred quality greater than 20 and at least

150 bp were considered for clustering."

ORIGIN

Alignment Scores:

Pred. No.: 2.42e-96 Length: 685

Score: 865.00 Matches: 171

Percent Similarity: 96.28% Conservative: 10

Best Local Similarity: 90.96% Mismatches: 7

Query Match: 93.51% Indels: 0

DB: 7 Gaps: 0

US-09-830-972-2\_copy\_975\_1163 (1-189) x CO503803 (1-685)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysValThrGlyValValPheGlyAlaSer 21

Db 72 GTTGTGACCTCTTCTTACTGCGAGACATTAAAGACAGAGGTGTGTTGGTCCAGC 131

Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

Db 132 TTGTTCTCTGCTCTCTCATTAACAGTGTTCAGCATCGTGAGCGTGACAGCTTACATTGCC 191

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

Db 192 TTGGCCCTGCTTCTGTGACCATCAGCTTTTAGGATATATCAAGGGAGTTTATCCAGGCAATC 251

Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81

Db 252 CAAAAGTCCGATGAAGCCATCCATTTAGGCTTACTTTGGAGTCTGATGTAGTGTGTCT 311

Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101

Db 312 GAAGAGCTGATTACAGAAATACAGCAGTGTGTGCTTGGTCACTCAACGGCACAGTCAAG 371

Qy 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121

Db 372 GAGCTGAGAGCGCTCTTCTCGTGTGATCACTTGTGTTGATTCTCTCAAGTTTGCAGTGTG 431

Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuLeuAla 141

Db 432 ATGTGGTGTTCACCTTACGTTGGTGTGCTTGTAAATGCTGTGACATTACTGATCTGCT 491

Qy 142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161

Db 492 TTGATTTTCGTTTTCAGTGTCTCTGTTTATTATGAGACATCAGGCCAGATCGACCAT 551

Qy 162 TyrLeuGlyLeuAlaAenLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

Db 552 TATTGGGACTAGTGAACAAGACGTCAGATCGATGGCCAAAGATCCCAAGATCCCAAGATC 611

Qy 182 ProGlyLeuLysArgLysAlaAsp 189

Db 612 CCTGGCTGAAGCGCAAACTGAG 635

RESULT 63

AF125103

LOCUS

DEFINITION Homo sapiens neuroendocrine specific protein c homolog mRNA,

complete cds.

ACCESSION AF125103

VERSION AF125103.1 GI:5107001

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 1798)

AUTHORS

Zhang,Q.H., Ye,M., Wu,X.Y., Ren,S.X., Zhao,M., Zhao,C.J., Fu,G.,

Shen,Y., Fan,H.Y., Lu,G., Zhong,M., Xu,X.R., Han,Z.G., Zhang,J.W.,

Tao,J., Huang,Q.H., Zhou,J., Hu,G.X., Gu,J., Chen,S.J. and Chen,Z.

Cloning and functional analysis of cDNAs with open reading frames

for 300 previously undefined genes expressed in CD34+ hematopoietic

stem/progenitor cells

Genome Res. 10 (10), 1546-1560 (2000)

JOURNAL

MEDLINE

PUBMED

REFERENCE

2 (bases 1 to 1798)

AUTHORS

Ye,M., Zhang,Q., Zhou,J., Shen,Y., Guan,Z., Wu,X., Fan,H., Mao,H.,

Dai,M., Huang,Q., Chen,S. and Chen,Z.

TITLE Human neuroendocrine specific protein c homolog mRNA, complete cds  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 1798)  
AUTHORS Ye,M., Zhang,Q., Zhou,J., Shen,Y., Guan,Z., Wu,X., Fan,H., Mao,H., Dai,M., Huang,Q., Chen,S. and Chen,Z.

TITLE Direct Submission  
JOURNAL Submitted (02-FEB-1999) Shanghai Institute of Hematology, Shanghai Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road II, Shanghai 200025, P. R. China

## FEATURES

Location/Qualifiers  
1..1798  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cell\_type="CD34+ hematopoietic stem/progenitor cells"  
215..814  
/codon\_start=1  
/product="neuroendocrine specific protein c homolog"  
/protein\_id="AAD39920.1"  
/db\_xref="GI:107002"  
/translation="MDGQKQKWKVLDLYWRDIIKTVGVFGASFLLLSLTVFSIV  
SVYIALALSLSTFSFRIYGVIOAIQKSDGHPFRAYLESEVAISELVQKYSNSA  
LHVNCTIKELRFLVDLDVLSKFAVLMVFTVVGALFNLGLLILALISLQCS  
YLHRHQADIDHYGLGNKXNDAMAKIQAKPLGRKAE"

## ORIGIN

Alignment Scores:  
Pred. No.: 1.27e-95 Length: 1798  
Score: 864.00 Matches: 182  
Percent Similarity: 97.88% Conservative: 3  
Best Local Similarity: 96.30% Mismatches: 3  
Query Match: 93.41% Indels: 2  
DB: 3 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x AFI25103 (1-1798)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 248 GTGTGTGACCTCTCTGCTGAGAGACATTAGAGACATGGAGTGGTGTGGTCCAGC 307  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 308 CTATTCTCTGCTTTCATTGACAGTATTACCACTGTGAGGCTAACAGCCTACATTGCC 367  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 368 TTGGCCCTGCTCTCTGTCACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 427  
QY 62 GlnLysSerAspGlnGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 428 CAGAAATCAGATGAGAGCCACCATTTCAGGGCATATCTGGAATCTGGAAGTTGCTATATCT 487  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 488 GAGGAGTTGGTTCAGAGTACAGTAATCTCTGCTTGGTCATGTGACACTGACAGTAAG 547  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 548 GAACTCAGCGCGCTCTCTTCTAGTATGATTTAGTTGATTTCTCTGAAAGTTGCACTGTG 607  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeuAla 141  
DB 608 ATGTGGGTATTTACCTATGTTGGTCCCTGTGTTTAATGGTCTACACTACTGATTTGGCT 667  
QY 142 LeuIleSerLeu-PheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 668 CTCATTTCTCCTCTCAGTGTTCCTGTTATTTA-GAAGCGCATCAGGCACAGATAGTCA 726  
QY 161 sTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 727 TTATCTAGGACTTGCATAAATAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAAT 786  
QY 181 eProGlyLeuLysArgLysAlaAsp 189

Db 787 CCTGTGATTGAAGCGCAAAGCTGAA 811

## RESULT 64

BU950008

LOCUS

DEFINITION

in3d05.yl HR85 islet Homo sapiens cDNA clone IMAGE:6126776 5'

similar to TR:Q9Y2Y7 Q9Y2Y7 POCEN-M. [2] TR:094962 ; mRNA

sequence.

ACCESSION

BU950008

VERSION

BU950008.1

KEYWORDS

EST

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 569)

AUTHORS

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,

Lenishka,I., Scarce,M., Brestelli,J., Gradwohl,G., Clifton,S.,

Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,

Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,

Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,

Williams,T., Jackson,Y. and Bowers,Y.

TITLE

Endocrine Pancreas Consortium

JOURNAL

Unpublished (2000)

COMMENT

Other\_ESTR: in63d05.xl

Contact: Douglas Melton, Klaus H. Kaestner, &amp; Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:

Washington University Genome Sequencing Center For information on

obtaining a clone please contact: Dr. Hiroshi Inoue

(hinoue@im.wustl.edu)

Seq primer: -40RP from Gibco

High quality sequence stop: 488.

Location/Qualifiers

1..569

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6126776"

/tissue type="Purified pancreatic islet"

/lab host="DH10B"

/clone lib="HR85 islet"

/note="Organ: Pancreas; Vector: pBluescript SK(-); Site\_1:

NotI; Site\_2: XhoI; cDNA made by oligo-dr priming.

Size-selected on agarose gel. Average insert size ~1kb. 5'

XhoI site was destroyed after directional cloning.

Amplified once. Contact information: Hiroshi Inoue, MD,

Metabolism Div. (Alan Permutt Lab), Washington University

School of Medicine, Box 8127, 660 South Euclid Ave., St.

Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:

314-362-1916, Fax: 314-747-2692."

## ORIGIN

Alignment Scores:  
Pred. No.: 3.29e-96 Length: 569  
Score: 863.00 Matches: 175  
Percent Similarity: 97.80% Conservative: 3  
Best Local Similarity: 96.15% Mismatches: 4  
Query Match: 93.30% Indels: 0  
DB: 5 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BU950008 (1-569)

QY 8 TrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSer 27

DB 12 TGGAGAGACATTAAGAGATTGGAGTGGTGTGGTGGCAGCCTATTCTCTGCTGCTTCA 71

```

Qy 28 LeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerVal 47
Db 72 TTGACAGATTTCAGCATTTGTAGGTTACACGCTACATGCTTGGCCCTCTCTGTG 131
Qy 48 ThrIleSerPheArgIleTyrIleGlyValIleGlnAlaIleGlnLysSerAspGluGly 67
Db 132 ACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATCCAGAAATCAGATGAAGCC 191
Qy 68 HisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluLeuValGlnLys 87
Db 192 CACCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGATGGTTTCAGAAG 251
Qy 88 TyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArgArgLeuPhe 107
Db 252 TACAGTAATCTGCTCTGTGTCATGTGACATGACGATTAAGGAACCTCAGCGCTCTTC 311
Qy 108 LeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTyrValPheThrTyr 127
Db 312 TTAGTTGATGATTTAGTTGATTTCTGGAAGTTTGCAGTGTGATGTTGCTATTTACCTAT 371
Qy 128 ValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeuIleSerLeuPheSer 147
Db 372 GTTGGTGGCTTTGTTTAATGGTGTGACACTACTGATTTTGGCTCTCATTTCACTCTT 431
Qy 148 IleProValIleTyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsn 167
Db 432 GTTCTGTTATTTATGAACGCATCAGCCACAGATAGATCATATTTAGGACTTGCAT 491
Qy 168 LysSerValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLysArgLys 187
Db 492 AAGAATGTTAAAGATGCTATGGCTAAAATCCAAAGCAAAATCCCTGGATTGAAGCGCAA 551
Qy 188 AlaAsp 189
Db 552 GCTGAA 557

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RESULT 65
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LOCUS 60324368F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5284672 5',
DEFINITION mRNA sequence.
ACCESSION BI544917
VERSION BI544917.1 GI:15432229
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/
JOURNAL 1 (bases 1 to 731)
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiruki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL1719 row: h column: 17
High quality sequence stop: 724.
Location/Qualifiers
1..731
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5284672"
/tissue type="hippocampus"
/lab_host="DH10B"

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## FEATURES

source

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/clone lib="NIH_MGC_95"
/notes=Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTNN-3', size-selected for average
insert size 2.5 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NHGM/NHGRI, National Institutes of Health). Note: this
is a NIH_MGC Library."

```

## ORIGIN

```

Alignment Scores:
Pred. No.: 6,25e-96 Length: 731
Score: 862.00 Matches: 175
Percent Similarity: 98.33% Conservative: 2
Best Local Similarity: 97.22% Mismatch: 3
Query Match: 93.19% Indels: 0
DB: 4 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x BI544917 (1-731)
Qy 2 ValValAspLeuLeuTyrTyrArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 191 GTTGTTCACCTCTCTGTACTCGAGAGACATTAAAGAAGACTGGAGTGGTGTGGTCCAGC 250
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 251 CTATTCTCTGCTCTTCATTTGACAGATATTGACGATTTGAGCGTAACAGCCTACATGCC 310
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 311 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 370
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 371 CAGAAATCAGATGAAGCCACCCATTGAGGCATATCTGGAATCTGAAGTGTCTATATCT 430
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 431 GAGGAGTTGGTTTCAGAAAGTACAGTAATCTCTGCTCTGCTCATGTGAACCTGACCATTAAG 490
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 491 GAATCAGGGCCCTCTCTTAGTTGATGATTAGTTGATTTCTCTGAAGTTTGCAGTGTG 550
Qy 122 MetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
Db 551 ATGTGGGTATTTACCTATGTTGGTGCCTGTTTAAATGGTCTGACACTACTGATTTGGCT 610
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 611 CTCATTTCACTCTCTCAGTGTCTCTGTTTATTATGAACGGCATCAGGCACAGATAGATCAT 670
Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 671 TAICTAGACTTTCGCAATAGATGTTAAAGATGCTATGTTAAATAATCCAGCAAGCAAAATC 730

RESULT 66
BU364240
LOCUS 603585074F1 CSEQCHN72 Gallus gallus cDNA clone CHES1539d19 5', mRNA
DEFINITION sequence.
ACCESSION BU364240
VERSION BU364240.1 GI:25872241
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 820)

```

**AUTHORS** Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
 Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
**TITLE** A Comprehensive Collection of Chicken cDNAs  
**JOURNAL** Curr. Biol. 12 (22), 1965-1969 (2002)  
**MEDLINE** 22335534  
**PUBMED** 12445392  
**COMMENT** Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.

**FEATURES**

source

1. 820  
 Location/Qualifiers  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="Compton Line 151"  
 /db\_xref="taxon:9031"  
 /clone="CHEST539d19"  
 /sex="Female"  
 /tissue\_type="cerebrum"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="CSPQCHN72"  
 /note="Organ: Brain; Vector: pBluescript II KS(+); Site\_1:  
 EcoRI; Site\_2: NotI; This normalized library was  
 constructed from 1 million independent clones. cDNA  
 synthesis was initiated using an oligo(dT) primer, using  
 methylated C in the first strand synthesis reaction.  
 Following this first strand reaction, double-stranded cDNA  
 was blunted, ligated to NotI adapters, digested with  
 EcoRI, size-selected, and cloned into the NotI and EcoRI  
 compatible sites of a custom modified MCS of the  
 pBluescript (KS+) vector. The library was normalized in 2  
 rounds using conditions adapted from Soares et al., PNAS  
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
 (1996): 791, except that a significantly longer  
 reannealing hybridization was used."

**ORIGIN**

Alignment Scores:  
 Pred. No.: 7,368-96 Length: 820  
 Score: 862.00 Matches: 173  
 Percent Similarity: 96.30% Conservative: 9  
 Best Local Similarity: 91.53% Mismatches: 6  
 Query Match: 93.13% Indels: 1  
 DB: 5 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BU364240 (1-820)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 156 GTTGTGACCTCTTACTGGCGAGACATTAAAGACAGAGTGTGTGTGTCAGC 215  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThAlaTyrIleAla 41  
 Db 216 TTGTTCTGCTGCTCTCATTAACAGTGTTCAGCATCGTGAGCGTGACAGCTTACATTGCC 275  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 276 TTGGCGCCCTCTTCTGTGACCATCAGCTTTAGATATACAGGGAGTTATCCAGGCAATC 335  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 336 CAAAGTCCGATGAAGGCCATCCATTAGGCTTACTTGGAGTCTGATGCTGTGCT 395  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 396 GAAGAGCTGATTGAGAAATACAGCAGTGTGTGCTTGTGTCATCATCAACGGCAGCTCAAG 455  
 QY 102 GluLeuArgAlaLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121

Db 456 GAGCTGACAGCCCTCTTCTCGTTGATGACTTGGTTGATTCTCTGAAGTTTCAGTGTG 515  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
 Db 516 ATGTGGGTGTTTCACTTACGTGTGTCCTTGTATATGCTGTGACATTACTGATCGCT 575  
 QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 576 TTGATTTCTGCTGTTTCAGTGTCTCTGTTATTTATGAGAGACATCAGGCCAGATCGACCAT 635  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 636 TATTTGGGAGCTAGTGAACAAGACCTCAAGATGGATGGCAAGATCCAAGCAAGATC 695  
 QY 182 Pro-GlyLeuLysArgLysAlaAsp 189  
 Db 696 CCTGGCCTGAAGCGCAAACTGAG 720  
 RESULT 67  
 BU848611  
 LOCUS  
 DEFINITION AGNCOURT 10276498 NIH MGC 144 Mus musculus cDNA clone  
 IMAGE:6596409 5', mRNA sequence.  
 ACCESSION BU848611  
 VERSION BU848611.1 GI:24033573  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 REFERENCE 1 (Bases 1 to 813)  
 NIH-MGC http://mgi.nci.nih.gov/.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Dr. Michael Brownstein  
 cDNA Library Preparation: Michael Brownstein Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LCM2825 row: p column: 09  
 High quality sequence stop: 160.  
 Location/Qualifiers  
 1. 813  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:6596409"  
 /lab\_host="DH10B (T1-phage-resistant)"  
 /clone\_lib="NIH MGC 144"  
 /note="Organ: Brain; Vector: pDNR-LIB; Site\_1: SfiI  
 (ggccatagggcc); Site\_2: SfiI (ggccgctggcc); cDNA made  
 by oligo-dT priming and directionally cloned. 5' and 3'  
 adaptors were used in cloning as follows:  
 5'-AAGCAGTGTGATCAACGACGATGCGCATACGCGCGG-3' and  
 5'-ATTCTAGAGCGGCGCGCATG-dt(30)NN-3'. Full-length  
 enriched library was constructed using the Clontech  
 Creator SMART kit and size-selected to contain the 0.2-0.5  
 kb size fraction (other fractions present in NIH\_MGC\_143).  
 Library created in the laboratory of M. Brownstein (NIH).  
 NIH). Note: this is a NIH\_MGC Library."

**ORIGIN**

Alignment Scores:  
 Pred. No.: 2,27e-95 Length: 813  
 Score: 858.00 Matches: 178  
 Percent Similarity: 97.28% Conservative: 1  
 Best Local Similarity: 96.74% Mismatches: 4  
 Query Match: 92.76% Indels: 1

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DB:
US-09-830-972-2_COPY_975_1163 (1-189) x B0848611 (1-813)
Qy 2 ValValAspLeuLeuTyrTrpArgAspLeuLeuValPheGlyAlaSer 21
Db 159 GTTGTGACCTCCCTGCTCTGAGAGACATTAAGAGACTGGAGTGGTGTGGTCCAGC 218
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerLeuValSerValThrAlaTyrLeuAla 41
Db 219 TTATTCCTGCTGCTCTGAGAGCTTTCAGCATTTGTCAGTGTACGGCTTACATGGC 278
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLeuGlyValIleGlnAlaIle 61
Db 279 TTGGCCCTGCTCTGCTGACTATCAGCTTTAGGATATATAGGGTGTGATCCAGCTATC 338
Qy 62 GlnIysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 339 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCCATATCA 398
Qy 82 GluGluLeuValGlnIleTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLeu 101
Db 399 GAGGATTTGGTTTCAGAAATATAGTAATTCCTGCTGCTGTCATGTGAACAGCACATATAA 458
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLeuPheAlaValLeu 121
Db 459 GAATTGAGGGCTCTCTCTAGTTGATGATTTAGTTGATTCCTGGAAGTTGCAGTGTG 518
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheGlnGlyLeuThrLeuLeuIleLeuAla 141
Db 519 ATGTGGGTATTTACTTACGTGGTGGCTTGTTCATATGTTGACACTACTGGATTTAGCT 578
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 579 CTGATCTCACCTTCAGTATTCCTGTGTATATATGAACGGCATGCGGCGCATAGATCAT 638
Qy 162 TyrLeuGlyLeuAlaAsnIysSerValIysAspAlaMet-AlaIleGlnAlaIleIle 181
Db 639 TATCTAGGACTTGCAAAACAGAGCGTAAAGATGCCATGCCATGNNCAAAATCCAAAGCAAAAT 698
Qy 181 eProGlyLeu 184
Db 699 CCCTGGATTG 708

RESULT 68
BG427864 713 bp mRNA linear EST 14-MAR-2001
LOCUS 602501551F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4614924 5',
DEFINITION mRNA sequence.
ACCESSION BG427864
VERSION BG427864.1 GI:13334370
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 713)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCN1367 row: f column: 13
High quality sequence stop: 712.
Location/Qualifiers
1. 713
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4614924"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH_MGC_75"
/notes="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccattatggcc); Site_2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGGCCATATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGGCGCGCATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 4,44e-95 Length: 713
Score: 855.00 Matches: 178
Percent Similarity: 96.28% Conservative: 3
Best Local Similarity: 94.68% Mismatches: 7
Query Match: 92.43% Indels: 1
DB: 4 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x BG427864 (1-713)
Qy 2 ValValAspLeuLeuTyrTrpArgAspLeuLeuValPheGlyAlaSer 21
Db 146 GTTGTGACCTCCCTGCTCTGAGAGACATTAAGAGACTGGAGTGGTGTGGTCCAGC 205
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerLeuValSerValThrAlaTyrLeuAla 41
Db 206 CTATTCCTGCTGCTCTTCATTGACAGTATTCAGCATTTGACGGTGAACAGCCCTACATGCC 265
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLeuGlyValIleGlnAlaIle 61
Db 266 TTGGCCCTGCTCTGCTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 325
Qy 62 GlnIysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 326 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 385
Qy 82 GluGluLeuValGlnIleTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLeu 101
Db 386 GAGAGTGTGGTTTCAGAGTACAGTAATCTGCTCTTGGTCAATGTAACCTGCACGATAAAG 445
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLeuPheAlaValLeu 121
Db 446 GAACTCAGGCGCTCTTCTTAGTTGATGATTTAGTTGATTCCTGGAAGTTGCAGTGTG 505
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
Db 506 ATGTGGGTATTTACTATGTTGGTGC-CTGTTTAAATGGTCTGACACTACTGATTTGGCT 564
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 565 CTCATTTTCATCTTCAGTGTTCCTGTCATTTATGAACGGCATCAGGCACATAGATCAT 624
Qy 162 TyrLeuGlyLeuAlaAsnIysSerValIysAspAlaMetAlaIleGlnAlaIleIle 181
Db 625 TATCTAGGACTTGCAAAATAGAAATGTTACAGATCTTAATGTTAAATCCAAAGCAAAATC 684
Qy 182 ProGlyLeuIysArgLeuAlaAsp 189
Db 685 CCTGGATTGAAGCGCAAGGTGAAT 708

RESULT 69
CD511521 758 bp mRNA linear EST 06-JUN-2003
LOCUS CD511521
DEFINITION AGENCOURT 14353136 NIH_MGC_187 Homo sapiens cDNA clone
IMAGE:30405928 5', mRNA sequence.
```

```

ACCESSION   CD511521
VERSION     CD511521.1  GI:31443239
SOURCE      EST.
ORGANISM    Homo sapiens (human)
REFERENCE   1 (bases 1 to 758)
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-re@mail.nih.gov
            Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDCM193 row: n column: 17
            High quality sequence stop: 614.
            Location/Qualifiers
                1..758
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:30405928"
                /lab_host="DH10B (T1 phage-resistant)"
                /clone_lib="NIH_MGC_187"
                /note="Organ: Blood vessels - aorta, basilar and artery;
                Vector: pDNR-LIB; Site 1: Sfil (ggccattatggcc); Site 2:
                Sfil (ggccgctcgcc); 5' and 3' adaptors were used in
                cloning as follows: 5' adaptor sequence:
                5'-CACGCGCATATGGCC-3' and 3' adaptor sequence:
                5'-ATTCTAGAGCGGCGGCGGCACATG-DT(30)BN-3' (where B = A,
                C, or G and N = A, C, G, or T). Average insert size 1.4 kb
                (range 0.5-4.0 kb). 14/15 colonies contained inserts by
                PCR. This library was enriched for full-length clones and
                was constructed by Clontech Laboratories (Palo Alto, CA).
                Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 5,58e-95 Length: 758
Score: 854.50 Matches: 178
Percent Similarity: 97.31% Conservative: 3
Best Local Similarity: 95.70% Mismatches: 3
Query Match: 92.38% Indels: 2
DB: 6 Gaps: 1

US-09-830-972-2_COPY_975_1163 (1-189) x CD511521 (1-758)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 148 GTTTGTGACCTCCTCTACTGAGAGACATTAAAGAGACTGGAGTGGTGTGGTCCACG 207
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 208 CTTATTCCTGCTGCTTTCATGTGACGATTTACGATTTGAGCGTACACGCTTACATTGCC 267
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 268 TTGGCCCTGCTCTGTGACCATCAGCTTTAGATATACAGGGTGTGATCCAGCTATC 327
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 328 CAGAAATCAGATGAAGGCCACCATTCAGGGCATATCTGGAATCTGGAAGTTGCTATCT 387
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101

388 GAGGAGTTGGTTCAAGATACAGTAATTCCTGCTCTGTGTCATGTAAGCTGCAGATAAG 447
102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
448 GAACCTCAGCGCCCTCTCTTAGTTAGTATGATTAGTTGATTCCTCAAGTTTCAGTGTG 507
122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
508 ATGTGGGTATTTACCTATGTTGGTCCCTGTTTATATGCTGTCACACTACTGATTTGGCT 567
142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
568 CTCATTTCACCTTCCTGAGTGTCTCTGTTATTTATGAACGCGCATCAGGCACAGATGATCAT 627
162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMet-AlaLysIleGlnAlaLysIle 181
628 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAA 687
181 ePro---GlyLeuLys 185
688 TCCCTCGGATGAAA 703

RESULT 70
LOCUS      BI394814
DEFINITION BI394814 646 bp mRNA linear EST 06-AUG-2001
            PgpIn.pk009.15 Normalized Chicken Pituitary/Hypothalamus/Pineal
            Library Gallus gallus cDNA clone pgpin.pk009.15 5' similar to
            gi|5902016 ref|NP_008939.1| reticulon 4; neuroendocrine-specific
            protein C like (foccon) [Homo sapiens] gi|13637055 ref|XP_002439.3|
            neuroendocrine-specific protein C like (foccon) [Homo sapiens]
            GI|AAD27783.1|AF077050_1 (AF077050) neuroendocri, mRNA sequence.
            BI394814
            EST.
            KEYWORDS
            SOURCE      Gallus gallus (chicken)
            ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
            REFERENCE   1 (bases 1 to 646)
            AUTHORS     Porter,T.E. and Cogburn,L.A.
            TITLE       ESTs from Normalized Chicken pituitary/Hypothalamus/Pineal cDNA
            JOURNAL     library USDA/IFAPES Animal Genome Project
            COMMENT     Unpublished (2001)
            Contact: Larry A. Cogburn
            University of Delaware
            Townsend Hall, Newark, DE 19717, USA
            Tel: 302-831-1335
            Fax: 302-831-2822
            Email: cogburn@udel.edu, www.chickest.udel.edu.
            Location/Qualifiers
                1..646
                /organism="Gallus gallus"
                /mol_type="mRNA"
                /strain="Commercial broiler chicken"
                /db_xref="taxon:9031"
                /clone="pgpin.pk009.15"
                /sex="Male and Female"
                /tissue type="Pituitary Gland/Hypothalamus/Pineal Gland"
                /dev stage="Embryonic (dl2,dl4,dl9); post-hatch
                (w1,w3,w5,w7,w9)"
                /lab host="E. Coli EMDH10B"
                /clone_lib="Normalized Chicken
                Pituitary/Hypothalamus/Pineal Library"
                /note="Vector: pCMVSPORT6; Library made from equivalent
                pools of total RNA isolated from each tissue at different
                ages. Single pass sequencing from 5'-end"

ORIGIN
Alignment Scores:
Pred. No.: 6,82e-95 Length: 646
Score: 853.00 Matches: 170

```

Percent Similarity: 95.21% Conservatives: 9  
 Best Local Similarity: 90.43% Mismatches: 9  
 Query Match: 92.22% Indels: 0  
 DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x B1394814 (1-646)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 51 GTTGTGACCTCTTACTGCGGACATTAAGAAGACAGGAGTGGTGTGGTCCAGC 110  
 Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 111 TTGTTCTCGTCTCTCATTAACAGTGTTCAGCATCGTGGAGTGTACAGCTTACATGCC 170  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 171 TTGGCCCTGCTTCTGTGACCATCAGCTTTTAGGATATACAAAGGAGTGTATCCAGCAATC 230  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 231 CAAAAGTCGATGAAGCCATCCATTTAGGCTTACTTGGAGTCTGTAGTGTGTCT 290  
 Qy 82 GluLeuLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 291 GAAGAGCTGATTAGAAATACAGCAGTGTGTGCTTGTGTACATCAACGGCAGTCAAG 350  
 Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 351 GAGCTGAGACCCCTCTTCTCGTGTGAGTGTGGTGAATCTCTGAAAGTTTGCAGTGTG 410  
 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
 Db 411 ATGTGGGTGTTCACTAGCTGTGGCTGTTGTTTAAATGCTGACATTAATGATGCT 470  
 Qy 142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 471 TTGATTTGCTGTTCAGTGTCTCTGTTATTATGAGAGACATCAGGCCAGATCCAGCAN 530  
 Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 531 TATTGGGACTTNTGAACAAGACGTCAAAGATCGGATGCGAAGATCCAAAGATCAAGATC 590  
 Qy 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 591 CCNNNTGAAGCCNNNACTGAG 614

## RESULT 71

BUI39629  
 LOCUS 603134795F1 CSEQCHL24 Gallus gallus CDNA clone ChEST117m23 5', mRNA  
 DEFINITION sequence.

ACCESSION BUI39629

VERSION BUI39629.1 GI:25354039

KEYWORDS EST.

SOURCE Gallus gallus (chicken)

## ORGANISM

Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

1 (bases 1 to 1028)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,

Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken CDNAS

Curr. Biol. 12 (22), 1965-1969 (2002)

22335534

12445392

Contact: Simon Hubbard

Department of Biomolecular Sciences

University of Manchester Institute of Science and Technology

(UMIST)

PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930

Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.  
 FEATURES Location/Qualifiers  
 source 1..1028

/organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="White Leghorn, HiseX"  
 /db\_xref="taxon:9031"  
 /clone="ChEST117m23"  
 /dev\_stage="16 day embryo"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQCHL24"  
 /note="Organ: brain; Vector: pBluescript II KS(+); Site 1:  
 EcoRI; Site 2: NotI; Modification of pBluescript II KS(+)  
 [Srratagen] vector to accommodate cDNA produced with the  
 T-trimmed protocol (Construction of uni-directionally  
 cloned cDNA libraries from messenger RNA for improved 3'  
 end DNA sequencing by Glenn Fu, et al. U.S. Patent #  
 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.  
 Ligate in double stranded adaptor containing BspI and  
 BamHI sites [5'ggccgctgcagcccgatcgaaaaaag]  
 [5'aattcttttttcggatccgggctgcagc]"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.32e-94 Length: 1028  
 Score: 853.00 Matches: 174  
 Percent Similarity: 95.81% Conservative: 9  
 Best Local Similarity: 91.10% Mismatches: 6  
 Query Match: 92.22% Indels: 2  
 DB: 5 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BUI39629 (1-1028)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 Db 186 TCAGTTCTTCCACCTCTTACTGCGGAGACATTAAGAAGACAGGAGTGGTGTGGTGCC 245  
 Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 246 AGCTTGTCTCTGCTGCTCTCATTAACAGTGTTCAGCATCGTGAGCGTGACAGCTTACATT 305  
 Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 306 GCCTTGGCCCTGCTTCTGTGACCATCAGCTTAGGATATACAAAGGAGTGTATCCAGCA 365  
 Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 366 ATCCAAAGTCCGATGAAGGCCATCCATTTAGGCTTACTTGGAGTCTGTAGTGTG 425  
 Qy 81 SerGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 Db 426 TCTGAAGAGCTGATTCAGAAATACAGCAGTGTGTGCTTGTGTACATCAACGGCAGTC 485  
 Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 486 AAGAGCTGAGAGCCCTCTTCTCGTGTGAGTCTTGGTGTCTCTGAAGTGTGAGTG 545  
 Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 Db 546 TTGATGTGGGTGTTCACCTACGTTGGTGGCTTGTATTAATGCTGTGACATTAATGACTG 605  
 Qy 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 Db 606 GCTTTGATTTTCGCTGTTCAGTGTCTCTGTTATTATGAGAGACATCAGGCCAGATCGAC 665  
 Qy 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAla-LysIleGlnAlaL 180  
 Db 666 CATATTGAGACTAGTGAACAAGACGTCAAAGATCGGATCGCAAAAGATCCAGCAAA 725  
 Qy 180 silePro-GlyLeuLysArgLysAlaAsp 189  
 Db 726 GATCCCTGGGCTTGAAGCGCAAAACTGAG 754

```

RESULT 72
BG109465      819 bp  mRNA  linear  EST 30-JAN-2001
LOCUS        602280543F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4368011 5',
DEFINITION   mRNA sequence.
ACCESSION   BG109465
VERSION     BG109465.1 GI:12602971
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Mammalia; Eukarya; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 819)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10021 row: f column: 12
High quality sequence stop: 647.
Location/Qualifiers
1. 819
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4368011"
/tissue_type="osteosarcoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 86"
/notes="Organ: bone; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.533 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 1.1e-94 Length: 819
Score: 852.50 Matches: 180
Percent Similarity: 96.8% Conservative: 3
Best Local Similarity: 95.24% Mismatches: 5
Query Match: 92.16% Indels: 2
DB: 4 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x BG109465 (1-819)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleValysThrGlyValValPheGlyAlaSer 21
Db 19 GTTGTGTGACCTCCTCTACTGGAGACATTAAAGACTGGAGTGGTGTGGTCCAGC 78

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 79 CTATTCTCTGCTTTCATTGACAGTATTGAGCATTTGAGCGTAAACAGCTACATTGCC 138

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 139 TTGGCCCTGCTCTGTGACCATCATCAGTTTAGGATATACAAGGGGTGTGATCCAGCTATC 198

QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 199 CAGAAATCAGATGAAGGACCCCATTCAGGCATATCTGGAATCTGAAGTGTCTATATCT 258

QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 259 GAGGAGTTGGTTTCAGAAGTACAGTAATCTCTGCTCTTGTGTCATGTGAACTGCACGATAAG 318

```

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QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 319 GAATTCAGCGCCCTCTCTCTAGTTGATGATTTAGTTGATTTCTCTGAAGTTGCAGG--TTG 376

QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
Db 377 ATGTGGGTATTTACCTATGTTGGTCCCTTGTATATGTCGACACTGACTGATTTGGCT 436

QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 437 CTCATTTCACTCTTCAGTGTTCCTGTTATTATGAACGGCATCAGGCACAGATAGATCAT 496

QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAla-LysIle 181
Db 497 TATCTAGGACTTGCAATTAAGAATGTTAAAGATGCTATGGCTAAATCCAAAGCCAAAAT 556

QY 181 eProGlyLeuLysArgLysAlaAsp 189
Db 557 CCTGGATTGAAGCGCAAGCTGAA 581

RESULT 73
CO581452      960 bp  mRNA  linear  EST 20-JUL-2004
LOCUS        ILLUMIGEN MCO_47216 Katze_MMLV Macaca mulatta cDNA clone
DEFINITION   IBIUW:17799 5' similar to Bases 83 to 959 highly similar to human
RTN4 (Hs.436349), mRNA sequence.
ACCESSION   CO581452
VERSION     CO581452.1 GI:50412806
KEYWORDS    EST.
SOURCE      Macaca mulatta (rhesus monkey)
ORGANISM    Macaca mulatta
Eukaryota; Eukarya; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
1 (bases 1 to 960)
Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)
Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.06.24. 532 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
http://www.macaque.org
PCR Primers
FORWARD: CCTCACTAAAGGGAACAA
BACKWARD: CACTATAGGCGGAATTGGTA
Insert Length: 960 Std Error: 0.00
Plate: CL000396 row: H column: 08
Seq primer: CCTCACTAAAGGGAACAA
POLYA-Yes.
Location/Qualifiers
1. 960
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/mol_type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"
/clone="IBIUW:17799"
/sex="female"
/dev_stage="adult"
/lab_host="Electromax DH10B"
/clone_lib="Katze_MMLV"
/notes="Organ: liver; Vector: pDONR 222; Site 1: BsrG I;
Site 2: BsrG I; created from CloneMiner cDNA Library
Construction kit (catalog #18249-029)"

ORIGIN
Alignment Scores:

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Pred. No.: 1.59e-94 Length: 960  
 Score: 852.00 Matches: 175  
 Percent Similarity: 96.28% Conservative: 6  
 Best Local Similarity: 93.09% Mismatches: 6  
 Query Match: 92.11% Indels: 1  
 DB: 7 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CO581452 (1-960)

Qy 3 ValAspLeuLeuTyrTrpArgAspIleValysThrGlyValValPheGlyAlaSerLeu 22  
 Db 84 GTTGACCTCTCTAGTGAGAGACTTGAAGAATAATGGAGTGGTGTGGCGCAGCCTA 143  
 Qy 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
 Db 144 TTCTGTGCTTCTCTTGACAGTATTGACGATTTGAGTGTAAAGCCTACATTGCCTTG 203  
 Qy 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrIleValysGlyValIleGlnAlaLeu 62  
 Db 204 GCCCTGTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAAGCTATCCAG 263  
 Qy 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
 Db 264 AAATCAGATGAAGGCCACCCATTGAGGCATATTCTGGAATCTGAAGTTGGCATATCTGAG 323  
 Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGlu 102  
 Db 324 GAGTTGGTTTCAGAGTACAGTAATCTGCTCTTGTCATGTGAAGTGCACGATTAAGGAA 383  
 Qy 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
 Db 384 CTCAGGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTGTAAGTTTGCAGTGTTCATG 443  
 Qy 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeu 142  
 Db 444 TGGGTATTATACCTATGTTGGTGGCTTGTGTTAATGGTCTGACGCTACTGATTTGGCTCTC 503  
 Qy 143 IleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTyr 162  
 Db 504 ATTTCACTCTTCAGTGTCTGTTATTTATGACGGCATGACGGCAGATAGATCATAT 563  
 Qy 163 LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePr 182  
 Db 564 CTAGGACTTGCAATAAGATGTTAAAGATGCTATGCTTAAATCCCGAGGAAATCC 623  
 Qy 182 oGlyLeuLysArgLysAlaAsp 189  
 Db 624 TGGATTGAAGCGCCAAGCTGAA 645

RESULT 74  
 BG400408  
 LOCUS BG400408 905 bp mRNA linear EST 12-MAR-2001  
 DEFINITION 602464428F1 NIH\_MGC\_75 Homo sapiens cDNA clone IMAGE:4592670 5',  
 mRNA sequence.

ACCESSION BG400408

VERSION BG400408.1 GI:13293856

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 905)

TITLE NIH-MGC http://mgi.nci.nih.gov/

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov  
 Plate: L1CM1331 row: g column: 07  
 High quality sequence stop: 708.

# FEATURES

## source

1. .905  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4592670"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /notes="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:  
 SfiI (ggccattggcc); Site 2: SfiI (ggccattggcc); 5' and  
 3' adaptors were used in cloning as follows: 5' adaptor  
 sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:  
 5'-ATTCTAGAGCCGCGCGGCATG-3' (where B = A, C, G, or T). Average insert size 1.65  
 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA). Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 2.59e-94 Length: 905  
 Score: 850.00 Matches: 177  
 Percent Similarity: 95.79% Conservative: 5  
 Best Local Similarity: 93.16% Mismatches: 6  
 Query Match: 91.89% Indels: 2  
 DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BG400408 (1-905)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleValysThrGlyValValPheGlyAlaSer 21  
 Db 153 GTTGTGACCTCTCTAGTACGAGACATTAAGAAGACTGGAGTGGTGTGGCGCAGC 212  
 Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 213 CTATTCTCTGCTCTTCATTTGACAGTATTCAGCATTTGTGAGCGTAAAGCCTACATGCC 272  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 273 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 332  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 333 CAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGAAGTTGCTATATCT 392  
 Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 393 GAGAGTTGGTTTCAAGATACAGTATTTCTGCTCTTGTCTATGTGAAGTGCACGATTAAG 452  
 Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 453 GAACTCAGGGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAAGTTTGCAGTGTG 512  
 Qy 122 Met-TrpValPheThrTyrValGlyAlaLeuPheAsn-GlyLeuThrLeuLeuLeuAla 141  
 Db 513 ATCGTGGGTATTTACCTATGTTGGTGGCTGTTTACTGGGTCTGACACTACTGATTTGGG 572  
 Qy 141 laLeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspH 161  
 Db 573 CTCTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAAACGGCATCAGGCACAGATAGTC 632  
 Qy 161 isTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysI 181  
 Db 633 ATTATCTAGGACTTGCAATAAGAAATGTTAAAGATGCTATGGGTAAATCCAGCAAAAA 692  
 Qy 181 leProGlyLeuLysArgLysAlaAsp 189  
 Db 693 TCCTGGATTGAAGCGCCAAGTTGAA 718

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RESULT 75
BG427986      743 bp  mRNA  linear  EST 14-MAR-2001
LOCUS        602500385F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4613876 5',
DEFINITION   mRNA sequence.
ACCESSION    BG427986
VERSION      BG427986.1 GI:13334492
KEYWORDS     EST.
ORGANISM     Homo sapiens (human)
COMMENT      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCMI384 row: j column: 21
            High quality sequence stop: 716.
            Location/Qualifiers
                1..743
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:4613876"
                    /lab_host="DH10B (T1 phage-resistant)"
                    /clone_lib="NIH_MGC_75"
                    /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:
                    SfiI (ggccgctggcc); Site 2: SfiI (ggccattatggcc); 5' and
                    3' adaptors were used in cloning as follows: 5' adaptor
                    sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
                    5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A,
                    C, or G and N = A, C, G, or T). Average insert size 1.65
                    kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
                    by PCR. This library was enriched for full-length clones
                    and was constructed by Clontech Laboratories (Palo Alto,
                    CA). Note: this is a NIH_MGC Library."
            ORIGIN
            source
            Alignment Scores:
            Pred. No.:      2 6e-94      Length:      743
            Score:          849.00      Matches:      178
            Percent Similarity: 95.26%      Conservative: 3
            Best Local Similarity: 93.68%      Mismatches: 7
            Query Match:      91.78%      Indels:      2
            DB:              4          Gaps:      0
            US-09-830-972-2_COPY_975_1163 (1-189) x BG427986 (1-743)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Dbb 163 GTTGTGTGACCTCCTGCTACTGGAGACATTTAAGAGACGTGGAGTGGTGTGGTCCAGC 222
Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThAlaTyrIleAla 41
Dbb 223 CTATTTCCTGCTCTTTCATTGACAGTATTACAGATTTGAGCGGTAAACGCCCTACATTC 282
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Dbb 283 TTGGCCCTGCTCTCTGTGACCATGAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 342
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Dbb 343 CAGAAATCAGATGAAGGGCCACCCCATTCAGGGCATATCTGGAATCTCTGAAGTTGCTATCT 402

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Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Dbb 403 GAGGAGTTGGTTCAGAGTACAGTAATCTCTCTTGTGTCATGTGAACCTGCACGATAAG 462
Qy 102 GluLeuArgAlaGlyLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Dbb 463 GAATCAGGCGCCCTCTCTTCTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 522
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
Dbb 523 ATGTGGGTATTTACCTATGTTGGTGCCTGTTTAAATGCTCTGACACTACTGATTTGGCT 582
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHi 161
Dbb 583 CTCATTTTCCACTCTTCTAGTTCCTGTTTATTTATGACGGCATCAGGCACAGATAGATCA 642
Qy 161 sTyrLeuGlyLeuAlaAsnLysSerVal-LysAspAlaMetAlaLysIleGlnAlaLysI 181
Dbb 643 TTAICTAGGACTTGCATAATAGATGTTTCACAGATGCTAATGGTAAATAATCCAGCAAA 702
Qy 181 leProGlyLeuLysArgLysAlaAsp 189
Dbb 703 TCCCTGGATTGAAGCGCAAGCTGAC 728
RESULT 76
BUI38907      759 bp  mRNA  linear  EST 25-NOV-2002
LOCUS        60313909F1 CSEQCHL24 Gallus gallus cDNA clone CHEST115a3 5', mRNA
DEFINITION   sequence.
ACCESSION    BUI38907
VERSION      BUI38907.1 GI:25353139
KEYWORDS     EST.
SOURCE       Gallus gallus (chicken)
ORGANISM     Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
            1 (bases 1 to 759)
REFERENCE    Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
            Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
            A Comprehensive Collection of Chicken CDNA
            Curr. Biol. 12 (22), 1965-1969 (2002)
JOURNAL
MEDLINE
PUBMED
PUBMED
12445392
COMMENT      Contact: Simon Hubbard
            Department of Biomolecular Sciences
            University of Manchester Institute of Science and Technology
            (UMIST)
            PO Box 88, Manchester, M60 1QD, UK
            Tel: 01612008930
            Fax: 01612360409
            Email: Simon.Hubbard@umist.ac.uk.
            Location/Qualifiers
                1..759
                    /organism="Gallus gallus"
                    /mol_type="mRNA"
                    /strain="White Leghorn, Hisex"
                    /db_xref="taxon:9031"
                    /clone="CHEST115a3"
                    /dev_stage="16 day embryo"
                    /lab_host="DH10B"
                    /clone_lib="CSEQCHL24"
                    /note="Organ: brain; Vector: pBluescript II KS(+); Site 1:
                    EcoRI; Site 2: NotI; Modification of pBluescript II KS(+)
                    [Stratagene] vector to accommodate cDNA produced with the
                    T-strapped protocol (Construction of uni-directionally
                    cloned cDNA libraries from messenger RNA for improved 3'
                    end DNA sequencing by Glenn Fu et al. U.S. Patent #
                    6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
                    Ligate in double stranded adaptor containing BspI and
                    BamHI sites [5'ggccgctgacggccgcatcgagaaaaag]
                    [5'aattcttttttcggatccggggtgcacgc]"
            ORIGIN

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## Alignment Scores:

Pred. No.: 4,74e-94 Length: 759  
 Score: 847.00 Matches: 172  
 Percent Similarity: 96.28% Conservatives: 9  
 Best Local Similarity: 91.49% Mismatches: 7  
 Query Match: 91.57% Indels: 1  
 DB: Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BU138907 (1-759)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 137 GTTGTTCACCTCTTACTGCGAGACATTAAGAAGACAGAGTGTTGTGTGCAGC 196  
 Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 197 TTGTTCCTGCTCTCATTAACAGTGTTCAGATCGTGGCGAGCAGCTTACATTCGC 256  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 257 TTGGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAGGGAGTTATCCAGGCATC 316  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 317 CAAAAGTCCGATGAAGGCCATCCATTTAGGGCTTACTTGGAGTCTGATGTAGCTGTCT 376  
 Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 377 GAAGAGCTGATTCAGAAATACAGCAGTGTGTGCTTGGTCACATCAACGCCAGTCAG 436  
 Qy 102 GluLeuArgLeuLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 437 GAGCTGAGAGCCCTCTCTCTGTTGATGACTTGGTTGATTTCTGAGTTTGCAGTTG 496  
 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 497 ATGTGGGTGTTCATACGTGTGGTCTGCTTTAAATGGTCTGACATTTACTGATCTGC 556  
 Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 557 TTGATTTCCGTGTTCAGTGTCTCTGTTGATTTATATGAGAGACATCAGGCCCGCCAG 616  
 Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 617 TATTTGGACTAGTGAACAGAGAGCTCAA-GATGCGATGCCAAGATCCAGCAGCAGATC 675  
 Qy 182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 676 CCTGGGCTGAAGCGCAAACTGAG 699

## RESULT 77

CK791443  
 LOCUS  
 DEFINITION AGENCOURT 18667576 NIH MGC 230 Mus musculus CDNA clone  
 IMAGE:30848940 5', mRNA sequence.

ACCESSION CK791443

VERSION CK791443.1 GI:42803439

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 826)

NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

CONTACT: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)

Tissue Procurement: Shioko Kimura/Atsushi Yamada, (NCI,CCR)

## CDNA Library Preparation: Express Genomics

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

Plate: NDAM1156 row: a column: 13

High quality sequence stop: 680.

## FEATURES

source

Location/Qualifiers

1..826  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:30848940"  
 /tissue\_type="Pooled thyroids from 5 mice"  
 /lab\_host="DH10B Tona"  
 /clone\_lib="NIH\_MGC\_230"  
 /notes="Organ: thyroid; Vector: pExpress-1; Site 1: NotI;  
 Site 2: NotI; RNA obtained from 5 normal wild-type mice  
 thyroid. CDNA was primed using oligo-dT primer:  
 5'-pGACTAGTTCTAGATCGAGCGCGCC(T)25-3' and cloned into  
 the EcoRV/NotI sites of pExpress-1. Size-selection 1.4 kb  
 resulted in an average insert size of 1.2 kb. Normalized  
 version of this library is NIH\_MGC\_189library constructed  
 by Express Genomics (Frederick, MD). Note: this is a  
 NIH\_MGC Library."

## ORIGIN

Alignment Scores: 6,17e-94 Length: 826  
 Pred. No.: 846.50 Matches: 179  
 Score: 98.36% Conservatives: 1  
 Percent Similarity: 97.81% Mismatches: 2  
 Best Local Similarity: 91.51% Indels: 2  
 Query Match: 7  
 DB: Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CK791443 (1-826)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 171 GTTGTTCACCTCTTACTGCGAGACATTAAGAAGACAGTGTGTGTGTGCAGC 230  
 Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 231 TTATTCCTGCTGCTCTGACAGTGTTCAGATTTGTAAGCGCTCAGTTGCC 290  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 291 TTGGCCCTGCTCTCTGATGACTATCAGCTTTAGGATATATAAAGGTTGTGATCCAAGCTATC 350  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 351 CAGAAATCAGATGAAGGCCACCCATTCAGGCATATTTGGAATCTGAAGTTGCCATATCA 410  
 Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 411 GAGGAATTTGGTTCCAGAAATATAGTAACTCTGCTCTTGGTCATCTGAACACACCAATAAAA 470  
 Qy 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 471 GAATTGAGCGCTCTCTTCTTAGTTGATGATTTAGTTAGTTCCCTGAAGTTTGCAGTTTG 530  
 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 531 ATGTGGGTATTTACTTACGTGTGGTGGCTTGTTCATAGTTTGACACTACTGATTTTAGCT 590  
 Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 591 CTGATCTCACTCTTCTAGTATTCCTGTTATATATATGAACGGCATCAGGCCGAGATAGATCAT 650  
 Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 651 TATCTAGGACTTGC-AACAAGAGCGTTAAGGATGCCATGGCCAAAATCCAG---CAAATC 705

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Qy 182 ProGlyLeu 184
Db 707 COTGGATTG 715

RESULT 78
LOCUS CD623552 659 bp mRNA linear EST 12-JAN-2004
DEFINITION 5608673H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD623552
VERSION CD623552.1 GI:40271817
EST. Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
JOURNAL extension cloning of partial genes
COMMENT Genomics 84 (1), 205-210 (2004)
CONTACT: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES
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            /clone_lib="FLP"
            /note="Vector: pDrive Cloning Vector"
ORIGIN
Alignment Scores:
Pred. No.: 5,16e-94 Length: 659
Score: 846.00 Matches: 172
Percent Similarity: 99.88% Conservative: 4
Best Local Similarity: 96.63% Mismatches: 2
Query Match: 91.46% Indels: 0
DB: 6 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x CD623552 (1-659)

Qy 12 LysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPhe 31
Db 654 AGGAAGACTGGAGTGGTGGTGGCCAGCCTATTCTCTGCTGCTTTTCATTGACAGTATTC 595

Qy 32 SerIleValSerValThrAlaTyrlleAlaLeuAlaLeuSerValThrIleSerPhe 51
Db 594 AGCATTGTGAGCGTAACAGCCTACATTGCTTGGCCCTGCTCTCTGTGACCATCAGCTTT 535

Qy 52 ArgIleTyrlsGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArg 71
Db 534 AGGATATACAGGGTGTGATCCAACTATCCAGAAATCAGATGAAGGCCACCCATTTCAGG 475

Qy 72 AlaTyrlLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrlSerAsnSer 91
Db 474 GCATATCTGGAATCTGAAGTTGCTATATCTAGAGGAGTTGGTTCAGAAAGTACAGTAATTC 415

Qy 92 AlaLeuGlyHisValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAspAsp 111
Db 414 GCTCTTGGTCATGTGAACATGACAGATAAGGAACCTCAGCGCCCTCTTCTTAGTTGATGAT 355

Qy 112 LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrlValGlyAlaLeu 131
Db 354 TTAGTTGATTCTCTGAAGTTTGACGTGTGATGCGGTATTACCTATGTTGGTCCCTTG 295

Qy 132 PheAsnGlyLeuThrLeuLeuIleAlaLeuIleSerLeuPheSerIleProValIle 151
Db 294 TTTAATGGTCTGACACTACTGATTTTGGCTCTCAATTCATCTCTCAGTGCTCTCTTATT 235

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Qy 152 TyrGluArgHisGlnValGlnIleAspHisTyrlLeuGlyLeuAlaAsnLysSerVallys 171
Db 234 TATGAACGGCATCAGGCACAGATAGATCATTTATCTAGGACTTGGCAATAAGAAATTTAAA 175

Qy 172 AspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLysArgLysAlaAsp 189
Db 174 GATGCTATGGCTAAATTCAGCAAAATACTGATTTGAAGCCCAAGCTGAA 121

RESULT 79
LOCUS CD623553 660 bp mRNA linear EST 12-JAN-2004
DEFINITION 5608673J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD623553
VERSION CD623553.1 GI:40271818
EST. Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
JOURNAL extension cloning of partial genes
COMMENT Genomics 84 (1), 205-210 (2004)
CONTACT: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES
    source
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            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone_lib="FLP"
            /note="Vector: pDrive Cloning Vector"
ORIGIN
Alignment Scores:
Pred. No.: 5,17e-94 Length: 660
Score: 846.00 Matches: 172
Percent Similarity: 98.88% Conservative: 4
Best Local Similarity: 96.63% Mismatches: 2
Query Match: 91.46% Indels: 0
DB: 6 Gaps: 0

US-09-830-972-2_COPY_975_1163 (1-189) x CD623553 (1-660)

Qy 12 LysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPhe 31
Db 6 AGGAAGACTGGAGTGGTGGTGGCCAGCCTATTCTCTGCTGCTTTTCATTGACAGTATTC 65

Qy 32 SerIleValSerValThrAlaTyrlleAlaLeuAlaLeuSerValThrIleSerPhe 51
Db 66 AGCATTGTGAGCGTAACAGCCTACATTGCTTGGCCCTGCTCTCTGTGACCATCAGCTTT 125

Qy 52 ArgIleTyrlsGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArg 71
Db 126 AGGATATACAGGGTGTGATCCAACTATCCAGAAATCAGATGAAGGCCACCCATTTCAGG 185

Qy 72 AlaTyrlLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrlSerAsnSer 91
Db 186 GCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAAGTACAGTAATTC 245

Qy 92 AlaLeuGlyHisValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAspAsp 111
Db 246 GCTCTTGGTCATGTGAACATGACAGATAAGGAACCTCAGCGCCCTCTTCTTAGTTGATGAT 305

Qy 112 LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrlValGlyAlaLeu 131
Db 306 TTAGTTGATTCTCTGAAGTTTGACAGTGTGATGGGTATTACCTATGTTGGTCCCTTG 365

Qy 132 PheAsnGlyLeuThrLeuLeuIleAlaLeuIleSerLeuPheSerIleProValIle 151

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Db 366 TTTAATGCTGTGACACTACTGATTGCTGCTCATTTCACTCTTCAGTGTTCCTGTTATT 425
Qy 152 TTTGluARHISGlnValGlnleAspHisTyrLeuGlyLeuAlaAenLysSerVallys 171
Db 426 TATGACGGCATCAGCCACAGATAGATCATTTCTAGGACTTGCATAATGAAATGTTAAA 485
Qy 172 AspAlaMetAlaLysleGlnAlaLysleProGlyLeuLysArgLysAlaAasp 189
Db 486 GATGCTATGGCTAAATCCAAGCAAAATCCCTGGATTGAAGCGCAAGCTGAA 539

RESULT 80
BE733819
LOCUS 601569133P1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843729 5',
DEFINITION mRNA sequence.
ACCESSION BE733819
VERSION BE733819.1 GI:10147721
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 716)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL 1 (bases 1 to 716)
COMMENT NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Straubeberg, Ph.D.
Email: csapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at: image.llnl.gov
Plate: LUCM539 row: a column: 10
High quality sequence stop: 716.
FEATURES
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3843729"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_21"
/note="Organ: placenta; vector: pOTB7; Site: 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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## ORIGIN

```

Alignment Scores:
Pred. No.: 5.81e-94 Length: 716
Score: 846.00 Matches: 181
Percent Similarity: 96.84% Conservative: 3
Best Local Similarity: 95.26% Mismatches: 4
Query Match: 91.46% Indels: 3
DB: 2 Gaps: 0
```

```
US-09-830-972-2_COPY_975_1163 (1-189) x BE733819 (1-716)
```

```

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 142 GTTGTCACCTCTGTTACTGAGAGACATTAAGAAGACTGGAGTGTGTTGGTCCAGC 201
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 202 CTATTCTGCTGCTTTTCATTGACAGATTCAGCATTGTGAGCGTAACAGCGCTACATTGCC 261
```

```

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 262 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCTATC 321
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 322 CAGAAATCAGATGAAGGCCACCCCATTCAGGCGCATATCTGGAATCTGAAGTTGCTATATCT 381
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAenSerThrIleLys 101
Db 382 GAGGAGTGTGTTCAGAAGTACAGTAATCTGCTTCTGTCATGTGAATCGCAGATAAG 441
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 442 GAATCAGCGCCCTCTTCTTAGTTGATGATTAGTTAGTTCTCTGAAAGTTGCGAGTGTG 501
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 502 ATGTGGGTATTTACCTATGTTGGTGCCTTGTAAATGCTCTGACACTACTGAT-TTGGCT 560
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
Db 561 CTCAATTCACCTCTTCAGTGTCTCTGTTATTATGAACGGCATCAGGCACAGATAGATCAT 620
Qy 162 TyrLeuGlyLeuAlaAenLysSerValLysAspAlaMetAlaLysIleGln-AlaLysIle 181
Db 621 TATCTAGGACTTGCATAATAGAATGTTAAGATGCTATGCTAAATCCAAAGCAGAAAT 680
Qy 181 e-ProGlyLeuLysArgLysAlaAasp 189
Db 681 CCCCTGGATTGAAGCGCAAGTGAAT 706
```

## RESULT 81

```
CR755232/c
```

```
LOCUS
```

```
DEFINITION
```

```
CR755232 Rattus norvegicus muscle Sprague-Dawley Rattus norvegicus
```

```
cDNA clone GP0AAA15ZC09, mRNA sequence.
```

```
ACCESSION
```

```
CR755232
```

```
VERSION
```

```
CR755232.1 GI:51867189
```

```
KEYWORDS
```

```
Rattus norvegicus (Norway rat)
```

```
SOURCE
```

```
Rattus norvegicus
```

```
ORGANISM
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
```

```
Rattus.
```

```
REFERENCE
```

```
1 (bases 1 to 1054)
```

```
AUTHORS
```

```
Cros,N., Tkatchenko,A.V., Pisani,D.F., Leclerc,L., Leger,J.J.,
```

```
Marini,J.F. and Dechesne,C.A.
```

```
TITLE
```

```
Analysis of altered gene expression in rat soleus muscle atrophied
```

```
by disuse
```

```
JOURNAL
```

```
J. Cell. Biochem. 83 (3), 508-519 (2001)
```

```
MEDLINE
```

```
21479502
```

```
PUBMED
```

```
11596118
```

```
COMMENT
```

```
Contact: Genoscope
```

```
Genoscope - Centre National de Sequencage
```

```
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
```

```
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
```

```
Genoscope sequence ID: GP0AAA15ZC09RPI.
```

```
FEATURES
```

```
Location/Qualifiers
```

```
1..1054
```

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/organism="Rattus norvegicus"
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```
/mol_type="mRNA"
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```
/strain="Sprague-Dawley"
```

```
/db_xref="taxon:10116"
```

```
/clone="GP0AAA15ZC09"
```

```
/sex="Female"
```

```
/tissue_type="muscle"
```

```
/clone_lib="Rattus norvegicus muscle Sprague-Dawley"
```

```
/note="Vector: pCRII-TOPO; Pietu G., Cros N., Leger J.J.,
```

```
Dechesne C.A. Subtracted library from atrophied and
```

```
control soleus muscles Subtraction was performed
```

```
according to Diatchenko et al. (Diatchenko L, Lau YF,
```

Campbell AP, Chenchik A, Mocadam F, Huang B, Lukyanov S, Lukyanov K, Gurskaya N, Sverdlov ED, Siebert PD.  
 Suppression subtractive hybridization: a method for generating differentially regulated or tissue-specific cDNA probes and libraries. Proc Natl Acad Sci U S A. 1996; 93 :6025-30) Rats were female Sprague Dawley between 200 and 220g. Soleus muscle atrophy was performed by 14 days of hindlimb suspension."

## ORIGIN

Alignment Scores:  
 Pred. No.: 2,73e-93 Length: 1054  
 Score: 842.50 Matches: 180  
 Percent Similarity: 94.76% Conservative: 1  
 Best Local Similarity: 94.24% Mismatches: 7  
 Query Match: 91.08% Indels: 3  
 DB: 7 Gaps: 1

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CR755232 (1-1054)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 DB 925 GTTGTCTTCTCTTCTACTGGAGACATTAAGAAGACTGGAGTGGTGTGGTCCAGC 866  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 DB 865 TTATGCCCTGCTGCTTTCTTACAGTGTTCAGCATTTGTCAGTGAACGGCCTATATTGCC 806  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 DB 805 TTGGCCCTGCTCTCGTGACTATCAGTTTAGGATATATAGGGGTGTATCCAGGCTATC 746  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 745 CAGAAATCAGATGAAGGCCACCATTCAGGCATATTTAGATCTGAAGTTGCTATATCA 686  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 DB 685 GAGGAATTTGGTTTCAGAAATACAGTAATCTGCTCTGTGTCATGTAAGCAGACATAAAA 626  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 DB 625 GAATGAGCGCGCTTTCTTAGTGTATGATTTAGTTGATTCCTCGAAGTTGTCAGTGTG 566  
 QY 122 MetTrpValPheThrTyrValGlyAla---LeuPheAsnGlyLeuThrIleLeuLeuLeu 140  
 DB 565 ATGTGGGTGTTTACTATGTTTGTGCTGCTTGTCAATGGTCTGACACTACTGATTTTA 506  
 QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
 DB 505 GCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGAT 446  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLys--IleGlnAlaL 180  
 DB 445 CATATCTAGGACTTGCAACAGAGTGTTAAGGATGCCATGGGCCATATCCAGCAA 386  
 QY 180 ylleProGlyLeuLysArgLysAlaAsp 189  
 DB 385 AAATCCCTGGATTGAAGCGCAAGCAGAT 357

## RESULT 82

BU949473

LOCUS in67h09.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6127360 5',  
 DEFINITION similar to TR:Q9Y2Y7 Q9Y2Y7 FOOCEN-M. [2] TR:O94962 ;, mRNA  
 sequence.

ACCESSION BU949473

VERSION BU949473.1 GI:24200824

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 609)  
 Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,  
 Lemishka,L., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,  
 Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,  
 Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,  
 Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,  
 Williams,T., Jackson,Y. and Bowers,Y.  
 Endocrine Pancreas Consortium  
 Unpublished (2000)  
 Other ESTs: in67h09.x1  
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium  
 Harvard University, Howard Hughes Medical Institute  
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
 MA 02138  
 Tel: 617-495-1812  
 Fax: 617-495-8557  
 Email: dmelton@biohp.harvard.edu  
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:  
 Washington University Genome Sequencing Center For information on  
 obtaining a clone please contact: Dr. Hiroshi Inoue  
 (hinoue@im.wustl.edu)  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 471.

## FEATURES

source

1..609  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6127360"  
 /tissue\_type="Purified pancreatic islet"  
 /lab\_host="DH10B"  
 /clone\_lib="HR85 islet"  
 /note="Organ: Pancreas; Vector: pBluescript SK(-); Site\_1:  
 Note1: Site 2: XhoI; cDNA made by oligo-dr priming.  
 Size-selected on agarose gel. Average insert size ~1kb. 5'  
 XhoI site was destroyed after directional cloning.  
 Amplified once. Contact information: Hiroshi Inoue, MD,  
 Metabolism Div. (Alan Permutt Lab), Washington University  
 School of Medicine, Box 8127, 660 South Euclid Ave., St.  
 Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:  
 314-362-1916, Fax: 314-747-2692."

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.44e-93 Length: 609  
 Score: 842.00 Matches: 172  
 Percent Similarity: 97.22% Conservative: 3  
 Best Local Similarity: 95.56% Mismatches: 5  
 Query Match: 91.03% Indels: 0  
 DB: 5 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BU949473 (1-609)

QY 10 AspIleLysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThr 29  
 DB 1 GACATTAAGAAGATTGGAGTGGTGTGGTGCCAGCCTATTCCCTGCTCTTCATTGACA 60  
 QY 30 ValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIle 49  
 DB 61 GTATTACAGATTGTGAGCGTAACAGCTACATTGGCTTGGCCCTCTCTGTGACCATC 120  
 QY 50 SerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisPro 69  
 DB 121 AGCTTTAGGATATACAGGGTGTGATCCAGCTATCCAGAAATCAGATGAAGCCACCCA 180  
 QY 70 PheArgAlaTyrLeuGluSerGluValAlaIleSerGluLeuValGlnLysTyrSer 89  
 DB 181 TTCAGGGCATATCTGGAAATCTGAAGTTCCTATATCTGAGGAGTTGGTTCAAGATGACTGT 240  
 QY 90 AsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLeuArgArgLeuPheLeuVal 109  
 DB 241 AATCTGCTCTTGGTTCATGTGAATGACATGACGACGATAAAGGAACCTCAGCGCCTCTTCTAGTT 300

```

Qy 110 AspAspLeuValAspSerLeuLysPheAlaValLeuMetTTPValPheThrTyrValcIy 129
Db 301 GATGATTAGTTGATCTCTGAGTTTGCAAGTTTGATGGTATTTACCTAATGTTGGT 360
Qy 130 AlaLeuPheAnGlyLeuThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 149
Db 361 GCCTTTGTTAATGGTCTGACACTACTGATTGTTGGCTCTCAATTCACCTCTTCAGTGTTCCT 420
Qy 150 VallileTyrGluArgHisGlnValGlnIleAspHisTyrLeuGlyLeuAlaAsnLysSer 169
Db 421 GTTATTATTATGAACGCGCATCAGCGACAGATAGATCATTATCTAGGACTTGCAGAAAT 480
Qy 170 VallysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLysArgLysAlaAsp 189
Db 481 GTTAAAGATGCTATGGCTAAATCCAGCAAAATCCCTGGATTGAAGCGCAAGCTGAA 540

RESULT 83
CD000871
LOCUS
DEFINITION AGENCOURT 13650322 NIH MGC 186 Homo sapiens cDNA clone
IMAGE:30321390 5', mRNA sequence.
ACCESSION CD000871
VERSION CD000871.1 GI:30295402
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Straubeberg, Ph.D.
Email: c3apbb-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM120 row: 1 column: 07
High quality sequence stop: 530.
FEATURES
Location/Qualifiers
1..735
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30321390"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_186"
/notes="Organ: Pooled-Skin; Vector: pNIR-LIB; Site 1: SfII
(ggcatatggcc); Site 2: SfII (ggccgctcgcc); Library is
oligo-dT primed and directionally cloned. cDNA was
prepared from a pooled samples of tissues from Skin,
meninges, duramater, pia matter and choroid plexus.
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCCATTATGGC-3' and 3' adaptor
sequence: 5'-ATTAGAGCGGCGGCGGCGCATG-dT(30)BN-3'
(where B = A, C, G or N = A, C, G, or T). Average
insert size 1.47 kb (range 0.50-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library"

Alignment Scores:
Pred. No.: 2,51e-93 Length: 735
Score: 841.00 Matches: 176
Percent Similarity: 97.27% Conservative: 2
Best Local Similarity: 96.17% Mismatches: 3

```

```

Query Match: 90..92% Indels: 2
DB: 6 Gaps: 0
US-09-830-972-2_COPY_975_1163 (1-189) x CD000871 (1-735)
Qy 2 ValValAspLeuLeuTyrTipArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 189 GTTGTTCACCTCCTCTGTTACTGGAGAGACATTAAAGAAGACTGGAGTGGTGGTGGTGGCCAGC 248
Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 249 CTATTCTCTGCTGCTTTCATTGACAGTATTGACGATTGTGAGCGTAACAGCCCTACATTGCC 308
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 309 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAAGCTATC 368
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 369 CAGAAATCAGATGAAGGCCACCCATTTCAGGCATATCTGGAATCTGAAGTTGCTATATCT 428
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
Db 429 GAGGAGTTGGTTTCAGAGTACAGTAATTCTGCTCTTGGTTCATGTGTAACATGCACGATAAG 488
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 489 GAATCTAGGCGCTCTCTCTAGTTGATGATTAGTTAGTTCTCTGAAAGTTTGCAGTGTG 548
Qy 122 MetTrpValPheThrTyrVal-GlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAl 141
Db 549 ATGTGGGTATTACCTATGTTTGGTGGCTTGTAAATGGTCTGACACTACTGATTTTGGC 608
Qy 141 AleuLysSerLeuPheSer-IleProValIleTyrGluArgHisGlnValGlnIleAsp 161
Db 609 TCTCATTTCACTCTTCAGTGGTTCCTGTTATTATGAACGCGCATCAGGCACAGATAGATC 668
Qy 161 IstYrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysI 181
Db 669 ATTATCTAGGACTTGCATATAAATGTTAAGATGCTATGGCTAAATCCAGCCANAA 728
Qy 181 lePro 182
Db 729 TCCCT 733
RESULT 84
BUI09449
LOCUS
DEFINITION BUI09449 915 bp mRNA linear EST 25-NOV-2002
603126259F1 CSRQCHL13 Gallus gallus cDNA clone CHEST95f15 5', mRNA
sequence.
ACCESSION BUI09449
VERSION BUI09449.1 GI:25312699
KEYWORDS EST.
ORGANISM Gallus gallus (chicken)
Gallus gallus
Gallus gallus
REFERENCE 1 (bases 1 to 915)
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 22335534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

```

FEATURES  
source

Location/Qualifiers  
1. .915  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="White Leghorn, Hisex"  
/db\_xref="taxon:9031"  
/clone="ChST95f15"  
/dev\_stage="22"  
/lab\_host="DH10B"  
/clone\_lib="CSQCHL13"  
/note="Organ: limbs; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; Modification of pBluescript II KS(+) [Stratagene] vector to accommodate cDNA produced with the T-trimmed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BspI and BamHI sites [5'ggccgctgcagcccgatccgaaaaaag] [5'aattcttttttcggatccgggctgcacgc]"

## ORIGIN

Alignment Scores:  
Pred. No.: 4,55e-93 Length: 915  
Score: 840.00 Matches: 171  
Percent Similarity: 95.77% Conservative: 10  
Best Local Similarity: 90.41% Mismatches: 8  
Query Match: 90.81% Indels: 1  
Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BU109449 (1-915)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
Db :: 186  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db :: 187  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db GCTTGGCCCTGCTTCTGTGACCATCAGCTTAGATATACAGGGAGTATCCAGGCA 306  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db ATCCAAAAGTCGATGAAGGCCCATCCATTAGGGCTTACTTGGAGCTCTGATGTAGCTGTG 366  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
Db TCTGAAGAGCTGATTTCAGAAATACAGCAGTGTGTGCTTGGTGCATCAACGGCACAGTC 426  
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db AAGGAGCTGAGACGGCTCTCTCTGTGATGCTTGTGATCTCTGAGTT-CCATGT 485  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db TTGATGTGGGTCTTCACCTACGTTCCTGCTTGTAAATGGTCTGCATTTACTGATCTG 545  
QY 141 AlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAsp 160  
Db GTTGTGATTTCTGCTGTTGAGTCTTCTGTTATATGAGACATCAGGCCAGATCCGAC 605  
QY 161 HistyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db CATTATTGGGACTAGTAGCAAGAACGTCRAAGATGCGATGGCAAGATCCAAAGCAAG 665  
QY 181 IleProGlyLeuLysArgLysAlaAsp 189  
Db ATCCCTGGGCTGAAGCGCAAAATTGAG 692

RESULT 85

## CN791158

LOCUS 4125836 BARC 8BOV Bos taurus cDNA clone 8BOV\_41013 5', mRNA  
DEFINITION linear  
sequence.  
ACCESSION CN791158  
VERSION CN791158.1 GI:47687138  
KEYWORDS EST.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
REFERENCE 1 (bases 1 to 677)  
AUTHORS Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassel,C.P. and Matukumalli,L.K.  
TITLE Intestinal Muscle and Analysis of a cDNA Library Generated From Intestinal Muscle and Epithelial Tissues of Holstein Cattle Unpublished (2004)  
JOURNAL  
COMMENT Contact: Richard G. Baumann  
ANRI Bovine Functional Genomics Lab

BLDG 162: BARC-EAST, Beltsville, MD 20705, USA

Tel: 3015048604

Fax: 3015048744

Email: rbaumann@barc.usda.gov

Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim\_alt', -trim\_fasta. Vector identified by cross match using options -minmatch 12 -minscore 18  
Plate: 41 row: O column: 13

Seq primer: CCTATTAGGTGACACTATAGAAC

High quality sequence stop: 677.

## FEATURES

source

Location/Qualifiers  
1. .677  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/strain="Holstein"  
/db\_xref="taxon:9913"  
/clone="8BOV\_41013"  
/sex="Female"  
/tissue\_type="Epithelial, Muscle"  
/dev\_stage="Lactating, Neonatal"  
/lab\_host="DH10B ToNA"  
/clone\_lib="BARC 8BOV"  
/note="Organ: Intestine; Vector: pCMVSPORT6.1; Site\_1: NotI; Site\_2: EcoRI; Normalized cow cDNA intestinal library in pCMVSPORT6.1, constructed from equimolar mRNA pools derived from 5 sources, 4 lactating intestinal, 1 neonatal intestinal 4/5 Lactating, Proximal Duodenum, Jejunum, distal ileum, Colon, 1/5 Neonatal, Proximal Duodenum, Jejunum, Distal Ileum"

## ORIGIN

## Alignment Scores:

Pred. No.: 3.94e-93 Length: 677  
Score: 839.00 Matches: 170  
Percent Similarity: 98.85% Conservative: 2  
Best Local Similarity: 97.70% Mismatches: 2  
Query Match: 90.70% Indels: 0  
Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CN791158 (1-677)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 156 GTTGTGACCTCCTCTACTGGAGACATTAAGAAGACTGGAGTGGTGTGGTCCAGC 215  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 216 TTGTTCTCTGCTCTCTGCTGACAGTATTGACATTGTGAGTGTACCGCTACATTGCC 275  
QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 276 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 335



QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 336 CAGAAATCTGATGAGGCCACCCATTGAGGCATATTTGGAACTGGAAGTGTCTATATCT 395  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 396 GAGGAGTGTGTTCAAGAGTACAGCAATCTGCTCTTGGTCTATGTTAACTGACCAATAAAA 455  
 QY 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 456 GAATCTAGAGCCCTCTTCTAGTTGATGATTTAGTTGATTTCTGGAAGTTTGCAGTGTG 515  
 QY 122 MetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 516 ATGTGGGTATTACCTATGTTGGTCTTGTTCATAGTCTGACACTACTAAATTTGGCT 575  
 QY 142 LeuLysSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 576 CTGATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCGCAATAGATCAT 635  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAla 175  
 Db 636 TATCTGGACTTGCATAAAGATGTTAAAGATCTATGGCT 677  
 RESULT 86  
 CR753971  
 LOCUS CR753971 1057 bp mRNA linear EST 02-SEP-2004  
 DEFINITION cDNA clone GP0AA15ZC09, mRNA sequence.  
 ACCESSION CR753971  
 VERSION CR753971.1 GI:51865928  
 KEYWORDS EST.  
 SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 1057)  
 Cros.N., Tkatchenko,A.V., Pisani,D.F., Leclerc,L., Leger,J.J.,  
 Marini,J.F. and Dechesne,C.A.  
 Analysis of altered gene expression in rat soleus muscle atrophied  
 by disease  
 J. Cell. Biochem. 83 (3), 508-519 (2001)  
 21479502  
 11596118  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Genoscope sequence ID : GP0AA15ZC09Cp1.  
 Location/Qualifiers  
 1. 1057  
 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /clone="GP0AA15ZC09"  
 /sex="Female"  
 /tissue\_type="muscle"  
 /clone\_lib="Rattus norvegicus muscle Sprague-Dawley"  
 /note="Vector: pCRII-TOPO; Pietu G., Cros N., Leger J.J.,  
 Dechesne C.A. Subtracted library from atrophied and  
 control soleus muscles Subtraction was performed  
 according to Diatchenko et al. (Diatchenko L, Lau YF,  
 Campbell AP, Chenchik A, Moqadam F, Huang B, Lukyanov S,  
 Lukyanov K, Gurskaya N, Sverdlov ED, Siebert PD.  
 Suppression subtractive hybridization: a method for  
 generating differentially regulated or tissue-specific  
 cDNA probes and libraries. Proc Natl Acad Sci U S A. 1996;  
 93 :6025-30) Rats were female Sprague Dawley between 200  
 and 220g. Soleus muscle atrophy was performed by 14 days  
 of hindlimb suspension."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 2,68e-92 Length: 1057  
 Score: 834.50 Matches: 178  
 Percent Similarity: 95.31% Conservatives: 5  
 Best Local Similarity: 92.71% Mismatches: 5  
 Query Match: 90.22% Indels: 4  
 DB: 7 Gaps: 1  
 US-09-830-972-2\_COPY\_975\_1163 (1-189) x CR753971 (1-1057)  
 QY 2 ValValAspLeu-LeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaLase 21  
 Db 136 GTTGTGGACCTCATCTACTTGGAGAGACATTAAGAGACTGGAGTGGTGTGTAGTGCAG 195  
 QY 21 rLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaIleAl 41  
 Db 196 CTTATTCTCTGCTGCTCTAAACAGTGTTCAGCATTTATCAGTGTAAACGGCCTACATTGC 255  
 QY 41 aLeuAla---LeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAl 60  
 Db 256 CTTGGCCCATAGACTCTCGGTAAATATAAGCTTTAGGATATATAAGGCGGTGATACAGGC 315  
 QY 60 alieGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 316 TATCCAGAAATCAGATGAGGCCACCCATTTCAGGGCATATTTAGAATCTCGAAGTTGCTAT 375  
 QY 80 eSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIle 100  
 Db 376 ATCAGAGGAATTTGGTTCAAAATATACAGTAATTTCTGCTCTTGGTTCATGTGAACACACAAT 435  
 QY 100 eLysGluLeuArgArgPheLeuValAspAspLeuValAspSerLeuLysPhe-Alav 120  
 Db 436 AAAGAACTCAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTTCCCTGAGATTTGCGAG 495  
 QY 120 alLeuMetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleL 140  
 Db 496 TGTGTGATGGGTGTTTACTTATGTTGGTCCCTTGTTCATGTTCTGACACTACTGATTT 555  
 QY 140 euAlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAl 160  
 Db 556 TAGCTCTGATCTCACTCTTCAGTATTCTCTGTTATTTATGAACGGCATCAGGTGCGAGATAG 615  
 QY 160 spHisTyr-LeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAla 179  
 Db 616 ATCATTTATCATAGGACATTCGAACAGAGATTTAAGGATGCCATGGCCAAATCCAAGCA 675  
 QY 180 LysIleProGlyLeuLysArgLysAlaAsp 189  
 Db 676 AAAATCCCTGGATTGAAGCGCAAGCAGAT 705  
 RESULT 87  
 CR771568  
 LOCUS CR771568 684 bp mRNA linear EST 23-SEP-2004  
 DEFINITION DKFZp469C2337.r1.469 (synonym: pkid1) Pongo pygmaeus cDNA clone  
 DKFZp469C2337-5', mRNA sequence.  
 CR771568  
 ACCESSION CR771568.1 GI:52614841  
 VERSION EST.  
 KEYWORDS  
 SOURCE Pongo pygmaeus (orangutan)  
 ORGANISM Pongo pygmaeus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pongo.  
 1 (bases 1 to 684)  
 Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Schaipp,A.,  
 Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and  
 Wiemann,S.  
 Pongo pygmaeus mRNA (Ottenwaelder,B., Obermaier,B.,  
 Deutschenbaur,S., et al.)  
 Unpublished (2004)  
 Contact: MIPS  
 MIPS  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
 This is the 5' sequence of the clone insert. Clone from S. Wiemann,  
 Molecular Genome Analysis, German Cancer Research Center (DKFZ);  
 Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix  
 (Martinried/Germany) within the cDNA sequencing consortium of the  
 German Genome Project. This clone (DKFZp469C2337) is available at  
 the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in  
 Berlin, Germany. Please contact RZPD for ordering:  
 http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZp469C2337  
 Further information about the clone and the sequencing project is  
 available at http://mips.gsf.de/projects/cdna/

## FEATURES

1. 684

Location/Qualifiers  
 source  
 /organism="Pongo pygmaeus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9600"  
 /clone="DKFZp469C2337"  
 /tissue type="kidney"  
 /dev stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="469 (synonym: pkid1)"  
 /note="Vector: pSport1\_Sfi; Site\_1: SfiI; Site\_2: SfiIb"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1,66e-92 Length: 684  
 Score: 834.00 Matches: 169  
 Percent Similarity: 98.28% Conservative: 2  
 Best Local Similarity: 97.13% Mismatches: 3  
 Query Match: 90.16% Indels: 0  
 DB: 7 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CR771568 (1-684)

QY 2 ValValAspLeuLeuTyrTrpArgAspLeuTyrThrGlyValValPheGlyAlaSer 21  
 DB 162 GTTNTTGACCTCCTCTACTGGAGACATTAAGAAGACTGGAGTGGTGTGGTGGCCAGC 221  
 QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 DB 222 CTATTCTCGCTGCTTTCATTGACATGATTCAGCATTTGTGAGTGTAAACAGCCTACATTGCC 281  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 DB 282 TTGGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 341  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 342 CAGAAATCAGATGAAGGCCACCATTCAGGCATATCTGGAATCTGGAATCTGAAATGCTATATCT 401  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 DB 402 GAGGAGTGGTTCAGAGTACAGTAAATCTGCTCTTGTGTCATGTGAATCGACGATAAAG 461  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 DB 462 GNACTCAGCGCGCTCTTCTTAGTGTGATTTAGTTGATTTCTGAAATTTGCAAGTGTG 521  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
 DB 522 ATGGGGTATTTACCTATGTTGGTGCCTGTTTAAATGCTCTGACGCTACTGATTTGGCT 581  
 QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 DB 582 CTCATTTCACCTTCAGTGTGCTGCTGTTATTATGAACGGCATCAGGCCACAGATAGATCAT 641  
 QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAla 175  
 DB 642 TATCTAGGACTTGCATAAATAAGATGTTAAAGTGTATGGCT 683

## RESULT 88

BG428512

LOCUS

906 bp mRNA linear EST 14-MAR-2001

DEFINITION 602501030F1 NIH\_MGC\_75 Homo sapiens cDNA clone IMAGE:4614679 5',  
 mRNA sequence.  
 ACCESSION BG428512  
 VERSION BG428512.1 GI:13335018  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NIH-MGC http://mgs.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: CLONTECH Laboratories, Inc.  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LCM1366 row: 1 column: 08  
 High quality sequence stop: 730.

## FEATURES

Location/Qualifiers

1..906  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4614679"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NIH\_MGC\_75"  
 /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site\_1:  
 SfiI (ggccgctcgcc); Site\_2: SfiI (ggccattggcc); 5' and  
 3' adaptors were used in cloning as follows: 5' adaptor  
 sequence: 5'-CAGCGCATATGCC-3' and 3' adaptor sequence:  
 5'-ATTCTAGAGCGCGGCGCATG-dt(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size 1.65  
 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA). Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 4.39e-92 Length: 906  
 Score: 832.00 Matches: 180  
 Percent Similarity: 96.83% Conservative: 3  
 Best Local Similarity: 95.24% Mismatches: 5  
 Query Match: 89.95% Indels: 3  
 DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BG428512 (1-906)

QY 2 ValValAspLeuLeuTyrTrpArgAspLeuTyrThrGlyValValPheGlyAlaSer 21  
 DB 103 GTTGTGACCTCCTGCTACTGGAGACATTAAGAAGACTGGAGTGGTGTGGTGGCCAGC 162  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 DB 163 CTATTCTCGCTGCTTTCATTGACATGATTCAGCATTTGTGAGTGTGATCCAGCTACATTGCC 222  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 DB 223 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 282  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 283 CAGAAATCAGATGAAGGCCACCATTCAGGCATATCTGGAATCTGGAATGCTATATCT 342  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 DB 343 GAGGAGTGGTTCAGAGTACAGTAAATCTGCTCTTGGTTCATGTGAACTGACGATAAAG 402

Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 403 GAATCAGCCCTCTTCTTAGTATGATTAGTCTCTGAGATTGCGAGTTG 462  
 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAlaValLeuLeuAla 141  
 Db 463 ATGTGGGTATTTACTATGTTGGTGGCTTGTAAATGCTGACACTACTGATTTGGT- 521  
 Qy 142 LeuLeuSerLeuPheSerIleProValIleTyrGlu-ArgHisGlnValGlnIleAspHi 161  
 Db 522 CTCATTTTCTTCTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACATAGATCA 581  
 Qy 161 sTyrLeuGlyLeuAlaAlaLeuSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 582 TTATCTAGGACTTGCNAATAGATGTTAAAGATGCTATGCT-AAAATCCAGCAAAAT 640  
 Qy 181 eProGlyLeuLysArgLysAlaAsp 189  
 Db 641 CCCTGGATTGAAGCGCAAGTGAAT 665

RESULT 89  
 BUI16200  
 LOCUS 603002628F1 CSEQCHL15 Gallus gallus cDNA clone CHEST1198 5', mRNA  
 DEFINITION sequence.  
 ACCESSION BUI16200  
 VERSION BUI16200.1 GI:25322885  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 961)  
 Boardman,P.E., Sanz-Exquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
 A Comprehensive Collection of Chicken cDNAs  
 Curr. Biol. 12 (22), 1965-1969 (2002)  
 22335534  
 12445392  
 CONTACT: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
 source  
 1..961  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="Compton Line 151"  
 /db\_xref="taxon:9031"  
 /clone="CHEST1198"  
 /sex="Female"  
 /tissue\_type="cerebrum"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQCHL15"  
 /note="Organ: brain; Vector: pBluescript II KS(+); Site:1:  
 EcoRI; Site 2: NotI; Modification of pBluescript II KS(+)  
 T-trimmed protocol (Construction of uni-directionally  
 cloned cDNA libraries from messenger RNA for improved  
 end DNA sequencing by Glenn Fu, et al. U.S. Patent #  
 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.  
 Ligate in double stranded adaptor containing BglI and  
 BamHI sites [5'-ggccggtgcagcccgatccgatacaaaag  
 [5'-aattcttttttcgattccggggtgcagc]".

ORIGIN

## Alignment Scores:

Pred. No.: 9,73e-92 Length: 961  
 Score: 829.50 Matches: 171  
 Percent Similarity: 95.74% Conservative: 9  
 Best Local Similarity: 90.96% Mismatches: 8  
 Query Match: 89.68% Indels: 2  
 DB: 5 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BUI16200 (1-961)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 175 GTTGTTCACCTCTTACTGCGGAGACATTAAAGAGACAGAGTGGTGTGGTGGCCAGC 234  
 Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 235 TTGTTCCTGCTGCTCTCATTAACAGAGTGTTCAGCATCTGAGCGTGAGCGCTTACATGGCC 294  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 295 TTGGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAAAGGAGTTATCCAGGCAATC 354  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 355 CAAAAGTCCGATGAAGGCCATCCATTTAGGCTTACTTTGAGTCTGATGTAGCTGTGTCT 414  
 Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
 Db 415 GAAGAGCTGATTGAGAAATACAGCAGTGTGTGCTGTCATCACATCAACGGCACAGTCAAG 474  
 Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 475 GAGCTGAGAGCCTCTTCTCTGTTGATGACTTGGTGTATCTCTGAAGTTTGCAGTGTG 534  
 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 Db 535 ATGTGGGTGTCTACTTACGTTGGTGGCTTGTAAATGCTGCTGACATTTACTGATCTGCT 594  
 Qy 142 LeuLeuSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
 Db 595 TTGATTTTCGCTGTTTCAGTGTCTGTTATTTATGAGAGACATCAGGCCAGATCGACCAT 654  
 Qy 162 TyrLeuGlyLeuAlaAlaLeuLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 655 TATTGGGACTAGTGAACAGAGACGTCAGAGATGCGATGGC-RAGATCCAGCAAGAT- 712

182 ProGlyLeuLysArgLysAlaAsp 189  
 Db 713 CCTGGGCTGAAGCGCAAACTGAG 736

## RESULT 90

BQ807975

LOCUS

DEFINITION

MACACA MULATTA

ACCESION

VERSION

KEYWORDS

SOURCE

ORGANISM

MACACA MULATTA

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BQ807975 619 bp mRNA linear EST 31-JUL-2002  
 NISC kki2d10.y1 NCI CGAP Brn72 Macaca mulatta cDNA clone  
 IMAGE:5331139 5', mRNA sequence.

MACACA MULATTA

MACACA MULATTA

MACACA MULATTA

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MACACA MULATTA

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 Cercopithecoidea; Macaca.

1 (bases 1 to 619)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

cDNA Library Preparation:

cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC)  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: info@image.llnl.gov  
Plate: LLAM11840 row: H column: 20  
Seq primer: M13Rpl reverse primer (ABI).

## FEATURES

Location/Qualifiers  
1..619  
/organism="Macaca mulatta"  
/mol\_type="mRNA"  
/db\_xref="taxon:9544"  
/clone="IMAGE:5331139"  
/tissue\_type="hypothalamus"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NCI CGAP Brn72"  
/note="Organ: brain; Vector: pCMV-SPORT6.1; Site 1: NotI; Site 2: EcoRV; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.2 kb. Constructed by Invitrogen. Note: this is a NCI CGAP Library."

## ORIGIN

Alignment Scores:  
Pred. No.: 6e-92 Length: 619  
Score: 829.00 Matches: 167  
Percent Similarity: 98.84% Conservatve: 4  
Best Local Similarity: 96.53% Mismatches: 2  
Query Match: 89.62% Indels: 0  
DB: 5 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x B0807975 (1-619)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
DB 100 GTTGTGACCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 159  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 160 CTAATCTCTGCTCTTCTCATTCAGCATATTCAGCATGTGAGTGTAAACAGCCTACATATCC 219  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 220 TTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 279  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerLeuValAlaIleSer 81  
DB 280 CAGAAATCAGATGAAGGCCACCCATTCAGGCATATCTGGAATCTGGAAGTTGCCATATCT 339  
QY 82 GluGluLeuValGlnLysTrpSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
DB 340 GAGGAGTTGGTTTCAGAGTACAGTAATCTCTGTGTCATGTGAATCGCACGATAAAG 399  
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 400 GAACCTCAGCGCCCTCTCTAGTTCATGATTTAGTTGATTCTCTGAAAGTTGCCAGTGTG 459  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
DB 460 ATGTGGGTATTTACCTATGTTGGTGCCTTGTATATGCTCTGACGCTACTGATTTGGCT 519  
QY 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
DB 520 CTAATTCACCTCTCAGTGTCTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 579  
QY 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMet 174  
DB 580 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATG 618

## RESULT 91

CO505196  
LOCUS  
DEFINITION  
GGEZEB1026A09, g embryo breast muscle - EB1 Gallus gallus cdna clone  
GGEZEB1026A09, mRNA sequence.  
ACCESSION  
CO505196

CO505196.1 GI:50275382  
EST.  
KEYWORDS  
SOURCE  
ORGANISM  
Gallus gallus (chicken)  
Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.

## REFERENCE

AUTHORS  
1. (Bases 1 to 669)  
Alves, H.J., Jorge, E.C., Marchesin, M.L., Monteiro-Vitorello, C.B.,  
Patricio, M., Ledur, M.C. and Coutinho, L.L.  
Discovery of new genes expressed in the chicken breast muscle  
Unpublished (2004)  
Contact: Helena J. Alves  
Laboratory of Animal Biotechnology, Dep. of Animal Production  
ESALQ - University of Sao Paulo  
Av. Padua Dias, 11, Piracicaba, SP, 13418-900, Brazil  
Tel: 55 19 3429 4434  
Fax: 55 19 3429 4285  
Email: hjalves@esalq.usp.br and llcoutin@esalq.usp.br  
PCR Primers  
BACKWARD: T7.

## FEATURES

Location/Qualifiers  
1..669  
source  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9031"  
/clone="GGEZEB1026A09"  
/tissue\_type="breast muscle"  
/dev\_stage="embryos with 9 and 17 days old"  
/lab\_host="DH5 alpha"  
/clone\_lib="embryo breast muscle - EB1"  
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; This  
cDNA library was constructed with the SuperScript plasmid  
System with Gateway Technology kit (Invitrogen), following  
manufacturer's protocols. Plasmid DNA was purified using a  
modified alkaline lysis method. Sequencing reactions were  
conducted using the DYEnamic Cycle Sequencing kit for  
MegABACE (Amersham Biosciences) according to the  
manufacturer's recommendations. Clones were sequenced by  
the 5' end with T7 primer. Sequencing reactions were  
analyzed on MegABACE1000 DNA Sequencer (Amersham  
Biosciences). The quality and clustering of the ESTs were  
analyzed using the softwares Phred/Cap3. Only EST  
sequences with Phred quality greater than 20 and at least  
150 bp were considered for clustering."

## ORIGIN

Alignment Scores:  
Pred. No.: 6.7e-92 Length: 669  
Score: 829.00 Matches: 171  
Percent Similarity: 95.74% Conservatve: 9  
Best Local Similarity: 90.96% Mismatches: 7  
Query Match: 89.62% Indels: 2  
DB: 7 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x CO505196 (1-669)

QY 3 ValAspLeuLeuTyrTrp-ArgAspIleLysLysThrGlyValValPheGlyAlaSerLe 22  
DB 43 GTTGACCTCTTTACTGNCAGACATTAAGACAGGAGTGTGTGT-GTGCCAGCTT 101  
QY 22 uPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLe 42  
DB 102 GTTCCTGCTCTCTCATTAACAGTGTTCAGCATCGTCGAGCTGACAGCTTACATGCTT 161  
QY 42 uAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleG 62  
DB 162 GGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAGGAGGTATCCAGGCATCCA 221  
QY 62 nLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerLeuValAlaIleSerG 82  
DB 222 AAAGTCCGATGAAGGCCATCCATTTAGGCTTACTTGGAGTCTGATGTAGCTGTGCTGA 281

Qy 82 uGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAenSerThrIleLysG1 102  
 Db 282 AGAGCTGATTACAGAAATACAGCAGTGTGTCTTGGTACATCAACGCCAGTCAAGGA 341  
 Qy 102 uLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMe 122  
 Db 342 GCTGAGACGCCCTCTCTCGTGTGATGACCTTGGTGTGATCTCTGAGGTTCGAT 401  
 Qy 122 tTTPValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuLeuAlaLe 142  
 Db 402 GTGGGTGTTCACTACGTGTGTGCTGTGTGTAAATGGTCTGACATCTACTGATCTGGCTTT 461  
 Qy 142 uileSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHisTy 162  
 Db 462 GATTTCGCTGTTCACTGCTGCTGCTGTTATTTATGAGACATCAGGCCAGACCATTA 521  
 Qy 162 rLeuGlyLeuAlaAenLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIlePr 182  
 Db 522 TTTGGGACTAGTGAAACAGACGTCAAAGATGCGATGGCAAGATCCCAAGCAAGATCCC 581  
 Qy 182 oGlyLeuLysArgLysAlaAap 189  
 Db 582 TGGCTGAGCGCAAACTGAG 603

RESULT 92  
 B1547877  
 LOCUS 603192073F1 NIH\_MGC\_95 Homo sapiens cDNA clone IMAGE:5263026 5',  
 DEFINITION mRNA sequence.

ACCESSION B1547877  
 VERSION B1547877.1 GI:15435189  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 614)  
 NIH-MGC http://mgi.nci.nih.gov/.

REFERENCE Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
 Toshituki and Piero Carninci (RIKEN)

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: L1AM11663 row: b column: 19  
 High quality sequence stop: 614.

FEATURES  
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 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
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 /clone="IMAGE:5263026"  
 /tissue\_type="hippocampus"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH MGC 95"

/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site\_1: BamHI; Site\_2: SalI-XhoI (Gcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH\_MGC Library."

ORIGIN

# Alignment Scores:

Pred. No.: 7..89e-92 Length: 614  
 Score: 828.00 Matches: 169  
 Percent Similarity: 98.85% Conservative: 3  
 Best Local Similarity: 97.13% Mismatches: 2  
 Query Match: 89.51% Indels: 0  
 DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x B1547877 (1-614)

Qy 16 ValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSer 35  
 Db 7 GTGGTGTGTGGTGGCCGCTATTCTCTGCTGCTTTTCATTGACAGTATTTCAGCATTTGTGAGC 66  
 Qy 36 ValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLys 55  
 Db 67 GTAAACAGCCATACATTGCTTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAG 126  
 Qy 56 GlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGlu 75  
 Db 127 GGTGTGATCCAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAA 186  
 Qy 76 SerGluValAlaIleSerGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHis 95  
 Db 187 TCTGAAGTTGCTATATCTGAGGAGTTGGTTTTCAGAAATACAGTAAATCTCTGCTCTTTGGTCA 246  
 Qy 96 ValAenSerThrIleLysGluLeuValGlnLysTyrSerAenSerAlaLeuValAspSer 115  
 Db 247 GTGAACGTGACAGTAAAGGAACCTCCTCTTCTAGTGTGATGATTTAGTTGATTTCT 306  
 Qy 116 LeuLysPheAlaValLeuMetTTPValPheThrTyrValGlyAlaLeuPheAenGlyLeu 135  
 Db 307 CTGAAGTTGTCAGTGTGTGATGCTGGTATTATACCTATGTTGCTGCTTGTAAATGCTG 366  
 Qy 136 ThrLeuLeuLeuAlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHis 155  
 Db 367 ACACACTACTGATTTGGCTCTCTCATTTCACTCTTCAGTGTCTCTGTTATTATTGAACGCA 426  
 Qy 156 GlnValGlnIleAspHisTyrLeuGlyLeuAlaAenLysSerValLysAspAlaMetAla 175  
 Db 427 CAGGCACAGATAGATCATTAATCTAGGACTTGCATAAAGAAATGTTAAAGATGCTATGGCT 486  
 Qy 176 LysIleGlnAlaLysIleProGlyLeuLysArgLysAlaAap 189  
 Db 487 AAATCCAGCAAAATCCCTGATTCAGCGCAAGCTGAA 528

# RESULT 93

CR771272

LOCUS

DEFINITION

DKFZp469F2235\_r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone

CR771272

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CR771272.1 GI:52614545

EST.

Pongo pygmaeus (orangutan)

Pongo pygmaeus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.

1 (bases 1 to 644)

Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R.,

Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and

Wiemann, S.

Pongo pygmaeus mRNA (Poustka, A., Albert, R., Moosmayer, P., et al.)

Unpublished (2004)

Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert. Clone from S. Wiemann,

Molecular Genome Analysis, German Cancer Research Center (DKFZ);

Email s.wiemann@dkfz-heidelberg.de; any. Please contact RZPD for

ordering:

http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469F2235

Further information about the clone and the sequencing project is

available at <http://mips.gsf.de/projects/cdna/>.

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FEATURES
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        /clone="DKP2p459F2235"
        /issue_type="kidney"
        /dev_stage="adult"
        /lab_host="DH108"
        /clone_lib="469 (synonym: pkid1)"
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ORIGIN
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Pred. No.:      8,446-92      Length:      644
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Percent Similarity: 96.59%      Conservative: 2
Best Local Similarity: 95.45%      Mismatches: 6
Query Match:    89.51%      Indels:    0
DB:             7      Gaps:      0

US-09-830-972-2_COPY_975_1163 (1-189) x CR771272 (1-644)

QY      2 ValValAspLeuLeuTyrTrrArgAspIleLysThrGlyValValPheGlyAlaSer 21
DB      115 GTTGTGACCTCTCTACTCTGGAGACATTAAGAAAGACTGGAGTGGTGTGGTCCAGC 174

QY      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB      175 CTATTCTCTGCTCTTTCATTGACAGATTCAGCATTTGAGTGAACAGCCTACATTGCC 234

QY      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB      235 TTGGCCCTGCTTCTCTGTGACCATCAGCTTTAGGATATACAAAGGGTGTGATCCAGCTATC 294

QY      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB      295 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGGAATCTGATATCT 354

QY      82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
DB      355 GAGGAGTGGTNNTCAGAGTACAGTAATCTCTGCTCTTGGTCATGTGAACCTGACGATAAG 414

QY      102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
DB      415 GAAATTCAGCGCCTCTCTAGTTGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 474

QY      122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeuAla 141
DB      475 ATGTGGGTATTTACCTATGTATGTGGTCCCTGTGTTAATGGTCTGACGCTACTGATTTGGCT 534

QY      142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161
DB      535 CTCATTTCTCCTTCAGTGTTCCCGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 594

QY      162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIle 177
DB      595 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGTATGGCTAAATC 642

RESULT 94
CN429726
LOCUS      CN429726      708 bp      mRNA      linear      EST 16-MAY-2004
DEFINITION      17000599934467 GRN_PRENEU Homo sapiens cDNA 5', mRNA sequence.
ACCESSION      CN429726
VERSION      CN429726.1      GI:47417320
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 708)
AUTHORS      Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,

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Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 708 Std Error: 0.00.
FEATURES
  source
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        conditions. Embryoid bodies were generated in the presence
        of all-trans retinoic and mitogens."

ORIGIN
Alignment Scores:
Pred. No.:      9,666-92      Length:      708
Score:          828.00      Matches:    169
Percent Similarity: 98.95%      Conservative: 3
Best Local Similarity: 97.13%      Mismatches: 2
Query Match:    89.51%      Indels:    0
DB:             7      Gaps:      0

US-09-830-972-2_COPY_975_1163 (1-189) x CN429726 (1-708)

QY      16 ValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSer 35
DB      1 GTGTGTGTGGTGGCAGCCTATTCTCTGCTGCTTTTCATTGACAGTATTGAGCACTTGTGAGC 60

QY      36 ValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLys 55
DB      61 GTAAAGCCTACATTCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAG 120

QY      56 GlyValIleGlnAlaIleGlnLysSerAspGluHisProPheArgAlaTyrLeuGlu 75
DB      121 GGTGTGATCCAAAGCTATCCAGAAATCAGTGAAGGCCACCCATTTCAGGGCATATCTCGAA 180

QY      76 SerGluValAlaIleSerGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHis 95
DB      181 TCTGAAGTTGCTATATCTGAGGAGTGTGTTTCAGAAAGTACAGTAATTCCTCTTTGGTCTAT 240

QY      96 ValAsnSerThrIleLysGluLeuArgArgLeuPheLeuValAspLeuValAspSer 115
DB      241 GTGAATCTGCAGTAAGAAGAACTCAGGCGCTCTCTTAGTTGATGATTTAGTTGATTTCT 300

QY      116 LeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeu 135
DB      301 CTGAAGTTTGAGTGTGATGTGGGTATTTACCTATGTTGGTGTGCTTTTAAATGGTCTG 360

QY      136 ThrLeuLeuLeuLeuAlaLeuIleSerIlePheSerIleProValIleTyrGluArgHis 155
DB      361 ACATCTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCAT 420

QY      156 GlnValGlnIleAspHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAla 175
DB      421 CAGGCACAGATAGATCATTTATCTAGGACTTGCATAATAGAAATGTTAAAGATGCTATGGCT 480

QY      176 LysIleGlnAlaLysIleProGlyLeuLysArgLysAlaAsp 189
DB      481 AAAATCCAAAGCAAAATCCCTGGATTGAAGCGCAAAAGCTGAA 522

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RESULT 95  
BG568630  
LOCUS  
DEFINITION 602587637F1 NIH\_MGC\_76 Homo sapiens CDNA clone IMAGE:4716393 5',  
755 bp mRNA linear EST 10-APR-2001  
mRNA sequence.  
ACCESSION BG568630  
VERSION BG568630.1 GI:13576283  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 755)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strauberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: CLONETECH Laboratories, Inc.  
CDNA Library Preparation: CLONETECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCMI564 row: j column: 10  
High quality sequence stop: 719.  
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/clone\_lib="NIH\_MGC\_76"  
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3' adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CAGCGCATATGCGC-3' and 3' adaptor sequence:  
5'-ATTCTAGCGCGGCGCGCATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.85  
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

FEATURES  
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/notes="Organ: Liver; Vector: pDNR-LIB (Clontech); Site 1:  
SfiI (ggcgctcgcc); Site 2: SfiI (ggccattggcc); 5' and  
3' adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CAGCGCATATGCGC-3' and 3' adaptor sequence:  
5'-ATTCTAGCGCGGCGCGCATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.85  
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
Pred. No.: 1.06e-91 Length: 755  
Score: 828.00 Matches: 178  
Percent Similarity: 95.81% Conservative: 5  
Best Local Similarity: 93.19% Mismatches: 5  
Query Match: 89.51% Indels: 4  
DB: 4 Gaps: 0  
US-09-830-972-2\_COPY\_975\_1163 (1-189) x BG568630 (1-755)  
Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 178 GTTGTGACCTCTCTGTGACCATCAGCTTTAGGATATACAGGCTGTGTTGGTGCAGC 237  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 238 CTATTCCTGCTGCTTTCAATGACAGTATTTCAGCATTTGTGAGCGTACAGCTACATTGCC 297  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 298 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGCTGTGATCCAGCTATC 357  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 358 CAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGGAATCTGAAGTTGCTATATCT 417

Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValaAsnSerThrIleLys 101  
Db 418 GAGGAGTGGTTCAGAAGTACAGTAATCTGCTCTGGTCACTGTGAACCTGCACGATAAG 477  
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 478 GAACCTCAGGCGCTCTCTTAGTTAGTATGATTAGTTCTCTGAAGTTTGCAGTGTG 537  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
Db 538 ATGTGGGTATTACCTATGTTGGTGGCTTGTAAATGCTGCACACTACTGAT-TTGGCT 596  
Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
Db 597 CTCATTTCACCTCTCAGTGTCTCTGTTATTATGAACGGCATCAGGCACAGATAGATCAT 656  
Qy 162 TyrLeuGlyLeuAlaLeuLysSerValLysAspAla-MetalalysileGlnAla--Lys 180  
Db 657 TATCTAGGACTTGCAAATAGAATGTTACAGATGCTAATGTTAAATCCAAAGCAAAAA 716  
Qy 181 IleProGlyLeuLysArgLysAlaAsp 189  
Db 717 ATCCCTGGATTGAAGCGCAAAAGTGAA 743  
RESULT 96  
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DEFINITION BUI16870 934 bp mRNA linear EST 25-NOV-2002  
603138816F1 CSEQCHL15 Gallus gallus CDNA clone CHEST12704 5', mRNA  
sequence.  
ACCESSION BUI16870  
VERSION BUI16870.1 GI:25324153  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 934)  
Boardman, P.R., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)  
22335534  
12445392  
COMMENT  
Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: [Simon.Hubbard@umist.ac.uk](mailto:Simon.Hubbard@umist.ac.uk).  
Location/Qualifiers  
1. 934  
/organism="Gallus gallus"  
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/strain="Compton Line 151"  
/db\_xref="taxon:9031"  
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/notes="Organ: brain; Vector: pBluescript II KS(+); Site 1:  
EcoRI; Site 2: NotI; Modification of pBluescript II KS(+)  
[Stratagene] vector to accommodate cDNA produced with the  
T-trimmed protocol (Construction of uni-directionally  
cloned cDNA libraries from messenger RNA for improved 3'  
end DNA sequencing by Glenn Fu, et al. U.S. Patent #  
6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.  
Ligate in double stranded adaptor containing BglI and  
BamHI sites [5'ggcgctgagcccgatccgaaaaag]

[5'aattcttttttcggtccggggtgcagc]

ORIGIN

Alignment Scores:  
Pred. No.: 1.43e-91 Length: 934  
Score: 828.00 Matches: 169  
Percent Similarity: 96.20% Conservativity: 8  
Best Local Similarity: 91.85% Mismatches: 7  
Query Match: 89.51% Indels: 1  
DB: 5 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BULL16870 (1-934)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 173 GTGTGTGACCTCTTCTGACCATCAGCTTAGGATATACAGGAGTTCGTTGGTCCAGC 231

Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 232 TTGTTCTGCTGCTCTCAATTAACAGTTCAGCATCGTGAGCGTGACAGCTTACATTGCC 291

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 292 TTGGCCCTGCTTCTGTGACCATCAGCTTAGGATATACAGGAGTTCGTTGGTCCAGC 351

Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 352 CAAAGTCCGATGAAGGCCCATCCATTAGGGCTTACTTGGAGTCTGTAGTGTGTCT 411

Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101  
Db 412 GNAGAGCTGATTCAGAAATACAGCAGTGTGTGCTTGTTCATCATCAAGGCACAGTCAAG 471

Qy 102 GluLeuArgLeuPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 472 GAGCTGAGAGCGCTCTCTCTGATGACCTTGGTGTGATCTCTCAAGTTCGAGTGTG 531

Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
Db 532 ATGTGGGTTCACCTAGCTGGTGGTGGCTTGTATATGCTGTGACATTAATGCTGCT 591

Qy 142 LeuIleSerLeuPheSerIleProValIleTyrGluArgHisGlnValGlnIleAspHis 161  
Db 592 TTGATTTGCTGCTTACGTTCTCTGTTTATATGAGACATCAGGCCCGCATCGACCAT 651

Qy 162 TyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 652 TATTGGGACTAGTGAACAAGACCTCAAGATGCGATGGCAAGATCAAGCAAGATC 711

Qy 182 ProGlyLeuLys 185  
Db 712 CCTGGGCTGAAA 723

RESULT 97  
BG696431  
LOCUS BG696431.1 GI:13961567  
DEFINITION 991 bp mRNA linear EST 07-MAY-2001  
mRNA sequence.

ACCESSION BG696431  
VERSION 1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 991)  
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
CONTACT: Robert Strausberg, Ph.D.  
Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
Tissue Procurement: James Cleaver, M.D.  
CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA  
Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM10697 row: 0 column: 08  
High quality sequence stop: 763.  
Location/Qualifiers  
1. 991  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4802911"  
/lab\_host="DH10B (TI phage-resistant)"  
/clone\_lib="NCI CGAP Skn3"  
/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.5kb. Library constructed by Life  
Technologies. Note: this is a NCI CGAP Library."

FEATURES  
source

ORIGIN

Alignment Scores:  
Pred. No.: 2.76e-91 Length: 991  
Score: 826.00 Matches: 177  
Percent Similarity: 96.26% Conservativity: 3  
Best Local Similarity: 94.55% Mismatches: 5  
Query Match: 89.30% Indels: 3  
DB: 4 Gaps: 0

US-09-830-972-2\_COPY\_975\_1163 (1-189) x BG696431 (1-991)

Qy 4 AspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeuPhe 23  
Db 216 GACCTCTGTTACTCGAGACATTAAGAAGACTGGAGTGGTGTGGTGGCCAGCTATTC 275

Qy 24 LeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAla 43  
Db 276 CTGCTGCTTTCATTCAGCATTCAGCATTCGAGCTGAGCGTACAGCTATTCGCTTGGCC 335

Qy 44 -LeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLys 63  
Db 336 CCGTCTCTCTGACCATCAGCTTTAGGATATACAGGCTGTGATCCAAGCTATCCAGAA 395

Qy 63 sSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluG 83  
Db 396 ATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGAATCTGAAGTTGCTATATCTGAGGA 455

Qy 83 uLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnSerThrIleLysGluLe 103  
Db 456 GTAGTTTCAGAACTACAGTAATTCCTGCTCTGCTGATGTGAACGCAGATAAGGAAC 515

Qy 103 uArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTr 123  
Db 516 CAGGCGCTCTCTTCTTAGTGTATGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTTGATGTG 575

Qy 123 pValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu 143  
Db 576 GGTATTTACCTATGTTGGTGGCTTGTATTAATGAGCGCATCAGGCAACAGATCATTCATC 634

Qy 143 eSerLeuPheSerIleProValIleTyrGluArgHisGlnVal-GlnIleAspHisTyrL 163  
Db 635 TTCACTCTTCAGTGTCTCTGTTATTTATGAACGCGCATCAGGCAACAGATCATTCATC 694

Qy 163 euGlyLeuAlaAsnLysSerValLysAspAlaMetAlaLysIleGlnAlaLysIleProG 183  
Db 695 TAGGACTTGCATAAAGAAATGTCAAAGATGCTATGGGTAAATCAAGCAAAAAATCCCTG 754

Qy 183 lyLeuLysArgLysAla 188  
Db 755 GATTGAAGCGCAAAAGC 771

RESULT 98  
AW230936



**LOCUS** AW230936 543 bp mRNA linear EST 10-DEC-1999  
**DEFINITION** uc069f05.y1 NCI CGAP Mam1 Mus musculus cDNA clone IMAGE:2647809 5' similar to TR:O94962 O94962 KIAA0886 PROTEIN. ;, mRNA sequence.  
**ACCESSION** AW230936  
**VERSION** AW230936.1 GI:6560232  
**KEYWORDS** EST.  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus  
**REFERENCE** 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
**AUTHORS** NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
**TITLE** National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
**JOURNAL** Unpublished (1997)  
**COMMENT** Other ESTs: uc069f05.x1  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Gilbert Smith, Ph.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html  
**MG1:1028261**  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 437.  
**FEATURES** Location/Qualifiers  
 source 1..543  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:2647809"  
 /tissue\_type="tumor, biopsy sample"  
 /dev\_stage="3 months, virgin"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI-CGAP Mam1"  
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sali; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"  
**ORIGIN**  
 Alignment Scores:  
 Pred. No.: 1.56e-91 Length: 543  
 Score: 825.00 Matches: 170  
 Percent Similarity: 98.28% Conservative: 1  
 Best Local Similarity: 97.70% Mismatches: 3  
 Query Match: 89.19% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-830-972-2\_COPY\_975\_1163 (1-189) x AW230936 (1-543)  
 Qy 16 ValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSer 35  
 Db 22 GTGGTGTGTGGTGGCAGCTATTCTCTGCTGCTGACAGTTCAGATTGTCAGT 81  
 Qy 36 ValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLys 55  
 Db 82 GTACGGCTACATTCGCTGGCCCTGCTCTCTGACTATCAGCTTAGATATATAG 141  
 Qy 56 GlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGlu 75  
 Db 142 GGTGTGATCCAAAGTATCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATTTGAA 201  
 Qy 76 SerGluValAlaIleSerGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHis 95  
 Db 202 TCTGAAGTTGCATATCAGAGGAATGCTGTTGAGAAATATAGTATCTCTCTGTCAT 261  
 Qy 96 ValAsnSerThrIleLysGluLeuArgLeuPheLeuValAspLeuValAspSer 115

Db 262 GTGAACAGCACTAAAGAATTGAGCGCTCTCTTCTTAGTTGATGATTTAGTTGATTC 321  
 Qy 116 LeuLysPheAlaValLeuMetTrrValPheThrTyrValGlyAlaLeuPheAsnGlyLeu 135  
 Db 322 CTGAAGTTTCAGTGTGGTATTTACTTACGTTGGTCTTGTTCATATGGTTTG 381  
 Qy 136 ThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerIleProValIleTyrGluArgHis 155  
 Db 382 ACACACTACTGATTTAGCTCTGATCTCACTCTTCAGTATTTCTGTATATATGAACGGAT 441  
 Qy 156 GlnValGlnIleAepHisTyrLeuGlyLeuAlaAsnLysSerValLysAspAlaMetAla 175  
 Db 442 CAGCGCAGATAGATCATTTATCTAGGACTTGCACAAAGAGCGTTAAGGATGCATGCGC 501  
 Qy 176 LysIleGlnAlaLysIleProGlyLeuLysArgLysAlaAsp 189  
 Db 502 AAAATCCCAAGCANAATCCCTGGATTGAAGCGCANAGCAGAA 543  
**RESULT 99**  
**LOCUS** BI548612 815 bp mRNA linear EST 05-SEP-2001  
**DEFINITION** 603189563F1 NIH\_MGC\_95 Homo sapiens cDNA clone IMAGE:5261007 5', mRNA sequence.  
**ACCESSION** BI548612  
**VERSION** BI548612.1 GI:15435924  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
**REFERENCE** 1 (bases 1 to 815)  
**AUTHORS** NIH-MGC http://mgc.nci.nih.gov/  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
 High quality sequence stop: 757.  
**FEATURES** Location/Qualifiers  
 source 1..815  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5261007"  
 /tissue\_type="hippocampus"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH\_MGC 95"  
 /note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: Sali-XhoI (gtcag); Oligo-dt primed using primer 5'-TTTTTTTTTTTNN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH\_MGC Library."  
**ORIGIN**  
 Alignment Scores:  
 Pred. No.: 5.66e-91 Length: 815  
 Score: 822.50 Matches: 178  
 Percent Similarity: 95.26% Conservative: 3  
 Best Local Similarity: 93.68% Mismatches: 7

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Query Match:      88.92%      Indels:      3
DB:               4           Gaps:       0

US-09-830-972-2_COPY_975_1163 (1-189) x B1548612 (1-815)

QY 2 ValValAspLeuLeuTy-TpArgAspIleTySerThrGlyValValPheGlyAlaSer 21
DB 169 GTTGTGACCTCTCTGCTGAGAGACATTAGAAGACTGGAGTGGTGTGGTCCAGC 228
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyRileAla 41
DB 229 CTATTCTCTGCTTTCATTGACACTATTGACATTGTGAGCGTAACAGCCTACATTGCC 288
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTySerGlyValIleGlnAlaIle 61
DB 289 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATATCAAGGGTGTGATCCAGCTATC 348
QY 62 GlnTySerAspGluGlyHisProPheArgAlaTyRLeuGluSerGluValAlaIleSer 81
DB 349 CAGAATCAGATGAAGGCCACCGATTACGGCATATCTGGAACTCTGAAAGTTGCTATATCT 408
QY 82 GluGluLeuValGlnTySerAsnSerAlaLeuGlyHisValAsnSerThrIleLys 101
DB 409 GAGGAGTTGTTTCAAGTACAGTAATCTGCTCTTGGTCACTGTAAGTCAAGATAAG 468
QY 102 GluLeuArgArgLeuPheLeuValAsp-AspLeuValAspSerLeuLysPheAlaValLe 121
DB 469 GAACTCAGCGCGCTCTCTTCTAGTACATGATTAGTATTCTCTGAAAGTTTGCAGTGT 528
QY 121 uMetTrpValPheThrTyRValGlyValAlaPheAsnGlyLeuThrLeuLeuAl 141
DB 529 GATGGGGTATTACATGTTGGTGGCTTGTATTGATGCTGACACTACTGATTTTGGC 588
QY 141 aLeuIleSerLeuPheSer-IleProValIleTyRArgHisGlnValGlnIleAspH 161
DB 589 TCTCATTTCACTCTTCAGCTGTTCTGTTATTATTAACGGCATCAGGCACAGATAGATC 648
QY 161 iTyRLeuGlyLeuAlaSerValLysAspAlaMetAlaLysIleGlnAlaLysI 181
DB 649 ATTATCTAAGACTGC--AATAAGATGTTAAGGATGCTATGGTAAAAATCCAAGCAAAA 706
QY 181 leProGlyLeuLysArgLysAlaAsp 189
DB 707 TCCCTGGATTGAAGCGCAAGTTGAA 732

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## RESULT 100

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AV702687      719 bp      mRNA      linear      EST 08-OCT-2000
LOCUS      AV702687 ADB Homo sapiens cDNA clone ADBBB01 5', mRNA sequence.
DEFINITION      AV702687 ADB Homo sapiens cDNA clone ADBBB01 5', mRNA sequence.
ACCESSION      AV702687
VERSION      AV702687.1 GI:10719017
KEYWORDS      EST.
SOURCE      Homo sapiens (human)

```

## ORGANISM

```

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 719)
Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G.,
Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z.,
Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S.,
Zhong, M., Lu, G., Hu, R., Chen, J., Chen, Z. and Han, Z.
Homo sapiens cDNA ADB clones

```

## REFERENCE

```

AUTHORS      Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

```

## FEATURES

```

1..719
Location/Qualifiers
source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ADBBB01"
/tissue_type="Adrenal gland"
/dev stage="Adult"
/lab_host="SOLR"
/clone_lib="ADB"
/Note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

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## ORIGIN

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Alignment Scores:      7.26e-91      Length:      719
Score:      821.00      Matches:      171
Percent Similarity:      96.67%      Conservative:      3
Best Local Similarity:      95.00%      Mismatches:      5
Query Match:      88.76%      Indels:      1
DB:      1      Gaps:      0

US-09-830-972-2_COPY_975_1163 (1-189) x AV702687 (1-719)

QY 11 IleTySerThrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrVal 30
DB 1 ATTAAGAGACTGGAGTGGTGTGGTGCCAGCCTATTCTGCTGCTTTCATTGACAGTA 60
QY 31 PheSerIleValSerValThrAlaTyRileAlaLeuAlaLeuLeuSerValThrIleSer 50
DB 61 TTCAGCATTTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTGTGACCATCAGC 120
QY 51 PheArgIleTyRLeuGlyValIleGlnAlaIleGlnTySerAspGluGlyHisProPhe 70
DB 121 TTTAGGATATCAAGGGTGTGATCCAGCTATCCAGAAATCAGATGAAGGCCACCATTC 180
QY 71 ArgAlaTyRLeuGluSerGluValAlaIleSerGluGluLeuValGlnTySerAsn 90
DB 181 AGGCAATATCTGGAATCTGAAAGTTGCTATATCTGAGGAGTTGGTTTCAGAGTACAGTAAT 240
QY 91 SerAlaLeuGlyHisValAsnSerThrIleLysGlnLeuArgLeuPheLeuValAsp 110
DB 241 TCTGCTCTTGGTCACTGAACTGCACGCAATAAGGAACCTCAGCGCGCTCTTCTTAGTTGAT 300
QY 111 AspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyRValGlyVala 130
DB 301 GATTTAGTTGATCTCTGAAAGTTTGCAGTGTGATGGGTATTTACCTATGTTGGTGCC 360
QY 131 LeuPheAsnGlyLeuThrLeuLeuAlaLeuIleSerLeuPheSerIleProVal 150
DB 361 TTGTTTAATGCTCTGACACTACTGATTTTGGCTCTCTCATTTTCAGTGTTCCTGTT 420
QY 151 IleTyRLeuArgHisGlnValGlnIleAspHisTyRLeuGlyLeuAlaAsnLysSerVal 170
DB 421 ATTTATGAACGGCATCAGGCACAGATAGATCATTTATCTAGGACTTGGCAATAAGAAATGTT 480
QY 171 LysAspAlaMetAlaLysIleGlnAlaLysIlePro-GlyLeuLysArgLysAlaAsp 189
DB 481 AAAGATGCTATGGCTTAANATCCAGCAAAAAAATCTTGGATTGAGGCCANAGCTGAA 538

```

Search completed: June 19, 2005, 10:16:37  
Job time : 2588 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 12:31:51 ; Search time 170.11 Seconds  
(without alignments)  
2678.292 Million cell updates/sec

Title: US-09-830-972-29

Perfect score: 5923

Sequence: 1 MEDLDQSLVSSSDSPRPQ.....VKDAMAKIQKIPGLKRAE 1178

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_16Dec04.\*  
1: geneseqp1980s.\*  
2: geneseqp1990s.\*  
3: geneseqp2000s.\*  
4: geneseqp2001s.\*  
5: geneseqp2002s.\*  
6: geneseqp2003as.\*  
7: geneseqp2003bs.\*  
8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5882	99.3	1178	3	AAY71311 Human neu
2	5815	98.2	1192	4	AAU04591 Human Nog
3	5815	98.2	1192	5	ABP68600 Human pan
4	5815	98.2	1192	6	ABR59667 Human Nog
5	5815	98.2	1192	8	ADP45551 Human MAG
6	5810	98.1	1192	3	AAY56967 Human MAG
7	5810	98.1	1192	4	AAAB82349 Human NOG
8	5810	98.1	1192	5	ASG30938 Human NOG
9	5810	98.1	1192	5	ABR81078 Human neu
10	5810	98.1	1192	8	ADP67234 Human NOG
11	5810	98.1	1192	8	ADR13966 Human NOG
12	5808	98.1	1192	8	ADO08103 Human pol
13	5794	97.8	1192	7	ADK67502 Human RTN
14	5758	97.2	1192	8	ADO26400 Human tru
15	5526	93.3	1246	4	AAU33228 Novel hum
16	4560	77.0	983	6	ABU11573 Human MDD
17	4400	74.3	893	3	AAAY95012 Human sec
18	4296	72.5	1163	3	AAAY71310 Rat neu
19	4296	72.5	1163	5	ABB81074 Rat neuro
20	4296	72.5	1163	8	ADO26399 Rat trunc
21	4296	72.5	1163	8	ADP45572 Rat NOGOA
22	4294	72.5	1162	3	AAAY71557 Rat NOGO
23	4289	72.4	1162	8	ADT89537 Mus muscu
24	4286	72.4	1163	3	AAAY71384 Alternati
25	4277	72.2	1163	8	ADO08105 Mouse pol

26	3931	66.4	819	8	ADP45553 Human NiG
27	3388.5	57.2	974	3	AAAY71560 Rat NOGO
28	3146.5	53.1	642	2	AAW58383 Human sec
29	3146.5	53.1	642	4	ABR90682 Human BGL
30	2715	45.8	803	3	AAAY71562 Rat NOGO
31	2593.5	43.8	798	8	ADO26414 Rat trunc
32	2529.5	42.7	737	3	AAAY71386 Rat NOGO
33	2487.5	42.0	746	3	AAAY71391 Rat NOGO
34	2457	41.5	736	3	AAAY71398 Rat NOGO
35	2449.5	41.4	732	3	AAAY71399 Rat NOGO
36	2425.5	41.0	739	8	ADO26415 Rat trunc
37	2405.5	40.6	695	3	AAAY71387 Rat NOGO
38	2344.5	39.6	684	3	AAAY71394 Rat NOGO
39	1948.5	32.9	552	3	AAAY71388 Rat NOGO
40	1743	29.4	502	3	AAAY71396 Rat NOGO
41	1634.5	27.6	475	3	AAAY71389 Rat NOGO
42	1586.5	26.4	403	3	AAAY71563 Rat NOGO
43	1552.5	26.2	457	3	AAAY71392 Rat NOGO
44	1495.5	25.2	373	3	AAAY53624 A bone ma
45	1495.5	25.2	373	3	AAAY56969 Human MAG

## ALIGNMENTS

RESULT 1

AAAY71311  
ID AAY71311 standard; protein; 1178 AA.

XX AC

AAAY71311;

DT 02-NOV-2000 (first entry)

DE Human neurite growth inhibitor Nogo.

XX Human; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;

KW central nervous system; neoplastic disease; antiproliferative; glioma;

KW antisense gene therapy; neuroblastoma; menigioma; retinoblastoma;

KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;

KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;

KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;

KW structural plasticity; screening.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 187 /label= Unknown

FT Misc-difference 188 /label= Unknown

FT Misc-difference 189 /label= Unknown

FT Misc-difference 190 /label= Unknown

FT Misc-difference 221 /label= Unknown

FT Misc-difference 328 /label= Unknown

FT Misc-difference 477 /label= Unknown

FT Region 977..1012 /label= Unknown

FT Region 994..1174 /note= "Region specifically described in claim 16"

FT Region 1079..1114 /note= "Region specifically described in claim 16"

FT Region 1079..1114 /note= "Region specifically described in claim 16"

FN WO200031235-A2.

XX 02-JUN-2000.

XX 05-NOV-1999; 99WO-US026160.

PF

XX



XX	Key	Location/Qualifiers	Db	1054..1119	AGLSAAVPPTAPAAAGAPLMDFGNDVFPPAPRGPLPAAPPVAPERQPSWDSPVSSVTPAP	120	
FT	Domain	/label= Luminal extracellular domain	Qy	/note= "This sequence is specifically claimed"	SPLSAAAIVSPSKLPEDDEPPARPPPPASVSPQAEVWTPPAPAPAAPSTPAPAKRG	180	
FT	Peptide	/note= "This sequence is specifically claimed"	Db	/label= Pep1	SPLSAAAIVSPSKLPEDDEPPARPPPPASVSPQAEVWTPPAPAPAAPSTPAPAKRG	180	
FT	Peptide	/note= "Receptor binding inhibitory peptide. This sequence is specifically claimed"	Qy	/label= Pep2	SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDPFPVLLLETAASLPSTSP	240	
FT	Peptide	/note= "Receptor binding inhibitory peptide. This sequence is specifically claimed"	Db	/label= Pep3	SSGSVDETLFALPAASEPVIIRSSAENMDLKEQPGNTISAGQEDPFPVLLLETAASLPSTSP	240	
FT	Peptide	/note= "Receptor binding inhibitory peptide. This sequence is specifically claimed"	Qy	/label= Pep4	LSAASFKEHYLGNLSTVLPTGTLQENVSEASKEVSEKAKTLLIDRLDTFSELEYSEM	286	
FT	Peptide	/note= "Receptor binding inhibitory peptide. This sequence is specifically claimed"	Db	/label= Pep5	LSAASFKEHYLGNLSTVLPTGTLQENVSEASKEVSEKAKTLLIDRLDTFSELEYSEM	300	
FT	Peptide	/note= "Receptor binding inhibitory peptide. This sequence is specifically claimed"	Qy	/label= Pep6	GSSFSVSPKASAVIVANPREEIIIVKNKDEEKLVSNNILHQOELPTALTTLVKEDDEVV	346	
FT	Peptide	/note= "Receptor binding inhibitory peptide. This sequence is specifically claimed"	Db	/label= Pep7	GSSFSVSPKASAVIVANPREEIIIVKNKDEEKLVSNNILHQOELPTALTTLVKEDDEVV	360	
FT	Peptide	/note= "Receptor binding inhibitory peptide. This sequence is specifically claimed"	Qy	/label= Pep8	SSEKADSFNEKRVAVEAPMRBEYADFPKPERVWEVKDSKEDSDMLAAGKIESNLESKV	406	
FT	Peptide	/note= "Receptor binding inhibitory peptide. This sequence is specifically claimed"	Db	/label= Pep9	SSEKADSFNEKRVAVEAPMRBEYADFPKPERVWEVKDSKEDSDMLAAGKIESNLESKV	420	
FT	Peptide	/note= "Receptor binding inhibitory peptide. This sequence is specifically claimed"	Qy	/label= Pep10	DKKCFADSLQTNHEKDSSESSNDTSPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466	
FT	Peptide	/note= "Receptor binding inhibitory peptide. This sequence is specifically claimed"	Db	/label= Pep11	DKKCFADSLQTNHEKDSSESSNDTSPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	480	
XX	WO200151520-A2.		Qy		PLLEDPTSENKTDKKEI EKKKAQIVTEKNTSTKTSNPPFFVAAQDSEDTVVTTDNLTKYTE	526	
XX	19-JUL-2001.		Db		PLLEDPTSENKTDKKEI EKKKAQIVTEKNTSTKTSNPPFFVAAQDSEDTVVTTDNLTKYTE	540	
XX	12-JAN-2001; 2001WO-US001041.		Qy		EVVANMPEGLTPDLVQACESELNEVTGKIAYETKMDLVQTSSEVMQESLYPAAQICPSF	586	
XX	12-JAN-2000; 2000US-0175707P.		Db		EVVANMPEGLTPDLVQACESELNEVTGKIAYETKMDLVQTSSEVMQESLYPAAQICPSF	600	
PR	26-MAY-2000; 2000US-0207366P.		Qy		ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE	646	
PR	29-SEP-2000; 2000US-0236378P.		Db		ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE	660	
XX	(UYUA ) UNIV YALE.		Qy		EAMSVSL-KVSGIKKEIKPENINAAQOETAPYISACDLIKETKLSAEAPDFSDYSE	705	
XX	Strittmatter SM;		Db		EAMSVSL-KVSGIKKEIKPENINAAQOETAPYISACDLIKETKLSAEAPDFSDYSE	720	
XX	WPI; 2001-442138/47.		Qy		MAKVEQVPDHSSELVEDSSPDSEVDLFSDDSIIPDVQKQDETVMVKESLETETSFESMI	765	
DR	N-PSDB; AAS09453.		Db		MAKVEQVPDHSSELVEDSSPDSEVDLFSDDSIIPDVQKQDETVMVKESLETETSFESMI	780	
XX	Novel Nogo receptor protein useful for identifying modulator of Nogo protein or Nogo receptor protein, which is useful for treating central nervous system disorders.		Qy		EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLOWHEELSTAVY	825	
XX	Example 1; Page 101-104; 109pp; English.		Db		EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLOWHEELSTAVY	840	
XX	The sequence is the human Nogo protein, a 250kDa myelin-associated axon growth inhibitor. The invention relates to the use of the nogo receptor, nogo protein, their nucleic acids, vectors expressing them and antibodies against them, to isolate agents which block nogo receptor mediated axonal growth. The agent is useful for treating a central nervous system disorder which is a result of cranial or cerebral trauma, spinal cord injury, stroke or a demyelinating disease selected from multiple sclerosis, monophasis demyelination, encephalomyelitis, multifocal leukoencephalopathy, panencephalitis, Marchiafava-Bignami disease, pontine myelinolysis, adrenoleukodystrophy, Pelizaeus-Merzbacher disease, Spongy degeneration, Alexander's disease, Canavan's disease, metachromatic leukodystrophy, viral infection and Krabbe's disease		Qy		SNDDLFIKSKAQIRETETFSDDSPIIIDEFPPTLISSTKTSDFSKLAREYTDLEVSHKSEI	885	
CC			Db		SNDDLFIKSKAQIRETETFSDDSPIIIDEFPPTLISSTKTSDFSKLAREYTDLEVSHKSEI	900	
CC			Qy		ANAPDAGSIPCTPHELPHDLISLKNIQPKVEEKISFSDDFSNGKSATSQVLLLPDVSALGH	945	
CC			Db		ANAPDAGSIPCTPHELPHDLISLKNIQPKVEEKISFSDDFSNGKSATSQVLLLPDVSALGH	959	
CC			Qy		TOABIESIVKPKVLEKAEKCLPSDTEKEDRSPSAIFSADLKGTSVVDLLYWRDIKKTGV	1005	
CC			Db		TOABIESIVKPKVLEKAEKCLPSDTEKEDRSPSAIFSADLKGTSVVDLLYWRDIKKTGV	1019	
XX	Sequence 1192 AA;		Qy		VFGASLFLILSLTVFSIVSVTAIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLES	1065	
XX	Query Match 98.2%; Score 5815; DB 4; Length 1192;		Db		VFGASLFLILSLTVFSIVSVTAIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLES	1079	
XX	Best Local Similarity 97.2%; Pred. No. 2.8e-293;		Qy		EVAISEELVQKYSNSALGHVNCITIKELRLFLVDDLVDSLKFAVLMMVFTVYGALFNGLT	1125	
XX	Matches 1160; Conservative 4; Mismatches 13; Indels 16; Gaps 3;		Db		EVAISEELVQKYSNSALGHVNCITIKELRLFLVDDLVDSLKFAVLMMVFTVYGALFNGLT	1139	
Qy	1 MEDLDQSPVSSSDSPRPQAFKQVFRPEDEDEDEDEDEDEDEDEDEDEDELEVLKPKA 60		Qy		LLTALILSIFSVPVIYERHQAIQIDHYLGLANKVNDAMAKIQAKIPGLKRAE 1178		
Db	1 MEDLDQSPVSSSDSPRPQAFKQVFRPEDEDEDEDEDEDEDEDEDEDEDELEVLKPKA 60		Qy				
Qy	61 AGLSAAVPPTAPAAAGAPLMDFGNDVFPPAPRGPLPAAPPVAPERQPSWDSPVSSVTPAP 120		Qy				

DB 1140 LILALISLFSVPVIERHOAQIDHYGLANKVNDAMAKIOAKIPGLKRAE 1192

RESULT 3  
ID ABP68600  
XX ABP68600 standard; protein; 1192 AA.  
AC ABP68600;  
XX  
DT 14-JAN-2003 (first entry)  
XX  
DE Human pancreatic cancer expressed protein SEQ ID NO 71.  
XX  
KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;  
KW cytostatic; tumour.  
XX  
OS Homo sapiens.  
XX  
PN WO200260317-A2.  
XX  
PD 08-AUG-2002.  
XX  
PF 30-JAN-2002; 2002WO-US002781.  
XX  
PR 30-JAN-2001; 2001US-026530SP.  
PR 31-JAN-2001; 2001US-0265682P.  
PR 09-FEB-2001; 2001US-0267568P.  
PR 21-MAR-2001; 2001US-0278651P.  
PR 28-APR-2001; 2001US-0287112P.  
PR 16-MAY-2001; 2001US-0291631P.  
PR 12-JUL-2001; 2001US-0305484P.  
PR 20-AUG-2001; 2001US-0313999P.  
PR 27-NOV-2001; 2001US-0333626P.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;  
XX WPI; 2002-627435/67.  
DR N-PSDB; ABV94680.  
XX  
PT New isolated polynucleotide and pancreatic tumor polypeptides, useful for  
PT diagnosing, preventing and/or treating cancer, particularly pancreatic  
PT cancer.  
XX  
PS Claim 2; SEQ ID NO 71; 300pp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated polynucleotide (I) comprising: (a)  
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)  
CC complements of (a); (c) sequences consisting of at least 20 contiguous  
CC residues of (a); (d) sequences that hybridize to (a), under moderately  
CC stringent conditions; (e) sequences having at least 75% or 90% identity  
CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-  
CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer  
CC in a patient and compositions comprising polypeptides, polynucleotides,  
CC antibodies, fusion proteins, T cell populations and antigen presenting  
CC cells expressing the polypeptide are useful in treating pancreatic cancer  
CC and stimulating an immune response. The polynucleotides can be used as  
CC probes or primers for nucleic acid hybridisation, in the design and  
CC preparation of ribozyme molecules for inhibiting expression of the tumour  
CC polypeptides and proteins in the tumour cells, in vaccines and for gene  
CC therapy. Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1192 AA;

Query Match 98.2%; Score 5815; DB 5; Length 1192;  
Best Local Similarity 97.2%; Pred. No. 2.8e-293;  
Matches 1160; Conservative 4; Mismatches 13; Indels 16; Gaps 3;

QY 1 MEDLQSLVSSSDSPRPQPAFKYQFVREPEDEDEDEDEDEDEDELEEVLERKPA 60  
|||||  
61 AGLSAAVPVPTAPAGAPLMDFGNDVFPAPRGPLPAAAPPVAPERQPSWDPSVSTVPAP 120  
|||||  
61 AGLSAAVPVPTAPAGAPLMDFGNDVFPAPRGPLPAAAPPVAPERQPSWDPSVSTVPAP 120  
|||||  
121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAPPPSTPAAPKRG 180  
|||||  
121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAPPPSTPAAPKRG 180  
|||||  
181 SSGA-----VVXXXKIMDLKEQPGNTISAGQEDPPSPLLETAASPSLSP 226  
|||||  
181 SSGVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDPPSPLLETAASPSLSP 240  
|||||  
227 LSAASFKEHYLGNLSTVLPTTEGLQENVSSEASKEVSEKAKTLIDRLDTFFSELEYSEM 286  
|||||  
241 LSAASFKEHYLGNLSTVLPTTEGLQENVSSEASKEVSEKAKTLIDRLDTFFSELEYSEM 300  
|||||  
287 GSSFSVSPKASAVIVANPREIIVKNDKEEKLVSNNILHXQOELPTALTKLKEDEVV 346  
|||||  
301 GSSFSVSPKASAVIVANPREIIVKNDKEEKLVSNNILHXQOELPTALTKLKEDEVV 360  
|||||  
347 SSEKAKDSFNKRVAVEAPMREYADFKPFERVMEVKDSKEDSDMLAAGGKIESNLEKV 406  
|||||  
361 SSEKAKDSFNKRVAVEAPMREYADFKPFERVMEVKDSKEDSDMLAAGGKIESNLEKV 420  
|||||  
407 DKCFADSLQTNHEKDSSESSNDTSPSTPEGIKDRSGAYITCAPFNPAAATESIATNIF 466  
|||||  
421 DKCFADSLQTNHEKDSSESSNDTSPSTPEGIKDRSGAYITCAPFNPAAATESIATNIF 480  
|||||  
467 PLLDPTSENXTDEKKIEEKAQIVTEKNTSTKTNPPFVAAQSDSETDYVTTDLTKYTE 526  
|||||  
481 PLLDPTSENXTDEKKIEEKAQIVTEKNTSTKTNPPFVAAQSDSETDYVTTDLTKYTE 540  
|||||  
527 EVWANMPEGLTPDLVQACESELSNEVTGKTIAVETKMDLVOTSEVMQSLYPAAQLCPSP 586  
|||||  
541 EVWANMPEGLTPDLVQACESELSNEVTGKTIAVETKMDLVOTSEVMQSLYPAAQLCPSP 600  
|||||  
587 ESEATPSVLPDIMEAPLNSAVPSAGASVIOQSSSPLEASSVNYSEIKHEPENPPPYE 646  
|||||  
601 ESEATPSVLPDIMEAPLNSAVPSAGASVIOQSSSPLEASSVNYSEIKHEPENPPPYE 660  
|||||  
647 EAMSVSL-KVSGIKEEKEPENINAAQOETAPYISITACDLIKETKLSAEAPAPDSYSE 705  
|||||  
661 EAMSVSLKVSGIKEEKEPENINAAQOETAPYISITACDLIKETKLSAEAPAPDSYSE 720  
|||||  
706 MAKVEQPPVDRHSELVEDSSPDSEPVDLFSDDSIPDVPOKQDETVMVKESLTETSFESMI 765  
|||||  
721 MAKVEQPPVDRHSELVEDSSPDSEPVDLFSDDSIPDVPOKQDETVMVKESLTETSFESMI 780  
|||||  
766 EYENKEKLSALPPPEGKPYLESFSLKSLDNTKDTLLPDEVSTLSKKEKIPLOMEELSTAVY 825  
|||||  
781 EYENKEKLSALPPPEGKPYLESFSLKSLDNTKDTLLPDEVSTLSKKEKIPLOMEELSTAVY 840  
|||||  
826 SNDDLFTSKAQIETETFSDDSPDPIIIDEPTLISSTKDSFSLAREYTDLEVSHKSEI 885  
|||||  
841 SNDDLFTSKAQIETETFSDDSPDPIIIDEPTLISSTKDSFSLAREYTDLEVSHKSEI 900  
|||||  
886 ANAPDGAGSLPCTELPHDLSLKNQPKVVEKISFSDDFSKNGSATSKVLLLPDVSALGH 945  
|||||  
901 ANAPDGAGSLPCTELPHDLSLKNQPKVVEKISFSDDFSKNGSATSKVLLLPDVSALGH 959  
|||||  
946 TOABIESIVKPKVLEKAEKKLPDSTKEKDRSPSAISADLGKTSVVDLLIWRDIKKTGV 1005  
|||||  
960 TOABIESIVKPKVLEKAEKKLPDSTKEKDRSPSAISADLGKTSVVDLLIWRDIKKTGV 1019  
|||||  
1006 VFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAKSDEGHPFRAYLES 1065  
|||||  
1020 VFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAKSDEGHPFRAYLES 1079  
|||||  
1066 EVAISEELVQKYSNLSALGHVNCCTIKELRRLFLVDLVDLSKFAVLMWVFTYVGLFNGLT 1125  
|||||  
1080 EVAISEELVQKYSNLSALGHVNCCTIKELRRLFLVDLVDLSKFAVLMWVFTYVGLFNGLT 1139  
|||||

QY 1126 LILALISLFSVPVIERHQAIIDHYLGANKVNDAMAKIQAKIPGLKRAE 1178  
 |||||  
 Db 1140 LILALISLFSVPVIERHQAIIDHYLGANKVNDAMAKIQAKIPGLKRAE 1192

## RESULT 4

ABR59667  
 ID ABR59667 standard; protein; 1192 AA.

XX ABR59667;

XX 22-JUL-2003 (first entry)

XX Human NogoA protein.

XX Human; Nogo receptor; Ngr; CTS domain; neuroprotective; gene therapy;  
 KW axonal growth; central nervous system; CNS; Nogo; spinal cord injury;  
 KW cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;  
 KW demyelinating disease; multiple sclerosis; monophasic demyelination;  
 KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis.

XX Homo sapiens.

XX WO2003031462-A2.

XX 17-APR-2003.

XX 04-OCT-2002; 2002WO-US0322007.

XX 06-OCT-2001; 2001US-00972599.

XX (UYVA ) UNIV YALE.

XX Strittmatter SM;

XX WPI; 2003-393433/37.

XX N-PSDB; ACC81048.

XX New human Nogo receptor polypeptides and nucleic acids, useful for  
 PT decreasing inhibition of axonal growth by a central nervous system  
 PT neuron, or in treating central nervous system disease, disorder or  
 PT injury, e.g. spinal cord injury.

XX Disclosure; Page 131-135; 148pp; English.

CC The invention relates to a novel nucleic acid encoding a polypeptide  
 CC comprising amino acid residues 27-309 of a 473 amino acid sequence (Pl,  
 CC human Nogo receptor (Ngr) NTLRRCT domain), or residues 27-309 of Pl with  
 CC 1-20 conservative amino acid substitutions, and less than a complete CTS  
 CC domain, provided that a partial CTS domain, if present, consists of no  
 CC more than the first 39 consecutive residues. The nucleic acid of the  
 CC invention has neuroprotective activity. The polynucleotide may have a use  
 CC in gene therapy. The nucleic acid is useful for decreasing inhibition of  
 CC axonal growth by a central nervous system (CNS) neuron. The Ngr  
 CC polypeptide or an agent inhibits the binding of Nogo to Ngr or Ngr-  
 CC dependent signal transduction in the central nervous system neuron may be  
 CC used in treating central nervous system disease, disorder or injury, e.g.  
 CC spinal cord injury. Expression of an Ngr protein may be associated with  
 CC inhibition of axonal regeneration following cranial, cerebral or spinal  
 CC trauma, stroke or a demyelinating disease, such as multiple sclerosis,  
 CC monophasic demyelination, encephalomyelitis, multifocal  
 CC leukoencephalopathy, panencephalitis, or Krabbe's disease. The present  
 CC sequence is used in the exemplification of the invention

XX Sequence 1192 AA;

Query Match

Best Local Similarity 98.2%; Score 5815; DB 6; Length 1192;

Matches 1160; Conservative 97.2%; Pred. No. 2.8e-293;

Mismatches 13; Indels 16; Gaps 3;

QY 1 MEDLQSPLVSSSDSPRPQPAFKYQFVREPEDEEEDEDELEEVLERKPA 60

Db 1 MEDLQSPLVSSSDSPRPQPAFKYQFVREPEDEEEDEDELEEVLERKPA 60  
 QY 61 AGLSAAVPPTAPAAAGAPLMDFGNDVPPAPRGPLPAAAPPVAPERQSPWDSPVSVSTVPAP 120  
 Db 61 AGLSAAVPPTAPAAAGAPLMDFGNDVPPAPRGPLPAAAPPVAPERQSPWDSPVSVSTVPAP 120  
 QY 121 SPLSAAAAPSCKLPEDDEPPAPPPPPASVSPQAEVPTWTPAPAPAAPSTPAAPKRRG 180  
 Db 121 SPLSAAAAPSCKLPEDDEPPAPPPPPASVSPQAEVPTWTPAPAPAAPSTPAAPKRRG 180  
 QY 181 SSGA-----VVXXYKIMDLKQPGNTTISAGQEDPSPVLTAAASPSLS 226  
 Db 181 SSGVDETFLFALPAASEPVTIRSSAENMDLKEQPGNTTISAGQEDPSPVLTAAASPSLS 240  
 QY 227 LSAASFKEHYGLNLTSLVLTPTGTLQENVSSASKEVSEKAKTLLIDRLTTFSELEYSEM 286  
 Db 241 LSAASFKEHYGLNLTSLVLTPTGTLQENVSSASKEVSEKAKTLLIDRLTTFSELEYSEM 300  
 QY 287 GSSFVSVPKASAVIVANPREEIIIVKNKDEBEKLVSNILHXQQLPTALTCLKVKEDEV 346  
 Db 301 GSSFVSVPKASAVIVANPREEIIIVKNKDEBEKLVSNILHXQQLPTALTCLKVKEDEV 360  
 QY 347 SSEKAKOSFNEKRVAVAPMRREYADFKPFRVWEVKDSKEDSDMLAAGGKIESLSEKV 406  
 Db 361 SSEKAKOSFNEKRVAVAPMRREYADFKPFRVWEVKDSKEDSDMLAAGGKIESLSEKV 420  
 QY 407 DKCFCADSLQTNHEKDSSENDDTSPSTPEGIKDRSGAVITCAPFNPAATESIATNIF 466  
 Db 421 DKCFCADSLQTNHEKDSSENDDTSPSTPEGIKDRSGAVITCAPFNPAATESIATNIF 480  
 QY 467 PLEDDPTSENKTDKKEIEKKAQIVTEKNTSTKTNPPFVAAQDSEDTYVTTDNLTKVTE 526  
 Db 481 PLLGDPTSENKTDKKEIEKKAQIVTEKNTSTKTNPPFVAAQDSEDTYVTTDNLTKVTE 540  
 QY 527 EVVANMPGLTPDLVQACESELNEVTGTKIAYETKMDLVQTSVMQESLYPAAQLCPSP 586  
 Db 541 EVVANMPGLTPDLVQACESELNEVTGTKIAYETKMDLVQTSVMQESLYPAAQLCPSP 600  
 QY 587 EESATSPVLPDIWMEAPLNSAVPSAGASVIOQSSSPLEASSVNYESIKEPENPPPYE 646  
 Db 601 EESATSPVLPDIWMEAPLNSAVPSAGASVIOQSSSPLEASSVNYESIKEPENPPPYE 660  
 QY 647 EAMSVSL-KVSGIKKEIKPENINAALQETEPYISIACDLIKETKLSAEPAPOFSDYSE 705  
 Db 661 EAMSVSLKVKVSGIKKEIKPENINAALQETEPYISIACDLIKETKLSAEPAPOFSDYSE 720  
 QY 706 MAKVEQVPVPHSELVSSSDSPSEVDLFSDDSIIPDVQKQDETVMVKESLTETSFESMI 765  
 Db 721 MAKVEQVPVPHSELVSSSDSPSEVDLFSDDSIIPDVQKQDETVMVKESLTETSFESMI 780  
 QY 766 EYENKEKLSALPPREGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLOMEELSTAVY 825  
 Db 781 EYENKEKLSALPPREGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLOMEELSTAVY 840  
 QY 826 SNDDLFIKSAQIARETETFSDDSPIIEDEPTLISKTDSFSLAREYTDLEVSHKSEI 885  
 Db 841 SNDDLFIKSAQIARETETFSDDSPIIEDEPTLISKTDSFSLAREYTDLEVSHKSEI 900  
 QY 886 ANAPDGAGSLPCTELPHDLSLKNQPKVEEKISDFDKNGSATSKVLLLPDVSALGH 945  
 Db 901 ANAPDGAGSLPCTELPHDLSLKNQPKVEEKISDFDKNGSATSKVLLLPDVSALGH 959  
 QY 946 TQAEIESIVKPKVLEKAEKKLPDTEKEDRSPAIKPSADLGKTSVVDLLYWRDIKKTGV 1005  
 Db 960 TQAEIESIVKPKVLEKAEKKLPDTEKEDRSPAIKPSADLGKTSVVDLLYWRDIKKTGV 1019  
 QY 1006 VFGASLFLLSLTAVFSIVSVTAYIALALLSVTISFRIYKGVIOIKQSDGHPFRAYLES 1065  
 Db 1020 VFGASLFLLSLTAVFSIVSVTAYIALALLSVTISFRIYKGVIOIKQSDGHPFRAYLES 1079  
 QY 1066 EVAISEELVQKYSNLSALGHVNCCTIKELRRLFLVDDLVDSLKFAVLMWVFTTVGALFNGLT 1125  
 Db 1080 EVAISEELVQKYSNLSALGHVNCCTIKELRRLFLVDDLVDSLKFAVLMWVFTTVGALFNGLT 1139





RESULT 6	Db	241	LSAASFKEHYLGNLSTVLPTEGTLQENVSEAKVSEKAKTLLIDRLDTESELEYSEM	300
AA556967	Qy	287	GSSFSVSPKASAVIVANPREBIIIVKNKDEBEKLVSNILHXQBLPTALTKLVKDEYV	346
ID AAY56967 standard; protein; 1192 AA.	Db	301	GSSFSVSPKASAVIVANPREBIIIVKNKDEBEKLVSNILHXQBLPTALTKLVKDEYV	360
AC AAY56967;	Qy	347	SSEKAKDSFNEKRVAVEAPMEEEYADPKPFRVWVVKDSKEDSDMLAAGGKTESNLSKV	406
DT 25-APR-2000 (first entry)	Db	361	SSEKAKDSFNEKRVAVEAPMEEEYADPKPFRVWVVKDSKEDSDMLAAGGKTESNLSKV	420
DE Human MAGI polypeptide.	Qy	407	DKCFADSLQTNHEKDSSESNDDTSPFSTPEGIKDRSGAYITTCAPFNPAATESIATNIF	466
XX MAGI protein; neuroendocrine-specific protein; neuropathy; human;	Db	421	DKCFADSLQTNHEKDSSESNDDTSPFSTPEGIKDRSGAYITTCAPFNPAATESIATNIF	480
KW spinal injury; neuronal degeneration; neuromuscular disorder; cancer;	Qy	467	PLLEDPTSENXTDEKKIIEKKAQIVTEKNTSTKTSNPFVAQDSEYVTTDNLTKVTE	526
KW psychiatric disorder; developmental disorder; inflammatory disorder;	Db	481	PLLEDPTSENXTDEKKIIEKKAQIVTEKNTSTKTSNPFVAQDSEYVTTDNLTKVTE	540
XX stroke; cystostatic; cerebroprotective; neuroprotective.	Qy	527	EVVANMPGLTPDLVORACESELNEVTGKTAYETKMDLVOTSEVMQSLYPAAQLCPSP	586
OS Homo sapiens.	Db	541	EVVANMPGLTPDLVORACESELNEVTGKTAYETKMDLVOTSEVMQSLYPAAQLCPSP	600
XX WO200005364-A1.	Qy	587	ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSSPLEASSVNYESI KHEPENPPPYE	646
PD 03-FEB-2000.	Db	601	ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSSPLEASSVNYESI KHEPENPPPYE	660
XX 21-JUL-1999; 99WO-CB002360.	Qy	647	EAMSVSL-KVSGIKKEIKPENINAAQETAPYISACDLIKETKLSAEPAPDSYSE	705
PR 22-JUL-1998; 98GB-00016024.	Db	661	EAMSVSL-KVSGIKKEIKPENINAAQETAPYISACDLIKETKLSAEPAPDSYSE	720
PR 19-JUL-1999; 99GB-00016898.	Qy	706	MAKVEQPVPHSELVEDSSPDPVDFSDDSIDPVPOKQDETVMVKESITETSFESMI	765
XX (SMIK ) SMITHKLINE BEECHAM PLC.	Db	721	MAKVEQPVPHSELVEDSSPDPVDFSDDSIDPVPOKQDETVMVKESITETSFESMI	780
XX Michalovich D, Printha RK;	Qy	766	EYENKEKLSALPPGGKPYLESFKLSLNDNTKDTLLPDEVSTLSKKEKIPLOMEEELSTAVY	825
PI WPI; 2000-182693/16.	Db	781	EYENKEKLSALPPGGKPYLESFKLSLNDNTKDTLLPDEVSTLSKKEKIPLOMEEELSTAVY	840
XX N-PSDB; AA256886.	Qy	826	SNDDLFIKSAQIRETETFSOSSPIEIIIDEPPTLISSKTSFSLKARYTDLVSHKSEI	885
DR Novel polypeptides related to neuroendocrine-specific proteins and	Db	841	SNDDLFIKSAQIRETETFSOSSPIEIIIDEPPTLISSKTSFSLKARYTDLVSHKSEI	900
PT polynucleotides useful for diagnosis of various diseases and for	Qy	886	ANAPDGAGSLPCTELPHDLISLKNQPKVEEKISFSDDFSKNGSATSKVLLPPDVLSALCH	945
XX treatment of cancer and neurological disorders.	Db	901	ANAPDGAGSLPCTELPHDLISLKNQPKVEEKISFSDDFSKNGSATSKVLLPPDVLSALCH	959
PS Claim 2; Page 20-21; 35pp; English.	Qy	946	TQAEIESIVKPKVLEKEAEKLPDSTEKEDRSPSAIFSAIDLGKTSVVDLLYWRDIKKTGV	1005
XX The invention relates to human MAGI protein, which is similar to	Db	960	TQAEIESIVKPKVLEKEAEKLPDSTEKEDRSPSAIFSAIDLGKTSVVDLLYWRDIKKTGV	1019
CC neuroendocrine-specific protein. The MAGI protein can be expressed by	Qy	1006	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAKSDEGHPFRAYLES	1065
CC standard recombinant methodology. The MAGI polypeptides, polynucleotides	Db	1020	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAKSDEGHPFRAYLES	1079
CC and antibodies are useful for treating diseases, including neuropathies,	Qy	1066	EVATSEELVOKYSNLSALGHVNCITKELRRLFLVDDLVDSLKFAVLMMVFTVVGALFNGLT	1125
CC spinal injury, neuronal degeneration, neuromuscular disorders,	Db	1080	EVATSEELVOKYSNLSALGHVNCITKELRRLFLVDDLVDSLKFAVLMMVFTVVGALFNGLT	1139
CC psychiatric disorders and developmental disorders, cancer, stroke and	Qy	1126	LLILALISLSFVPIYERHQAQIDHYLGLANKNVKDMAKIQAKIPGLKRAE	1178
CC inflammatory disorders. The polynucleotide is also useful for chromosome	Db	1140	LLILALISLSFVPIYERHQAQIDHYLGLANKNVKDMAKIQAKIPGLKRAE	1192
CC localization and for tissue expression studies. The present sequence	Qy	1192	standard; protein; 1192 AA.	
CC represents the human MAGI protein	Db	1192	standard; protein; 1192 AA.	
XX Sequence 1192 AA;	Qy	1192	standard; protein; 1192 AA.	
Query Match 98.1%; Score 5810; DB 3; Length 1192;	Qy	1192	standard; protein; 1192 AA.	
Best Local Similarity 97.2%; Pred. No. 5.1e-293;	Qy	1192	standard; protein; 1192 AA.	
Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;	Qy	1192	standard; protein; 1192 AA.	
Qy 1 MEDLDQSLVSSSSPPRPQAFKQYFVREPEDEEEDEDEDEDELEVLKPKA 60	Qy	1192	standard; protein; 1192 AA.	
Db 1 MEDLDQSLVSSSSPPRPQAFKQYFVREPEDEEEDEDEDEDELEVLKPKA 60	Qy	1192	standard; protein; 1192 AA.	
Qy 61 AGLSAAVPPTAPAGAPLMDFGNDVPVPPAPRGPLPAAPPVAPERQSPVSVSTVPAP 120	Qy	1192	standard; protein; 1192 AA.	
Db 61 AGLSAAVPPTAPAGAPLMDFGNDVPVPPAPRGPLPAAPPVAPERQSPVSVSTVPAP 120	Qy	1192	standard; protein; 1192 AA.	
Qy 121 SPLSAAAVSPSKLPEDDEPPAPPPPPPPASVSPQAEVWTPPPAPAPAPPSTPAAPKRRG 180	Qy	1192	standard; protein; 1192 AA.	
Db 121 SPLSAAAVSPSKLPEDDEPPAPPPPPPPASVSPQAEVWTPPPAPAPAPPSTPAAPKRRG 180	Qy	1192	standard; protein; 1192 AA.	
Qy 181 SSGA-----VVVXXXKIMDLKEQPGNTISAGQEDPVSILLETAAAXPSLSP 226	Qy	1192	standard; protein; 1192 AA.	
Db 181 SSGVDETLFALPAASEPVIRSSAEMDLKQPGNTISAGQEDPVSILLETAAAXPSLSP 240	Qy	1192	standard; protein; 1192 AA.	
Qy 227 LSAASFKEHYLGNLSTVLPTEGTLQENVSEAKVSEKAKTLLIDRLDTESELEYSEM 286	Qy	1192	standard; protein; 1192 AA.	

XX NOGO-A; human; chromosome 2p21; neuropathy; spinal injury; brain injury;  
 KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;  
 KW neuromuscular disorder; psychiatric disorder; developmental disorder;  
 KW neuroprotective; nootropic; neuroleptic; antiparkinsonian;  
 KW cerebroprotective; neuroleptic; diagnosis; therapy.  
 XX Homo sapiens.  
 OS  
 XX WO200136631-A1.  
 PN  
 XX 25-MAY-2001.  
 XX  
 XX 14-NOV-2000; 2000WO-GB004345.  
 PF  
 XX 15-NOV-1999; 99GB-00026995.  
 PR  
 XX 24-JAN-2000; 2000GB-00001550.  
 PR  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 PA  
 XX Michalovich D, Prinjha R;  
 XX  
 XX WPI; 2001-343822/36.  
 DR  
 XX N-PSDB; AAF90324.  
 DR  
 XX  
 XX New polypeptide designated NOGO-C is a splice variant of the human NOGO  
 PT gene and may be useful in the treatment of neural disorders including  
 PT Alzheimer's and Parkinson's diseases.  
 PT  
 XX Disclosure; Page 26-27; 25pp; English.  
 PS  
 XX The present sequence is that of human NOGO-A. NOGO-A is a previously  
 CC known splice variant of the human NOGO gene on chromosome 2p21. The  
 CC invention relates to a novel splice variant, NOGO-C (see AAB82348). It  
 CC provides NOGO-C polypeptides and polynucleotides, and methods for  
 CC producing such polypeptides by recombinant techniques. Also disclosed are  
 CC methods for utilizing NOGO-C polypeptides and polynucleotides in the  
 CC treatment of diseases including neuropathies, spinal injury, brain  
 CC injury, stroke, neuronal degeneration, for example Alzheimer's disease  
 CC and Parkinson's disease, neuromuscular disorders, psychiatric disorders  
 CC and developmental disorders. Also provided are methods for identifying  
 CC agonists and antagonists for use in treating conditions associated with NOGO  
 CC -C imbalance, and diagnostic assays for detecting diseases associated  
 CC with inappropriate NOGO-C activity or levels  
 XX  
 SQ Sequence 1192 AA;

Query Match 98.1%; Score 5810; DB 4; Length 1192;  
 Best Local Similarity 97.2%; Pred. No. 5.1e-293;  
 Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

QY 1 MEDLDQSLVSSSDSPRPQAPFYQVREPEDEDEDEDEDEDEDEDEDEDEDELEVLKPA 60  
 Db 1 MEDLDQSLVSSSDSPRPQAPFYQVREPEDEDEDEDEDEDEDEDEDEDELEVLKPA 60

QY 61 AGLSAPVPTAPAAAGAPLMDFGNDVPPAPRGLPAAPVAPRQSPWSPSVSTVPAP 120  
 Db 61 AGLSAPVPTAPAAAGAPLMDFGNDVPPAPRGLPAAPVAPRQSPWSPSVSTVPAP 120

QY 121 SPLSAAVSPSKLPEDDEPPAPPPPPASVSPQAEVPTMTTAPAPAPSTTAPAKRRG 180  
 Db 121 SPLSAAVSPSKLPEDDEPPAPPPPPASVSPQAEVPTMTTAPAPAPSTTAPAKRRG 180

QY 181 SSGA-----VVXXXXXKINDLKEQPGNTISAGQEDFPVSLLETAASPSLSLP 226  
 Db 181 SSGVDETLFALPAASEPVTSRRAENNDLKEQPGNTISAGQEDFPVSLLETAASPSLSLP 240

QY 227 LSAASKEHYLGNLSTVLPTTEGTLOENVSEASKEYSEKAKTLLIDRLTFESELSEYSEM 286  
 Db 241 LSAASKEHYLGNLSTVLPTTEGTLOENVSEASKEYSEKAKTLLIDRLTFESELSEYSEM 300

QY 287 GSSFSVSPKASAVIVANPREEIIIVKNKDEBEKLVSNILHNQOELPTALTCLKVKEDEVV 346

Db 301 GSSFSVSPKASAVIVANPREEIIIVKNKDEBEKLVSNILHNQOELPTALTCLKVKEDEVV 360  
 QY 347 SSEKAKDSNEKRVAVEAPMRBEYADFPFERVWEVKSDSDMLAAGKIESNLESKY 406  
 Db 361 SSEKAKDSNEKRVAVEAPMRBEYADFPFERVWEVKSDSDMLAAGKIESNLESKY 420  
 QY 407 DKKCFADSLQTNHEKDSSESSNDDTSFSTPGEGIKDRSGAYITCAPNFNPAATESIATNLF 466  
 Db 421 DKKCFADSLQTNHEKDSSESSNDDTSFSTPGEGIKDRPGAYITCAPNFNPAATESIATNLF 480  
 QY 467 PLLEDPTSENXTDEKKIEBKAKIIVTEKNTSTKTSNPFVFAAQDSDTYVTTDNLTKVTE 526  
 Db 481 PLLGPTSENKTDEKKIEBKAKIIVTEKNTSTKTSNPFVFAAQDSDTYVTTDNLTKVTE 540  
 QY 527 EVVANMPEGLTPDLVQEAACESLNEVTGKIAYETKMDLVQTSVNMQESLYPAAQLCPSP 586  
 Db 541 EVVANMPEGLTPDLVQEAACESLNEVTGKIAYETKMDLVQTSVNMQESLYPAAQLCPSP 600  
 QY 587 ESEATPSPVLPDIVWEAPLNSAVPSAGASVIOQSSSPLEASSVNYESIKHPEPNPPYE 646  
 Db 601 ESEATPSPVLPDIVWEAPLNSAVPSAGASVIOQSSSPLEASSVNYESIKHPEPNPPYE 660  
 QY 647 EAMSVSL-KVSGIKKEIKPENINAALQETAPYISIACDLIKETKLSAEPAPDFSDYSE 705  
 Db 661 EAMSVSLKVVSGIKKEIKPENINAALQETAPYISIACDLIKETKLSAEPAPDFSDYSE 720  
 QY 706 MAKVQPPVDHSELVEDSSPDSEPVDLFSDDSIPDPVQKQDETVMVKESLSTETSPESMI 765  
 Db 721 MAKVQPPVDHSELVEDSSPDSEPVDLFSDDSIPDPVQKQDETVMVKESLSTETSPESMI 780  
 QY 766 EYENKEKLSALPEGGKPYLESFKLSLONTKDTLLPDEVSTLSKKEKIPLOMEELSTAVY 825  
 Db 781 EYENKEKLSALPEGGKPYLESFKLSLONTKDTLLPDEVSTLSKKEKIPLOMEELSTAVY 840  
 QY 826 SNDDLFIKSEAQIRETETFSDDSSPIEIIIDEPPTLISSKTDSPSKLAREYTDLEVSHKSEI 885  
 Db 841 SNDDLFIKSEAQIRETETFSDDSSPIEIIIDEPPTLISSKTDSPSKLAREYTDLEVSHKSEI 900  
 QY 886 ANAPGAGSLPCTELPHDLNLKNIQKVBEKISFSDDFSKNGSATSKVLLLPDVSALGH 945  
 Db 901 ANAPGAGSLPCTELPHDLNLKNIQKVBEKISFSDDFSKNGSATSKVLLLPDVSALGH 959  
 QY 946 TQAEIESIVKPVLEKEAEKLPSTDEKEDRSPSAIFSADLGKTSVVDLLYWRDKKTTGV 1005  
 Db 960 TQAEIESIVKPVLEKEAEKLPSTDEKEDRSPSAIFSADLGKTSVVDLLYWRDKKTTGV 1019  
 QY 1006 VFGASLFLLLSLTVFSIVSVTAIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLES 1065  
 Db 1020 VFGASLFLLLSLTVFSIVSVTAIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLES 1079  
 QY 1066 EVAISEELVQKYSNAGLGHVNCITIKELRLFLVDDLVDSLKEAVLMWVFTYVYVGFALFNGLT 1125  
 Db 1080 EVAISEELVQKYSNAGLGHVNCITIKELRLFLVDDLVDSLKEAVLMWVFTYVYVGFALFNGLT 1139  
 QY 1126 LLILALISLFSVPVIYERHOAODIHYVLGLANKNVKDMAKIOAKIPGLKRAE 1178  
 Db 1140 LLILALISLFSVPVIYERHOAODIHYVLGLANKNVKDMAKIOAKIPGLKRAE 1192

RESULT 8  
 ABG30938  
 ID ABG30938 standard; protein; 1192 AA.  
 XX  
 AC ABG30938;  
 XX  
 DT 21-OCT-2002 (first entry)  
 XX  
 DE Human NogoA protein.  
 XX  
 KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;  
 KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;  
 KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;  
 KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;

KW tissue hypertrophy; central nervous system; axon regeneration; NogoA;  
KW Nogo-associated disease; metastasis.  
XX Homo sapiens.  
XX WO200257483-A2.  
XX PD 25-JUL-2002.  
XX PF 18-JAN-2002; 2002WO-GB0000228.  
XX PR 18-JAN-2001; 2001GB-00001312.  
XX PA (GLAX ) GLAXO GROUP LTD.  
XX PA (SMK ) SMITHLINE BEECHAM PLC.  
XX Blackstock WP, Halé RS, Prinjha R, Rowley A;  
XX N-PSDB; ASK90134.  
XX Identifying modulators of Nogo or BACE activity for treating acute  
PT neuronal injuries, neoplastic or dysproliferative disorders, comprises  
PT providing and monitoring interaction between Nogo and BACE polypeptides.  
XX Disclosure; Page 59-62; 68pp; English.  
XX The present invention relates to a new method of identifying modulators  
CC of Nogo function or BACE activity. The method involves providing Nogo and  
CC BACE polypeptides capable of binding with each other, monitoring the  
CC interaction between these polypeptides, and determining if the test agent  
CC is a modulator of Nogo or BACE activity. The method is useful in treating  
CC acute neuronal injuries, such as spinal or head injury, stroke,  
CC peripheral nerve damage, and in neoplastic (e.g. Glioblastomas,  
CC neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.  
CC cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue  
CC hypertrophy) of the central nervous system. The BACE polypeptide is  
CC useful in screening methods to identify agents that may act as modulators  
CC of BACE activity and in particular agents that may be useful in treating  
CC Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,  
CC and the polynucleotide encoding the BACE polypeptide are useful in  
CC manufacturing a medicament for the treatment or prevention of disorders  
CC responsive to the modulation of Nogo activity, in alleviating the  
CC symptoms or improving the condition of a patient suffering from this  
CC disorder, in axon regeneration, or in preventing metastasis or spreading  
CC of a cancer. The polynucleotide may also be an essential component in  
CC assays, a probe, in recombinant protein synthesis, and in gene therapy  
CC techniques. The present amino acid sequence represents the human NogoA  
CC protein of the invention  
SQ Sequence 1192 AA;  
Query Match 98.1%; Score 5810; DB 5; Length 1192;  
Best Local Similarity 97.2%; Pred. No. 5.1e-293;  
Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;  
QY 1 MEDLDQSLVSSSSPPRPQAFKQYFVREPEDEEEDEDEDELEVLERKPA 60  
DB 1 MEDLDQSLVSSSSPPRPQAFKQYFVREPEDEEEDEDEDELEVLERKPA 60  
QY 61 AGLSAAPVPTAPAGAPLMDFGNDVPPAPRGPLPAAPVAPERQPSWDPSPVSTVPAP 120  
DB 61 AGLSAAPVPTAPAGAPLMDFGNDVPPAPRGPLPAAPVAPERQPSWDPSPVSTVPAP 120  
QY 121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPPVWTPPAPAPAPPSTPAAPKRRG 180  
DB 121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPPVWTPPAPAPAPPSTPAAPKRRG 180  
QY 181 SSGA-----VVVXXXKIMDLKEQPGNTISAGQEDFSPVLTAAASPSLSP 226  
DB 181 SSGVDETLFALPAASEPVRSSAMDLKQPGNTISAGQEDFSPVLTAAASPSLSP 240  
QY 227 LSAASFKEHYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRLDTFSELEYSEM 286

DB 241 LSAASFKEHYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRLDTFSELEYSEM 300  
QY 287 GSSFSVSPKAEASAVIVANPREEEIIVKQKDEBEKLVSNILHQQELPTALTKLVKEDRVV 346  
DB 301 GSSFSVSPKAEASAVIVANPREEEIIVKQKDEBEKLVSNILHQQELPTALTKLVKEDRVV 360  
QY 347 SSEKAKDSFNEKRVAVAPMREYADFKPFRVWEVKDSKEDSDMLAAGGKIESNLESKV 406  
DB 361 SSEKAKDSFNEKRVAVAPMREYADFKPFRVWEVKDSKEDSDMLAAGGKIESNLESKV 420  
QY 407 DKCFADSLQTNHEKDSSESNDTSPFSTPEGIKDRSGAYITCAPFNPAATESIATNIF 466  
DB 421 DKCFADSLQTNHEKDSSESNDTSPFSTPEGIKDRPGAYITCAPFNPAATESIATNIF 480  
QY 467 PLLEDPTSENXTDEKKIEEKAQIVTEKNTSTKNSPFFVAAQDSEDTYVTDNLTKYTE 526  
DB 481 PLLGDPTSENKTDEKKIEEKAQIVTEKNTSTKNSPFLVAAQDSEDTYVTDNLTKYTE 540  
QY 527 EVANMPGLTPDLVQACESELNEVTGKIAYETKMDLVOTSEVMQESLYPAAQLCPSPF 586  
DB 541 EVANMPGLTPDLVQACESELNEVTGKIAYETKMDLVOTSEVMQESLYPAAQLCPSPF 600  
QY 587 ESEATPSVLPDVMBAPLNSAVPSAGASVIQSPSSPLEASSVNYESIKHEPENPPPYE 646  
DB 601 ESEATPSVLPDVMBAPLNSAVPSAGASVIQSPSSPLEASSVNYESIKHEPENPPPYE 660  
QY 647 EAMSVSL-KVSGIKKEIKEPENINAAQETAPYISACDLIKETKLSAEPAFPDSYSE 705  
DB 661 EAMSVSLKKYSGIKKEIKEPENINAAQETAPYISACDLIKETKLSAEPAFPDSYSE 720  
QY 706 MAKVEQVPVPHSELVEDSSPDSEVDLFSDDSIDPVQKODETVMLVKESLETETSFESMI 765  
DB 721 MAKVEQVPVPHSELVEDSSPDSEVDLFSDDSIDPVQKODETVMLVKESLETETSFESMI 780  
QY 766 EYENKEKLSALPPGGKPYLESFKLSLONTKOTLLPDEVSTLSKKEKIPLQMBELSTAVY 825  
DB 781 EYENKEKLSALPPGGKPYLESFKLSLONTKOTLLPDEVSTLSKKEKIPLQMBELSTAVY 840  
QY 826 SNDDLFTSKAQIRETETFSDDSPIELIDREPTLISKTDSFSLAREYTDLEVSHKSEI 885  
DB 841 SNDDLFTSKAQIRETETFSDDSPIELIDREPTLISKTDSFSLAREYTDLEVSHKSEI 900  
QY 886 ANAPDAGAGSLPCTELPHDLSLKNQPKVEEKISPDSDDFSKNGSATSKVLLLPDVSALGH 945  
DB 901 ANAPDAGAGSLPCTELPHDLSLKNQPKVEEKISPDSDDFSKNGSATSKVLLLPDVSALA- 959  
QY 946 TQABIESIVKPKVLEKBAEKLPDSTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGV 1005  
DB 960 TQABIESIVKPKVLEKBAEKLPDSTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGV 1019  
QY 1006 VFGASLFLILLSTVFSIVSVTAYTALALLSVTISFRIYKGVIOAKISDEGHPFRAYLES 1065  
DB 1020 VFGASLFLILLSTVFSIVSVTAYTALALLSVTISFRIYKGVIOAKISDEGHPFRAYLES 1079  
QY 1066 EVAISELVOKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFVLMVFTVVGALFNGLT 1125  
DB 1080 EVAISELVOKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFVLMVFTVVGALFNGLT 1139  
QY 1126 LLILALISLSPVPIYERHQAQIDHYLGLANKNVKDMAKIQAQIPGLKRAE 1178  
DB 1140 LLILALISLSPVPIYERHQAQIDHYLGLANKNVKDMAKIQAQIPGLKRAE 1192  
RESULT 9  
ABB81078  
ID ABB81078 standard; protein; 1192 AA.  
XX AC ABB81078;  
XX DT 05-NOV-2002 (first entry)  
XX DE Human neurotransmitter receptor protein Nogo-A.

XX Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;  
KW central nervous system; peripheral nervous system; tranquilizer; Nogo;  
KW vulnerability; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;  
KW neurotic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;  
KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;  
KW neurotransmitter receptor; human; receptor.  
XX Homo sapiens.  
OS  
XX US2002072493-A1.  
PN  
XX 13-JUN-2002.  
PD  
XX  
PF  
XX 28-JUN-2001; 2001US-00893348.  
XX  
XX 19-MAY-1998; 98IL-00124500.  
PR  
XX 21-JUL-1998; 98WO-00214715.  
PR  
XX 22-DEC-1998; 98US-00218277.  
PR  
XX 19-MAY-1999; 99US-00314161.  
XX  
XX (YEDA ) YEDA RES & DEV CO LTD.  
PA  
XX Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;  
PI Moalem G;  
PI  
XX WPI: 2002-607255/65.  
DR  
XX N-PSDB; ABR86601.  
XX  
XX Promoting nerve regeneration and preventing neuronal degeneration in the  
PT central/peripheral nervous system from injury/disease, comprises  
PT administering nervous system-specific activated T cells/antigen, or  
PT analogs/peptides.  
XX  
XX Example; Page 53-56; 93pp; English.  
XX  
XX The invention relates to promoting nerve regeneration or conferring  
CC neuroprotection and preventing or inhibiting neuronal degeneration in the  
CC central/peripheral nervous system (NS). The method involves administering  
CC NS-specific activated T cells, NS-specific antigen, its analogue or its  
CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or  
CC combinations. The method is useful for promoting nerve regeneration and  
CC preventing neuronal degeneration in central/peripheral nervous system  
CC from injury/disease, where the injury is spinal cord injury, blunt  
CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or  
CC damage caused by surgery such as tumour excision. The disease is not an  
CC autoimmune disease or neoplasm. The disease results in a degenerative  
CC process occurring in either gray or white matter or both. The disease is  
CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,  
CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and  
CC vitamin deficiency, intervertebral disc herniation, prion diseases such  
CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral  
CC neuropathies associated with various diseases, including but not limited  
CC to uremia, porphyria, hypoglycemia, Sjogren larsson syndrome, acute  
CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary  
CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption  
CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and Igg gamma-  
CC pathies, complications of various drugs (e.g., metronidazole) and toxins  
CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia  
CC telangiectasia, Friedrich's ataxia, amyloid polynuropathies,  
CC adrenomyeloneuropathy, giant axonal neuropathy, Refsum's disease, Fabry's  
CC disease, or lipoproteinemia. The present sequence represents the human  
CC neurotransmitter receptor protein Nogo-A, an example of NS-specific  
XX antigen  
XX Sequence 1192 AA;  
SQ

Db 1080 EVAISEELVQKYSNLSALGHVNCITIKELRRLFLVDDLVDSLKFAVLMMVFTYVGFALFNGLT 1139

Qy 1126 LLLALISLFSVPVYERHQAIIDHYGLANKNVKDMAKIOAKIPGLKRAE 1178

Db 1140 LLLALISLFSVPVYERHQAIIDHYGLANKNVKDMAKIOAKIPGLKRAE 1192

RESULT 10

ADP67234

ID ADP67234 standard; protein; 1192 AA.

XX ADP67234;

AC

XX

DT 09-SEP-2004 (first entry)

XX

DE Human Nogo-A protein.

XX

KW human; Nogo-A; neurite outgrowth inhibitor; Nogo;

KW contactin-associated protein-1; Caspr; neuroprotective; gene therapy;

KW CNS; spinal cord injury; multiple sclerosis; epilepsy; stroke.

XX

OS Homo sapiens.

XX

PN WO2004052389-A2.

XX

PD 24-JUN-2004.

XX

PF 05-DEC-2003; 2003WO-GB005329.

XX

PR 06-DEC-2002; 2002US-0431549P.

PR 20-JUN-2003; 2003US-0480138P.

XX

PA (SICE-) SINGAPORE GEN HOSPITAL PTE LTD.

PA (FORR/) FORREST G R.

XX

PI Xiao Z;

XX

DR WPI; 2004-468705/44.

XX

PT New composition comprising Nogo and Caspr or a substance capable of

PT promoting interaction between Nogo and Caspr useful for treating injury

PT to or disease of the CNS, e.g., spinal cord injury, multiple sclerosis,

PT epilepsy or stroke.

XX

PS Disclosure; Page 14; 202pp; English.

XX

CC The invention relates to a novel composition comprising neurite outgrowth

CC inhibitor (Nogo) and contactin-associated protein-1 (Caspr) or its

CC mimetics or a substance capable of promoting interaction between Nogo and

CC Caspr, in combination with a carrier. A composition of the invention has

CC neuroprotective activity, and may have a use in gene therapy. The

CC composition is useful for treating injury to or disease of the CNS, e.g.

CC spinal cord injury, multiple sclerosis, epilepsy or stroke. The present

CC sequence represents human Nogo-A.

XX

SQ Sequence 1192 AA;

Query Match 98.1%; Score 5810; DB 8; Length 1192;

Best Local Similarity 97.2%; Pred. No. 5.1e-293;

Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

Qy 1 MEDLQSPLVSSSDSPRRPQAFKQFVREPEDEDEDEDEDEDEDELEVLKPA 60

Db 1 MEDLQSPLVSSSDSPRRPQAFKQFVREPEDEDEDEDEDEDEDELEVLKPA 60

Qy 61 AGLSAAPVPTAPAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQSPWDPSPVSTVPAP 120

Db 61 AGLSAAPVPTAPAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQSPWDPSPVSTVPAP 120

Qy 121 SPLSAAAVSPKLPDDEDPAPPPPPPPASVSQAEVWTPPPAPAPAPPSTPAAPKRG 180

Db 121 SPLSAAAVSPKLPDDEDPAPPPPPPPASVSQAEVWTPPPAPAPAPPSTPAAPKRG 180

Qy 181 SSGA-----VAXXXKIMDLKEQPGNTISAGQEDPPSVLLETAASPSLSP 226

Db 181 SSGVDETLFALPAASEPVISSAENMDLKEQPGNTISAGQEDPPSVLLETAASPSLSP 240

Qy 227 LSAAAFKEHEYLGNLSTVLPTEGLQENVSEASKEVSEKAKTLLIDRLTFESELEYSEM 286

Db 241 LSAAAFKEHEYLGNLSTVLPTEGLQENVSEASKEVSEKAKTLLIDRLTFESELEYSEM 300

Qy 287 GSSFSVSPKASAVIVANPREIIVKNKDEBEKLVNNILHXQOBLTALTTLKVKEDVV 346

Db 301 GSSFSVSPKASAVIVANPREIIVKNKDEBEKLVNNILHNQOBLTALTTLKVKEDVV 360

Qy 347 SSEKAKDSFNEKRVAVAPMEEEYADFKPFRVWEVKDSKEDSDMLAAGGKIESLESKV 406

Db 361 SSEKAKDSFNEKRVAVAPMEEEYADFKPFRVWEVKDSKEDSDMLAAGGKIESLESKV 420

Qy 407 DKCFADSLQTNHEKSESSNDTSPSTPEGIKORSNAVITCAPFNPAAATESIATNIF 466

Db 421 DKCFADSLQTNHEKSESSNDTSPSTPEGIKDRPCAVITCAPFNPAAATESIATNIF 480

Qy 467 PLLDPTSENXTDEKKEKKAQIVTEKNTSTKSNPFVAAQDSETDYVTDNLTKYTE 526

Db 481 PLLDPTSENXTDEKKEKKAQIVTEKNTSTKSNPFVAAQDSETDYVTDNLTKYTE 540

Qy 527 EVANMPGLTPDLVQEAECESLNEVTGKTIAYETKMDLVOTSEVMQSLYPAAQLCPSP 586

Db 541 EVANMPGLTPDLVQEAECESLNEVTGKTIAYETKMDLVOTSEVMQSLYPAAQLCPSP 600

Qy 587 ESEATPSVLPDVIWEAPLNSAVPSGASVIQSSSSPLEASSVNYESIKEPENPPYE 646

Db 601 ESEATPSVLPDVIWEAPLNSAVPSGASVIQSSSSPLEASSVNYESIKEPENPPYE 660

Qy 647 EAMSVSL-KVSGIKKEIKPENINAALOETAPYISIACDLIKETKLSAEPAPDSDYSE 705

Db 661 EAMSVSLKVSGIKKEIKPENINAALOETAPYISIACDLIKETKLSAEPAPDSDYSE 720

Qy 706 MAKVEQPVPHSELVEDSSPSEVDLFSDDSIIDPVPQKQDETVMVKESLTETSFESMI 765

Db 721 MAKVEQPVPHSELVEDSSPSEVDLFSDDSIIDPVPQKQDETVMVKESLTETSFESMI 780

Qy 766 EYENKEKLSALPPGGKPYLESFKLSLNDNTKDTLLPDEVSTLSKKEKIPLOMEELSTAVY 825

Db 781 EYENKEKLSALPPGGKPYLESFKLSLNDNTKDTLLPDEVSTLSKKEKIPLOMEELSTAVY 840

Qy 826 SNDDLFIKSEAQIRETETFSDDSPIIIDEPTLISSKTDSPSKLAREYTDLEVSHKSEI 885

Db 841 SNDDLFIKSEAQIRETETFSDDSPIIIDEPTLISSKTDSPSKLAREYTDLEVSHKSEI 900

Qy 886 ANAPDGAGSLPCTELPHDLSLKNQPKVEEKISFSDSPSKNGSATSKVLLLPDVSALGH 945

Db 901 ANAPDGAGSLPCTELPHDLSLKNQPKVEEKISFSDSPSKNGSATSKVLLLPDVSALA- 959

Qy 946 TQABIESIVPKVLEKBAEKLPDSTEKEDRSPSAIFSADLGKTSVVDLLYMRDIKKTGV 1005

Db 960 TQABIESIVPKVLEKBAEKLPDSTEKEDRSPSAIFSADLGKTSVVDLLYMRDIKKTGV 1019

Qy 1006 VFGASLFLLLSLTVFSIVSVTAYTALALLSVTISFRIYKGVIOAKQSDGHPFRAYLES 1065

Db 1020 VFGASLFLLLSLTVFSIVSVTAYTALALLSVTISFRIYKGVIOAKQSDGHPFRAYLES 1079

Qy 1066 EVAISEELVQKYSNLSALGHVNCITIKELRRLFLVDDLVDSLKFAVLMMVFTYVGFALFNGLT 1125

Db 1080 EVAISEELVQKYSNLSALGHVNCITIKELRRLFLVDDLVDSLKFAVLMMVFTYVGFALFNGLT 1139

Qy 1126 LLLALISLFSVPVYERHQAIIDHYGLANKNVKDMAKIOAKIPGLKRAE 1178

Db 1140 LLLALISLFSVPVYERHQAIIDHYGLANKNVKDMAKIOAKIPGLKRAE 1192

RESULT 11

ADRI3966

ID ADRI3966 standard; protein; 1192 AA.

XX











PI	Skerra A, Fiedler M;	
XX	WPI; 2004-376159/35.	
XX	New isolated truncated Nogo-A polypeptide that corresponds to a truncated	
PT	form of the Nogo-A protein, useful for identifying a compound having	
PT	detectable affinity to a Nogo-A protein.	
XX	Claim 1; Fig 6B; 80pp; English.	
XX	The present invention relates to an isolated truncated Nogo-A polypeptide	
CC	that corresponds to a truncated form of the Nogo-A protein from the rat	
CC	and from the human. The truncated polypeptide is useful for identifying a	
CC	compound having detectable affinity to a Nogo-A protein. The present	
CC	sequence is a Nogo-A polypeptide of the invention.	
XX	Sequence 1192 AA;	
SQ	Query Match 97.2%; Score 5758; DB 8; Length 1192;	
	Best Local Similarity 96.2%; Pred. No. 2.6e-290;	
	Matches 1148; Conservative 11; Mismatches 18; Indels 16; Gaps 3;	
Qy	1 MEDLDQSLVSSDPPRPQAFKQFVREPEDEDEDEDEDEDEDEDEDEDEDELEVLERKPA 60	
Db	1 MEDLDQSLVSSDPPRPQAFKQFVREPEDEDEDEDEDEDEDEDEDEDEDELEVLERKPA 60	
Qy	61 AGLSAAPVPTAPAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQSPWDPSPVSTVPAP 120	
Db	61 AGLSAAPVPTAPAGAPLMDFGNEFVFPAPRGPLPAAPPVAPERQSPWDPSPVSTVPAP 120	
Qy	121 SPLSAAAVSPSKLPEDDEPPAPPPPPASVSPQAEVPTWTPAPAPAPPSTPAAPKRRG 180	
Db	121 SPLSAAAVSPSKLPEDDEPPAPPPPPASVSPQAEVPTWTPAPAPAPPSTPAAPKRRG 180	
Qy	181 SSGA-----VWXXXKIMDLKQPGNTISAGQEDFPSVLLETAASLPSLP 226	
Db	181 SSGVDETLFALPAASEPVIRSSAENMELKQPGNTISAGQEDFPSVLLETAASLPSLP 240	
Qy	227 LSASFKEHYLGNLSTVLTGTLQENVSSASKEVSEKATLIDRLTFSELEYSEM 286	
Db	241 LSASFKEHYLENLSTVLTGTLQENVSSASKEVSEKATLIDRLTFSELEYSEM 300	
Qy	287 GSSFSVSPKASAVITVANPREIIVKNKDEBEKLVNNILHQQELPTALTCLKVEDEV 346	
Db	301 GSSFSVSPKASAVITVANPREIIVKNKDEBEKLVNNILHQQELPTALTCLKVEDEV 360	
Qy	347 SSEKAKDSFNKRVAVAPMREEVADPKPFRVVEVKDSKEDSDMLAAGGKIESNLSKV 406	
Db	361 SSEKAKDSFNKRVAVAPMREEVADPKPFRVVEVKDSKEDSDMLAAGGKIESNLSKV 420	
Qy	407 DKCFADSLQTNHEKDSSESSNDTSFPSTPEGIKDRSGAVITCAPFNPAATESIATNIF 466	
Db	421 DKCFADSLQTNHEKDSSESSNDTSFPSTPEGIKDRSGAVITCAPFNPAATESIATNIF 480	
Qy	467 PLEEDPTSENXTDEKKIEEKAQIVTEKNTSTKSNPFFVAQDSQSDTYVTTDLTKVTE 526	
Db	481 PLLGDPTSENKTDEKKIEEKAQIVTEKNTSTKSNPFLVAQDSQSDTYVTTDLTKVTE 540	
Qy	527 EVVANMPGLTPDLVQVACESSELNEVTGKIAYETKMDLVOTSEVMQESLYPAAQLCPSP 586	
Db	541 EVVANMPGLTPDLVQVACESSELNEVTGKIAYETKMDLVOTSEVMQESLYPAAQLCPSP 600	
Qy	587 EESATPSPLVDIVMEAPLNSAVPSAGASVIOQSSSPLEASSVNYESIKEHPENPPPYE 646	
Db	601 EESATPSPLVDIVMEAPLNSAVPSAGASVIOQSSSPLEASSVQYESIKHEPNPPPYE 660	
Qy	647 EAMSVSL-KVSGIKKEEIKPENINAAQETEPAYISACDLIKETKLSAEPAPDFSQYSE 705	
Db	661 EAMSVSLKKVSGIKKEEIKPENINAAQETEPAYISACDLIKETKLSAEPAPDFSQYSE 720	
Qy	706 MAKVEQVPVDSHSELVEDSSSPSEVDFLPSDDSIIPDVQKQDETVMVKESLTETSPFSMI 765	
Db	721 MAKVEQVPVDSHSELVEDSSSPSEVDFLPSDDSIIPDVQKQDETVMVKESLTETSPFSMI 780	

Qy	766 EYENKEKLALPPGGKPYLESFKLSLNTKDTLLPDEVSTLSKKEKIPLOWEELSTAVY 825	
Db	781 EYQKEKLALPPGGKPYLESFKLSLNTKDTLLPDEVSTLSKKEKIPLOWEELSTAVY 840	
Qy	826 SNDDLFIKSAQIRETETFSDDSPFIEIIDEPTTLISSKTSDFSKLAREYTTDLEVSHKSEI 885	
Db	841 SNDDLFIKSAQIRETETFSDDSPFIEIIDEPTTLISSKTSDFSKLAREYTTDLEVSHKSEI 900	
Qy	886 ANAPDGAGSLPCTELPHDLNLKNIQPKVEEKISFSDPSKNGSATSKVLLLPDVSALGH 945	
Db	901 AQAPDGAGSLPCTELPHDLNLKNIQPKVEEKISFSDPSKNGSATSKVLLLPDVSALA- 959	
Qy	946 TOAIESIVKPKVLEKAEKCLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGV 1005	
Db	960 TOAIESIVKPKVLEKAEKCLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGV 1019	
Qy	1006 VFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLES 1065	
Db	1020 VFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLES 1079	
Qy	1066 EVAISEELVQKYSNLSALGHVNCCTIKELRLFLVDDLVDSLKFAVLMMVFTTVGALFNGLT 1125	
Db	1080 EVAISEELVQKYSNLSALGHVNCCTIKELRLFLVDDLVDSLKFAVLMMVFTTVGALFNGLT 1139	
Qy	1126 LLILALISLSPVPIYERHQAQIDHYLGLANKNVKDMAKIOAKIPGLKRAE 1178	
Db	1140 LLILALISLSPVPIYERHQAQIDHYLGLANKNVKDMAKIOAKIPGLKRAE 1192	
RESULT 15		
AAU33228		
ID	AAU33228 standard; protein; 1246 AA.	
XX	AC AAU33228;	
XX	DT 18-DEC-2001 (first entry)	
XX	DE Novel human secreted protein #3719.	
XX	KW Human; vaccination; gene therapy; nutritional supplement;	
KW	stem cell proliferation; haematopoiesis; nerve tissue regeneration;	
KW	immune suppression; immune stimulation; anti-inflammatory; leukaemia.	
OS	Homo sapiens.	
XX	PN WO200179449-A2.	
XX	PD 25-OCT-2001.	
XX	PP 16-APR-2001; 2001WO-US0008656.	
XX	PR 18-APR-2000; 2000US-00552929.	
PR	26-JAN-2001; 2001US-00770160.	
XX	(HYSE-) HYSEQ INC.	
XX	Tang YT, Liu C, Drmanac RT;	
XX	WPI; 2001-611725/70.	
XX	Nucleic acids encoding a range of human polypeptides, useful in genetic	
PT	vaccination, testing and therapy.	
XX	Claim 20; Page 737; 765pp; English.	
XX	The invention relates to novel human secreted polypeptides. The	
CC	polypeptides and antibodies to the polypeptides are useful for	
CC	determining the presence of or predisposition to a disease associated	
CC	with altered levels of polypeptide. The polypeptides are also useful for	
CC	identifying agents (agonists and antagonists) that bind to them. Cells	
CC	expressing the proteins are useful for identifying a therapeutic agent	
CC	for use in treatment of a pathology related to aberrant expression or	

CC physiological interactions of the polypeptide. Vectors comprising the  
CC nucleic acids encoding the polypeptides and cells genetically engineered  
CC to express them are also useful for producing the proteins. The proteins  
CC are useful in genetic vaccination, testing and therapy, and can be used  
CC as nutritional supplements. They may be used to increase stem cell  
CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon  
CC and/or nerve tissue growth or regeneration; immune suppression and/or  
CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.  
CC AAU29510-AAU3304 represent the amino acid sequences of novel human  
CC secreted proteins of the invention  
XX  
SQ Sequence 1246 AA;

Query Match 93.3%; Score 5526.5; DB 4; Length 1246;  
Best Local Similarity 93.0%; Pred. No. 2.8e-278;  
Matches 1123; Conservative 13; Mismatches 39; Indels 33; Gaps 10;  
  
QY 1 MEDLDQSLVSSSDSPRPQAPKQYQVREPEDEEEEEEEEEDEDELEEVLERKPA 60  
DB MEDLDQSLVSSSDSPRPQAPKQYQVREPEDEEEEEEEEEDEDELEEVLERKPA 101  
  
QY 61 AGLSAAVPVTPAAGAPLMDFGNDFVPPAPRGPLPAAPVAPERQSPWDPSPVSSVTPAP 120  
DB AGLSAAVPVTPAAGAPLMDFGNDFVPPAPRGPLPAAPVAPERQSPWDPSPVSSVTPAP 161  
  
QY 121 SPLSAAVSPSKLPEDDEPPAPPPPPASVSPQAEFVWTPAPAPAPSTPAAPKRRG 180  
DB SPLSAAVSPSKLPEDDEPPAPPPPPASVSPQAEFVWTPAPAPAPSTPAAPKRRG 221  
  
QY 181 SSGA-----VVXXXKIMDLKEQPGNTISAGQDFPSPVLLETAASKPSLSP 226  
DB SSGVDETLFALPAASEPVIRSAENNDLKEQPGNTISAGQDFPSPVLLETAASKPSLSP 281  
  
QY 227 LSAASFKEHYLGNLSTVLPTGTLQENVSEASKEYSEKAKTLLIDRDLTFESELEYSEM 286  
DB LSAASFKEHYLGNLSTVLPTGTLQENVSEASKEYSEKAKTLLIDRDLTFESELEYSEM 341  
  
QY 287 GGSFVSVPKASNAVIANPREELIVKNDKEEKLVSNNILHXQOELPTALTCLKVKEDEVV 346  
DB GGSFVSVPKASNAVIANPREELIVKNDKEEKLVSNNILHXQOELPTALTCLKVKEDEVV 401  
  
QY 347 SZEKAKDSFNEKRVAVEAPMREYADFKPERVWEVKDSKEDSMDLAAGKIESNLESKV 406  
DB SZEKAKDSFNEKRVAVEAPMREYADFKPERVWEVKDSKEDSMDLAAGKIESNLESKV 461  
  
QY 407 DKKCFADSLQTNHKESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAAATESIATNIF 466  
DB DKKCFADSLQTNHKESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAAATESIATNIF 521  
  
QY 467 PLLEDPTSENXTDEKKIEBKKAQIVTEKNTSTKTSNPPFFVAAQDSETDVTTDNLTKYTE 526  
DB PLLGDPSTENKTDKKEIEBKKAQIVTEKNTSTKTSNPPFLVAAQDSETDVTTDNLTKYTE 581  
  
QY 527 EVVANMPEGLTPDLVOEACESELNEVTGKIAYETKMDLVQTSSEVMQESLYPAAQLCPSP 586  
DB EVVANMPEGLTPDLVOEACESELNEVTGKIAYETKMDLVQTSSEVMQESLYPAAQLCPSP 641  
  
QY 587 ESEATPSVPLDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE 646  
DB ESEATPSVPLDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE 701  
  
QY 647 EAMSVSL-KVSGIKKEIKPENINAAALQETAPYISIACDLIKETKLSAEPAPDFSDYSE 705  
DB EAMSVSLKKVSGIKKEIKPENINAAALQETAPYISIACDLIKETKLSAEPAPDFSDYSE 761  
  
QY 706 MAKVEQVPDHSSELVSDSPDSEPDVDFSDDISPDVPQKQDETVMVLVKESLTETSPESMI 765  
DB MAKVEQVPDHSSELVSDSPDSEPDVDFSDDISPDVPQKQDETVMVLVKESLTETSPESMI 821  
  
QY 766 EYENKEKLSALPEGGKPYLESFKLSLNDNTKOTLLPDEVSTLSKKEKIPQMEELSTAVY 825  
DB EYENKEKLSALPEGGKPYLESFKLSLNDNTKOTLLPDEVSTLSKKEKIPQMEELSTAVY 881

QY 826 SNDDLFIKSAQIRETETFSDDSPLEIIDEFPPTLISSKTDSPSKLAREYTDLEVSHKSEI 885  
DB SNDDLFIKSAQIRETETFSDDSPLEIIDEFPPTLISSKTDSPSKLAREYTDLEVSHKSEI 941  
  
QY 886 ANAPDGAGSLPCTELPHDLNLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDPVSALGH 945  
DB ANAPDGAGSLPCTELPHDLNLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDPVSALA- 1000  
  
QY 946 TQAEIESIVKPKVLEKAEKPLPSDETEKEDRSPSAIFSADLQKTSVVDLLLYWRDIKKTGV 1005  
DB TQAEIESIVKPKVLEKAEKPLPSDETEKEDRSPSAIFSADLQKTSVVDLLLYWRDIKKTGV 1060  
  
QY 1006 VFGAS-LFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAKSDEGHPFRAY-- 1062  
DB VFGASVFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAKSDEGHPFRAYSIG 1120  
  
QY 1063 -LSEVAISEELVQKYSNSALGHV-NCTIKELRR--LFLVDDLVDLSLK-FAVLMMVFTY 1116  
DB NLESCLYLRELGSGRYSNSALGSMNCTVKNFRAPSFSSWMDLVDSLRSFAVLMMVFTY 1180  
  
QY 1117 VGALFNGLTLL-----ILALISLFSVPVIVYERHQAQIDHYLGLANKNVKQAMAKIQAKI 1170  
DB VGCL--GLMVLDTTGFWALNFTISSSGSWLIYERHQAQIDHYLGLANKNVKQAMAKIQAKI 1238  
  
QY 1171 PGLKPKAE 1178  
DB PGLKPKAE 1246

Search completed: June 16, 2005, 13:11:05  
Job time : 175.11 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:19:00 ; Search time 44.4839 Seconds  
(without alignments)  
1976.818 Million cell updates/sec

Title: US-09-830-972-29  
Perfect score: 5923  
Sequence: 1 MEDLDQSLVSSDPPRPQ.....VKDAMAKIQKIPGLKRAE 1178

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA.\*

- 1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/1aa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	931	15.7	199	2	US-08-700-607-1
2	931	15.7	201	4	US-09-949-016-9124
3	787.5	13.3	776	2	US-08-700-607-5
4	787.5	13.3	776	4	US-09-949-016-6998
5	727.5	12.3	439	4	US-09-949-016-9180
6	705	11.9	356	2	US-08-700-607-6
7	688	11.6	208	2	US-08-700-607-7
8	671	11.3	267	2	US-08-700-607-8
9	638	10.8	129	4	US-09-513-999C-5000
10	627.5	10.6	192	4	US-09-949-016-8859
11	541.5	9.1	168	4	US-09-149-476-563
12	522.5	8.8	219	4	US-09-270-767-45132
13	514	8.7	588	4	US-09-949-016-7290
14	513	8.7	241	2	US-08-700-607-3
15	347	5.9	68	4	US-09-513-999C-6304
16	344.5	5.8	75	4	US-09-621-976-4600
17	344.5	5.8	75	4	US-09-621-976-4601
18	316	5.3	8991	4	US-08-714-741-32
19	299	5.0	324	4	US-09-538-092-1246
20	296.5	5.0	2468	4	US-09-976-594-726
21	296.5	5.0	2468	4	US-09-538-092-1135
22	296.5	5.0	2522	4	US-09-949-016-10237
23	286	4.8	2753	4	US-09-949-016-7659
24	286	4.8	2753	4	US-09-949-016-7660
25	285	4.8	92	4	US-09-149-476-411
26	276.5	4.7	1786	3	US-08-973-462-8
27	267.5	4.5	1601	4	US-09-345-473E-40

28	265	4.5	1596	4	US-08-978-277A-4	Sequence 4, Appli
29	263.5	4.4	2409	6	5180808-2	Patent No. 5180808
30	263.5	4.4	2409	6	5180808-2	Patent No. 5180808
31	261	4.4	4377	4	US-09-949-016-6978	Sequence 6978, Ap
32	258	4.4	3913	4	US-09-949-016-10933	Sequence 10933, A
33	257.5	4.3	1781	4	US-09-961-403-13	Sequence 13, Appl
34	256	4.3	1780	1	US-08-769-309A-5	Sequence 5, Appli
35	256	4.3	1780	3	US-08-994-570-5	Sequence 5, Appli
36	252	4.3	114	4	US-09-513-999C-7861	Sequence 7861, Ap
37	249.5	4.2	2079	4	US-09-949-016-8301	Sequence 8301, Ap
38	240	4.1	1878	4	US-09-949-016-8902	Sequence 8902, Ap
39	240	4.1	1878	4	US-09-949-016-8903	Sequence 8903, Ap
40	238	4.0	1346	2	US-08-635-121-2	Sequence 2, Appli
41	238	4.0	1346	4	US-08-978-277A-2	Sequence 2, Appli
42	237.5	4.0	688	3	US-09-141-047-8	Sequence 8, Appli
43	237.5	4.0	1270	4	US-07-757-022B-44	Sequence 44, Appl
44	237.5	4.0	1311	4	US-07-757-022B-42	Sequence 42, Appl
45	237.5	4.0	1313	4	US-07-757-022B-142	Sequence 142, Appl

ALIGNMENTS

RESULT 1  
US-08-700-607-1  
; Sequence 1, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA: US/08700,607  
APPLICATION NUMBER: US/08700,607  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0114 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 199 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE: Consensus  
US-08-700-607-1

Query Match 15.7%; Score 931; DB 2; Length 199;  
Best Local Similarity 99.0%; Pred No. 1e-49;  
Matches 189; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 988 KTSVVDLLYMRDKTKTGTVFGASLFLLSLTVFSIVSVTAYIALLSVTISFRIYKGI 1047

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Db 9 KDKVLLYWRDVKKTGVFGASLFLLLSLTVFSIVSVTAIYALALSVTISPRIYKGI 68
QY 1048 QAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNCITIKELRRLFLVDDLVSLKF 1107
Db 69 QAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNCITIKELRRLFLVDDLVSLKF 128
QY 1108 AVLMMWFTYVGFALFNGLTLLILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDAKIQ 1167
Db 129 AVLMMWFTYVGFALFNGLTLLILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDAKIQ 188
QY 1168 AKIPGLKRAE 1178
Db 189 AKIPGLKRAE 199
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## RESULT 2

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US-09-949-016-9124
; Sequence 9124, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9124
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9124
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Query Match 15.7%; Score 931; DB 4; Length 201;

Best Local Similarity 99.0%; Pred. No. 1e-49; Mismatches 2; Indels 0; Gaps 0;

Matches 189; Conservative 0;

QY 988 KTSVLLYWRDVKKTGVFGASLFLLLSLTVFSIVSVTAIYALALSVTISPRIYKGI 1047

Db 11 KDKVLLYWRDVKKTGVFGASLFLLLSLTVFSIVSVTAIYALALSVTISPRIYKGI 70

QY 1048 QAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNCITIKELRRLFLVDDLVSLKF 1107

Db 71 QAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNCITIKELRRLFLVDDLVSLKF 130

QY 1108 AVLMMWFTYVGFALFNGLTLLILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDAKIQ 1167

Db 131 AVLMMWFTYVGFALFNGLTLLILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDAKIQ 190

QY 1168 AKIPGLKRAE 1178

Db 191 AKIPGLKRAE 201

## RESULT 3

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US-08-700-607-5
; Sequence 5, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 776 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307307
US-08-700-607-5
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Query Match 13.3%; Score 787.5; DB 2; Length 776;

Best Local Similarity 31.9%; Pred. No. 4.5e-40; Indels 207; Gaps 25;

Matches 229; Conservative 91; Mismatches 190;

QY 588 ESEATPSVLPDI--VMEAPLNSA-----VPSAGASVTPSSSPL-----ASSVNY----- 632

Db 141 EELGTGSLPDPVPGIESRGLFSSDGIEMTFAESTEVNKILADLPDQMAEAYKIDIT 200

QY 633 --BSIKHEPENPPPEEA-----MSVLSKVGIGKEIKPENINAA-----QET 675

Db 201 RPEEVKHQHPHELEDKDLDFKNKDTISIKPEGVREPK-PAPVEGKIIKDHLEEST 259

QY 676 EAPYISIAIDL-----IKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVED 722

Db 260 PAPYID--DLSEQRRAQITTPVKITLITEPSVE-----TTQKTPKQDICK 309

QY 723 SSPDSEFVDFGS---DDS-----IPDVPOKQ-----DETVMVKESLTETSF 761

Db 310 PSPDTVTPTVSEPDSPGSIPTPSSGTEPSAAESQKGSISEDELITAIKEA----- 363

QY 762 ESMIEYENKEKLSALPPEGKPYLESFKLSLNTKDTLLPDEVSTLSKKEKIPLOMEELS 821

Db 364 -KGLSYETAENPRPVQLADRP-----EYKARSGPTTIPSPLDHEA 403

QY 822 TAVYSNDLDFISKEAQIRETETFSDSPIIIDEFP-----TLISSTDSFS----- 868

Db 404 SSAESGD-----SEIELVSEDPMAAEDALPSGVVSGHVGPPSP 444

QY 869 -----KLAREYTDLEVSHKGEIANAPDAGSLPCTELPHDLISLKNIPKVEEKISFSD 921

Db 445 ASPSIQYSILREAREARLSELIIESCDASSA-----EESPKREQDSPMPKPSALD 496

QY 922 DF-----SKNGSATSKVLL-----LPPDVSAHGHTQAIESIVKP 956

Db 497 AIREETGVRAERAPRRRGLAEPGSLFDYFSTPEPQGPPELPPGDGAL-----EPETMPLP 551

QY 957 KVLEKEAEKKLPDSTEKEDRSPSA-----IFSADLGKTSVVDLLYWRDIK 1001

Db 552 -----RKPEEDSSSNQSPAATKGPGLGPGAPPPPLLF---LNKQKADLLYWRDIK 599



Db 257 YNRDIKQTGIVFGSFLLLFSLTQFVSVVAYLAAALSATISFRIYKSVQAVQKTD 316  
QY 1056 GHPFRAYLSEVAISELVQKYSNSALGHVNCCTIKELRBLFLVDDLSLKFAVLMWVFT 1115  
Db 317 GHPFKAYLEITLSQEQIKYTDCLQFYVNSTLXELRRLFLVQDLVDSLKFAVLMWLT 376  
QY 1116 YVGALENGTLTLLALISLFSVPVIYERHQAQIDHYGLGNKVKDAMAKIOAKIPGLKR 1175  
Db 377 YVGALENGTLTLLMAYVSMFTLPVVYVKEHQADQYGLVTRTHINAVVAKIOAKIPGAKR 436  
QY 1176 KAE 1178  
Db 437 HAE 439

RESULT 6  
US-08-700-607-6  
; Sequence 6, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0114 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 356 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 307309  
US-08-700-607-6

Query Match 11.9%; Score 705; DB 2; Length 356;  
Best Local Similarity 42.8%; Pred. No. 1.7e-35;  
Matches 168; Conservative 55; Mismatches 86; Indels 85; Gaps 11;  
QY 803 EVSTLSKKEKIPLOMEELSTAVNSDDLFTSKAEQIRFETETSDSSPIBIIDFPTLIS 862  
Db 30 QYSILREERAEJDSLI---IFSCDASSASESPKRE---QDSPMK-----PSALDA 77  
QY 863 KTDSPSKLAREYTDLEVSHKSEIANAPDGAGSL---PCTELPHDLSLKNIQPKVEKISF 919  
Db 78 -----IREETGVRAEERAPRRGLBPGSLDYPSTE-----PQPGPE----- 115

QY 920 SDDFSKNGSATSKVLLLPDVSAIGHQTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPS 979  
Db 116 -----LPPGDGAL-----EPETMLP-----RKPEEDSSSSNQSPA 145  
QY 980 A-----IFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVS 1024  
Db 146 ATKPGPLGPGAPPPLFP---LNKQKAIDLLYWRDIKQTGIVFGSFLLLSLTQPSVVS 202  
QY 1025 VTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISELVQKYSNSALGH 1084  
Db 203 VVAYLALAALSATISFRIYKSVLQAVQKTDGHPFKAYLELEITLSQEQIKYTDCLQFY 262  
QY 1085 VNCTIKELRRLFLVDDLSLKFAVLMWVFTVVGALFNGTLTLLALISLFSVPVIYERH 1144  
Db 263 VNSTLXELRRLFLVQDLVDSLKFAVLMWLTVVGALFNGTLTLLMAVSMFTLPVVYVXH 322  
QY 1145 QQAIDHYGLGNKVKDAMAKIOAKIPGLKRKAE 1178  
Db 323 QQAIDQYGLGLVTRTHINAVVAKIOAKIPGAKRHAE 356

RESULT 7  
US-08-700-607-7  
; Sequence 7, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0114 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 208 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 307311  
US-08-700-607-7

Query Match 11.6%; Score 688; DB 2; Length 208;  
Best Local Similarity 67.5%; Pred. No. 8.9e-35;  
Matches 129; Conservative 32; Mismatches 30; Indels 0; Gaps 0;  
QY 988 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 1047  
Db 18 KQAIDLLYWRDIKQTGIVFGSFLLLFSLTQFVSVVAYLAAALSATISFRIYKSVL 77



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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8859
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-8859

Query Match          10.6%; Score 627.5; DB 4; Length 192;
Best Local Similarity 61.1%; Pred. No. 4.1e-31;
Matches 116; Conservative 38; Mismatches 35; Indels 1; Gaps 1;

QY 990 SVVDLLYWDIKKTVGASLFLILSLTVFSIVSTAYATALLISVTSIFRIYKGVQA 1049
Db 3 SVHDLIFWDRDKTVGFTGLTLMLLSLAFAFVSIVSYLLIALLSVTSIFRIYKSVQA 62

QY 1050 IOKSDRGHPFRAYLSEVAISELVQKYSNSALGHVNCITKELRLFLVDDLDVSLKFAV 1109
Db 63 VQKSEGHFPKAYLDVDTLSSEAFHNYNMMVHNRALKLIIRLFVDELVDLSKLAV 122

QY 1110 LMVFTYVYGALFNGLLTLLILALISLFSVPVYERHQADHYLGLANKNVKDMAKIQAK 1169
Db 123 FWMIMTYVGAVENTLLILAEILLESVPVYKTKYQIDHYVYGIARDQTKSIVEKIQAK 182

QY 1170 IGPL-KRAE 1178
Db 183 LPIAKKRAE 192

RESULT 11
US-09-149-476-563
; Sequence 563, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
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; EARLIER FILING DATE: 1997-03-07
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; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
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; EARLIER APPLICATION NUMBER: 60/047,592

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; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
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US-09-513-999C-6304
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Best Local Similarity 100.0%; Pred. No. 1.6e-14;
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GenCore version 5.1.6  
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Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1714042

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5815	98.2	1192	9	US-09-972-599A-6
3	5815	98.2	1192	14	US-10-060-036-71
4	5810	98.1	1192	9	US-09-789-386-2
5	5810	98.1	1192	9	US-09-893-348-23
6	5810	98.1	1192	15	US-10-267-502-429
7	5810	98.1	1192	16	US-10-327-213-9
8	5810	98.1	1192	16	US-10-466-258-9
9	5810	98.1	1192	16	US-10-810-653-23
10	5794	97.8	1192	15	US-10-408-967-7
11	4296.5	72.5	1163	9	US-09-893-348-18
					Sequence 6, Appli
					Sequence 6, Appli
					Sequence 71, Appl
					Sequence 23, Appl
					Sequence 429, App
					Sequence 9, Appli
					Sequence 9, Appli
					Sequence 23, Appl
					Sequence 7, Appli
					Sequence 18, Appli

12	4296.5	72.5	1163	16	US-10-810-653-18	Sequence 18, Appli
13	4289	72.4	1162	16	US-10-633-423-10	Sequence 10, Appli
14	4289	72.4	1162	16	US-10-427-741-10	Sequence 10, Appli
15	4277.5	72.2	1163	15	US-10-267-502-431	Sequence 431, App
16	1495.5	25.2	373	9	US-09-789-386-6	Sequence 6, Appli
17	1495.5	25.2	373	9	US-09-765-205-6	Sequence 6, Appli
18	1495.5	25.2	373	9	US-09-893-348-24	Sequence 24, Appli
19	1495.5	25.2	373	14	US-10-060-036-72	Sequence 72, Appli
20	1495.5	25.2	373	15	US-10-408-967-8	Sequence 8, Appli
21	1495.5	25.2	373	16	US-10-810-653-24	Sequence 24, Appli
22	1495.5	25.2	373	17	US-10-347-669-6	Sequence 6, Appli
23	1487.5	25.1	373	16	US-10-466-258-4	Sequence 4, Appli
24	1417	23.9	289	9	US-09-789-386-4	Sequence 4, Appli
25	1225.5	20.7	379	14	US-10-205-194-164	Sequence 164, App
26	1187	20.0	360	9	US-09-893-348-20	Sequence 20, Appli
27	1187	20.0	360	16	US-10-810-653-20	Sequence 20, Appli
28	931	15.7	199	9	US-09-893-348-25	Sequence 25, Appli
29	931	15.7	199	15	US-10-660-946-1	Sequence 1, Appli
30	931	15.7	199	16	US-10-810-653-25	Sequence 25, Appli
31	924	15.6	199	15	US-10-408-967-9	Sequence 9, Appli
32	922	15.6	199	11	US-09-978-360A-467	Sequence 467, App
33	908	15.3	199	9	US-09-893-348-21	Sequence 21, Appli
34	908	15.3	199	16	US-10-810-653-21	Sequence 21, Appli
35	890	15.0	199	16	US-10-466-258-11	Sequence 11, Appli
36	791	13.4	777	14	US-10-205-219-93	Sequence 93, Appli
37	787.5	13.3	776	15	US-10-660-946-5	Sequence 5, Appli
38	787.5	13.3	776	15	US-10-267-502-430	Sequence 430, App
39	787.5	13.3	776	16	US-10-723-860-1481	Sequence 1481, Ap
40	779	13.2	780	15	US-10-267-502-432	Sequence 432, App
41	705	11.9	356	15	US-10-660-946-6	Sequence 6, Appli
42	704	11.9	593	15	US-10-108-260A-2892	Sequence 2892, Ap
43	688	11.6	208	15	US-10-660-946-7	Sequence 7, Appli
44	671	11.3	267	14	US-10-205-194-127	Sequence 127, App
45	671	11.3	267	15	US-10-660-946-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1  
US-09-758-140-6  
; Sequence 6, Application US/09758140  
; Patent No. US20020012965A1  
; GENERAL INFORMATION:  
; APPLICANT: Strittmatter, Stephen M.  
; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth  
; FILE REFERENCE: 44574-5073-US  
; CURRENT APPLICATION NUMBER: US/09/758,140  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/175,707  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: US 60/207,366  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/236,378  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-758-140-6

Query Match 98.2%; Score 5815; DB 9; Length 1192;  
Best Local Similarity 97.2%; Pred. No. 3.4e-261;  
Matches 1160; Conservative 4; Mismatches 13; Indels 16; Gaps 3;  
Qy 1 MEDLDQSLVSSSPRPQPAFKYQFVREDEDEDEDEDEDEDELEVLKPA 60  
Db 1 MEDLDQSLVSSSPRPQPAFKYQFVREDEDEDEDEDEDEDELEVLKPA 60  
Qy 61 AGLSAAPVFTAPAGAPLMDGNFVPPAPRGPLPAPVPAPERQSPVSTVPAP 120

Db 61 AGLSAAPVPTAPAAAGAPLMDFGNDFVPPAPRGPLPAAPVPAERQPSWDPSPVSVSTVPAP 120  
QY 121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSQAEPVMTTPAPAPAAAPSTPAAPKRRG 180  
Db 121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSQAEPVMTTPAPAPAAAPSTPAAPKRRG 180  
QY 181 SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASPSLSP 226  
Db 181 SSGVDETLFPALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASPSLSP 240  
QY 227 LSAAAPKEHYLGNLSTVLPTGTLQENVSEASKEVSEKAKTLLIDRLDTEFSELEYSEM 286  
Db 241 LSAAAPKEHYLGNLSTVLPTGTLQENVSEASKEVSEKAKTLLIDRLDTEFSELEYSEM 300  
QY 287 GGSFVSVPKASAVIVANPREELIVKNKDEEKLVSNNILHXQOELPTALTKLVKEDVV 346  
Db 301 GGSFVSVPKASAVIVANPREELIVKNKDEEKLVSNNILHXQOELPTALTKLVKEDVV 360  
QY 347 SSEKAKDSFNEKRVAVEAPMREYADFKPFRVWEVKDSKEDSDMLAAGKIESNLESKV 406  
Db 361 SSEKAKDSFNEKRVAVEAPMREYADFKPFRVWEVKDSKEDSDMLAAGKIESNLESKV 420  
QY 407 DKCFADSLQTNHKEKDESSNDTSPSTPEGIKDRSGAYITCAPNPAATESIATNIF 466  
Db 421 DKCFADSLQTNHKEKDESSNDTSPSTPEGIKDRSGAYITCAPNPAATESIATNIF 480  
QY 467 PLLEDPTSENKXTDEKKIEBKAKIIVTEKNTSTKTSNPFVVAQDSSTDYVTTDNLTKVTE 526  
Db 481 PLUGDPTSENKXTDEKKIEBKAKIIVTEKNTSTKTSNPFVVAQDSSTDYVTTDNLTKVTE 540  
QY 527 EVVANMPEGLTDPDLVQEAACESLNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQCPSP 586  
Db 541 EVVANMPEGLTDPDLVQEAACESLNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQCPSP 600  
QY 587 ESEATPSPVLPDIWVAPLNSAVPSAGASVIOPLSSSPLSEASVNYESIKHEPENPPPYE 646  
Db 601 ESEATPSPVLPDIWVAPLNSAVPSAGASVIOPLSSSPLSEASVNYESIKHEPENPPPYE 660  
QY 647 EAMSLSL-KVSGIKSEIKPENINAAALQETAPYISIACDLIKETKLSAPPDPDSYSE 705  
Db 661 EAMSLSLKVSGIKSEIKPENINAAALQETAPYISIACDLIKETKLSAPPDPDSYSE 720  
QY 706 MAKVEQVDPHSLVEDSDSPDSEVDLFSDDSIPTVPQKQDETWMLVKESLTSFESMI 765  
Db 721 MAKVEQVDPHSLVEDSDSPDSEVDLFSDDSIPTVPQKQDETWMLVKESLTSFESMI 780  
QY 766 EYENKEKLSALPPEGKPYLESFKLSLDNTKOTLLPDEVSTLSKKEKIPLOMEELSTAVY 825  
Db 781 EYENKEKLSALPPEGKPYLESFKLSLDNTKOTLLPDEVSTLSKKEKIPLOMEELSTAVY 840  
QY 826 SNDDLFIKSEAQIRETETSDSSPIEIIDFPPTLISKTDSPSKLAREYTDLEVSHKSEI 885  
Db 841 SNDDLFIKSEAQIRETETSDSSPIEIIDFPPTLISKTDSPSKLAREYTDLEVSHKSEI 900  
QY 886 ANAPDGAGSLPCTELPHDLISLKNIQPKVEEKISFSDDFKNGSATSKVLLLPDVSALGH 945  
Db 901 ANAPDGAGSLPCTELPHDLISLKNIQPKVEEKISFSDDFKNGSATSKVLLLPDVSALGH 959  
QY 946 TQAEIESIVKPKVLEKAEKKLPDTEKEDRSPSAIFSADLGTSVVDLLLYWRDIDKKTGV 1005  
Db 960 TQAEIESIVKPKVLEKAEKKLPDTEKEDRSPSAIFSADLGTSVVDLLLYWRDIDKKTGV 1019  
QY 1006 VFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLES 1065  
Db 1020 VFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLES 1079  
QY 1066 EVAISEELVQKYSNLSALGHVNTCIKELRLFLVDDLDVSLKFAVLMVFTYVVALENGLT 1125  
Db 1080 EVAISEELVQKYSNLSALGHVNTCIKELRLFLVDDLDVSLKFAVLMVFTYVVALENGLT 1139  
QY 1126 LLTALISLSPSVPIYERHQAQIDHYILGLANKNVKDMAKIOAKIPGLKEKAE 1178  
Db 1140 LLTALISLSPSVPIYERHQAQIDHYILGLANKNVKDMAKIOAKIPGLKEKAE 1192

## RESULT 2

US-09-972-599A-6  
; Sequence 6, Application US/099725599A  
; Patent No. US20020077295A1  
; GENERAL INFORMATION:  
; APPLICANT: STRITTMATTER, STEPHEN M.  
; TITLE OF INVENTION: NOCO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH  
; FILE REFERENCE: C077 CIP US  
; CURRENT APPLICATION NUMBER: US/09/972,599A  
; CURRENT FILING DATE: 2001-10-06  
; PRIOR APPLICATION NUMBER: PCT/US01/01041  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 09/758,140  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 60/236,378  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/207,366  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/175,707  
; PRIOR FILING DATE: 2000-01-12  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-972-599A-6

Query Match 98.2%; Score 5815; DB 9; Length 1192;

Best Local Similarity 97.2%; Pred. No. 3.4e-261;  
Matches 1160; Conservative 4; Mismatches 13; Indels 16; Gaps 3;

QY 1 MEDLDOSPLVSSSDSPRPQPAFKYQFVREPEDEDEDEDEDEDEDEDEDEDEDELEEVLERKPA 60  
Db 1 MEDLDOSPLVSSSDSPRPQPAFKYQFVREPEDEDEDEDEDEDEDEDEDEDEDELEEVLERKPA 60  
QY 61 AGLSAAPVPTAPAAAGAPLMDFGNDFVPPAPRGPLPAAPVPAERQPSWDPSPVSVSTVPAP 120  
Db 61 AGLSAAPVPTAPAAAGAPLMDFGNDFVPPAPRGPLPAAPVPAERQPSWDPSPVSVSTVPAP 120  
QY 121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSQAEPVMTTPAPAPAAAPSTPAAPKRRG 180  
Db 121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSQAEPVMTTPAPAPAAAPSTPAAPKRRG 180  
QY 181 SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASPSLSP 226  
Db 181 SSGVDETLFPALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASPSLSP 240  
QY 227 LSAAAPKEHYLGNLSTVLPTGTLQENVSEASKEVSEKAKTLLIDRLDTEFSELEYSEM 286  
Db 241 LSAAAPKEHYLGNLSTVLPTGTLQENVSEASKEVSEKAKTLLIDRLDTEFSELEYSEM 300  
QY 287 GGSFVSVPKASAVIVANPREELIVKNKDEEKLVSNNILHXQOELPTALTKLVKEDVV 346  
Db 301 GGSFVSVPKASAVIVANPREELIVKNKDEEKLVSNNILHXQOELPTALTKLVKEDVV 360  
QY 347 SSEKAKDSFNEKRVAVEAPMREYADFKPFRVWEVKDSKEDSDMLAAGKIESNLESKV 406  
Db 361 SSEKAKDSFNEKRVAVEAPMREYADFKPFRVWEVKDSKEDSDMLAAGKIESNLESKV 420  
QY 407 DKCFADSLQTNHKEKDESSNDTSPSTPEGIKDRSGAYITCAPNPAATESIATNIF 466  
Db 421 DKCFADSLQTNHKEKDESSNDTSPSTPEGIKDRSGAYITCAPNPAATESIATNIF 480  
QY 467 PLLEDPTSENKXTDEKKIEBKAKIIVTEKNTSTKTSNPFVVAQDSSTDYVTTDNLTKVTE 526  
Db 481 PLUGDPTSENKXTDEKKIEBKAKIIVTEKNTSTKTSNPFVVAQDSSTDYVTTDNLTKVTE 540  
QY 527 EVVANMPEGLTDPDLVQEAACESLNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQCPSP 586  
Db 541 EVVANMPEGLTDPDLVQEAACESLNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQCPSP 600







Best Local Similarity 97.2%; Pred. No. 5,9e-261; Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;	
QY 1 MEDLDQSLVSSSDSPRPQPAFKYQFVREPEDEEEEDDEDELEEVLERKPA 60	
DB 1 MEDLDQSLVSSSDSPRPQPAFKYQFVREPEDEEEEDDEDELEEVLERKPA 60	
QY 61 AGLSAAVPPTAPAAAGAPLMDFGNDVFPAPRGPPLPAAPVAPERQSPWDPSPVSTVPAP 120	
DB 61 AGLSAAVPPTAPAAAGAPLMDFGNDVFPAPRGPPLPAAPVAPERQSPWDPSPVSTVPAP 120	
QY 121 SPLSAAAVSPSKLPEDDEPPAPPPPPASVSQAEVWTPPPAPAPAPSTPAAPKRG 180	
DB 121 SPLSAAAVSPSKLPEDDEPPAPPPPPASVSQAEVWTPPPAPAPAPSTPAAPKRG 180	
QY 181 SSGA-----VVXXXKIMDLKEQPGNTISAGQEDFPSVLETAASPSLSP 226	
DB 181 SSGA-----VVXXXKIMDLKEQPGNTISAGQEDFPSVLETAASPSLSP 240	
QY 227 LSAASFKEHEYLGNLSTVLTPTGTLQENVSEASKEVSEKAKTLLIDRDLTFESELEYSEM 286	
DB 241 LSAASFKEHEYLGNLSTVLTPTGTLQENVSEASKEVSEKAKTLLIDRDLTFESELEYSEM 300	
QY 287 GSSFSVSPKAESAVIVANPREBIIIVKNKDEBEKLVSNILHXQBELPTALTKLVKEDVV 346	
DB 301 GSSFSVSPKAESAVIVANPREBIIIVKNKDEBEKLVSNILHXQBELPTALTKLVKEDVV 360	
QY 347 SSEKAKDSFNKRVAEAPMREYADFKPFRVWEVKDSKEDSMDLAAGGKIESNLSKV 406	
DB 361 SSEKAKDSFNKRVAEAPMREYADFKPFRVWEVKDSKEDSMDLAAGGKIESNLSKV 420	
QY 407 DKCFADSLQTNHKEKDSSESSNDTSPSTPEGIKORSGAVITCAPNPAATESIATNIF 466	
DB 421 DKCFADSLQTNHKEKDSSESSNDTSPSTPEGIKORSGAVITCAPNPAATESIATNIF 480	
QY 467 PLLDPTSENXTDKKIEBKAKQIVTEKNTSTKTSNPPFVAAQDSETDYVTTDNLTKYTE 526	
DB 481 PLLDPTSENXTDKKIEBKAKQIVTEKNTSTKTSNPPFVAAQDSETDYVTTDNLTKYTE 540	
QY 527 EVVANMPEGLTPDLVQACESELNEVTGKIAYETKMDLVQTSVMQESLYPAAQLCPSP 586	
DB 541 EVVANMPEGLTPDLVQACESELNEVTGKIAYETKMDLVQTSVMQESLYPAAQLCPSP 600	
QY 587 EBEATPSPVLPDIIVMEAPLNAVPSAGASVITQSSSPLEASSVNYESI KHEPENPPYE 646	
DB 601 EBEATPSPVLPDIIVMEAPLNAVPSAGASVITQSSSPLEASSVNYESI KHEPENPPYE 660	
QY 647 EAMSVSL-KVSGIKEEIKPENINAALQTEAPYISIACDLIKETKLSAEPAPDFS DYSE 705	
DB 661 EAMSVSLKVKSGIKEEIKPENINAALQTEAPYISIACDLIKETKLSAEPAPDFS DYSE 720	
QY 706 MAKVEQVPDHSSELVEDSPDVLPSDDSIPOVPQKQDETVMLVKESLTETSFESMI 765	
DB 721 MAKVEQVPDHSSELVEDSPDVLPSDDSIPOVPQKQDETVMLVKESLTETSFESMI 780	
QY 766 EYENKEKLSALPPEGKPYLESFKLSLONTKDTLLPDEVSTLSKKEKIPLOWEELSTAVY 825	
DB 781 EYENKEKLSALPPEGKPYLESFKLSLONTKDTLLPDEVSTLSKKEKIPLOWEELSTAVY 840	
QY 826 SNDDLFIKSAQIRIETETFSOSSPIEIIIDEPFTLISSTKTSFKLSAREYTDLEVSHKSEI 885	
DB 841 SNDDLFIKSAQIRIETETFSOSSPIEIIIDEPFTLISSTKTSFKLSAREYTDLEVSHKSEI 900	
QY 886 ANAPGAGSLPCTELPHDLSLKNIQPVKEEKISFSDDFSNGKSGATSCKVLLPPDVVSALGH 945	
DB 901 ANAPGAGSLPCTELPHDLSLKNIQPVKEEKISFSDDFSNGKSGATSCKVLLPPDVVSALA- 959	
QY 946 TQAEIESIVKPVLEKEKELPSDTEKEDRSPSAIFSA DLGKTSVVDLLLYWRDIIKKTGV 1005	
DB 960 TQAEIESIVKPVLEKEKELPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIIKKTGV 1019	
QY 1006 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAQKSDGHPFRAYLES 1065	

DB 1020 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAQKSDGHPFRAYLES 1079	
QY 1066 EVAISEELVOKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFAVLMWFTYVYGALPNGLT 1125	
DB 1080 EVAISEELVOKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFAVLMWFTYVYGALPNGLT 1139	
QY 1126 LILIALISLFSVPVIYERHQAOIDHYLGLANKVNDAMAKIOAKIPGLKRAE 1178	
DB 1140 LILIALISLFSVPVIYERHQAOIDHYLGLANKVNDAMAKIOAKIPGLKRAE 1192	
RESULT 6	
US-10-267-502-429	
; Sequence 429, Application US/10267502	
; Publication No. US20040071700A1	
; GENERAL INFORMATION:	
; APPLICANT: Kim, Jaeseob	
; APPLICANT: Galant, Ron	
; TITLE OF INVENTION: Obesity Linked Genes	
; FILE REFERENCE: LSD-07416	
; CURRENT APPLICATION NUMBER: US/10/267,502	
; CURRENT FILING DATE: 2003-01-27	
; NUMBER OF SEQ ID NOS: 439	
; SOFTWARE: PatentIn version 3.2	
; SEQ ID NO 429	
; LENGTH: 1192	
; TYPE: PRT	
; ORGANISM: Homo sapiens	
US-10-267-502-429	
Query Match 98.1%; Score 5810; DB 15; Length 1192;	
Best Local Similarity 97.2%; Pred. No. 5,9e-261;	
Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;	
QY 1 MEDLDQSLVSSSDSPRPQPAFKYQFVREPEDEEEEDDEDELEEVLERKPA 60	
DB 1 MEDLDQSLVSSSDSPRPQPAFKYQFVREPEDEEEEDDEDELEEVLERKPA 60	
QY 61 AGLSAAVPPTAPAAAGAPLMDFGNDVFPAPRGPPLPAAPVAPERQSPWDPSPVSTVPAP 120	
DB 61 AGLSAAVPPTAPAAAGAPLMDFGNDVFPAPRGPPLPAAPVAPERQSPWDPSPVSTVPAP 120	
QY 121 SPLSAAAVSPSKLPEDDEPPAPPPPPASVSQAEVWTPPPAPAPAPSTPAAPKRG 180	
DB 121 SPLSAAAVSPSKLPEDDEPPAPPPPPASVSQAEVWTPPPAPAPAPSTPAAPKRG 180	
QY 181 SSGA-----VVXXXKIMDLKEQPGNTISAGQEDFPSVLETAASPSLSP 226	
DB 181 SSGA-----VVXXXKIMDLKEQPGNTISAGQEDFPSVLETAASPSLSP 240	
QY 227 LSAASFKEHEYLGNLSTVLTPTGTLQENVSEASKEVSEKAKTLLIDRDLTFESELEYSEM 286	
DB 241 LSAASFKEHEYLGNLSTVLTPTGTLQENVSEASKEVSEKAKTLLIDRDLTFESELEYSEM 300	
QY 287 GSSFSVSPKAESAVIVANPREBIIIVKNKDEBEKLVSNILHXQBELPTALTKLVKEDVV 346	
DB 301 GSSFSVSPKAESAVIVANPREBIIIVKNKDEBEKLVSNILHXQBELPTALTKLVKEDVV 360	
QY 347 SSEKAKDSFNKRVAEAPMREYADFKPFRVWEVKDSKEDSMDLAAGGKIESNLSKV 406	
DB 361 SSEKAKDSFNKRVAEAPMREYADFKPFRVWEVKDSKEDSMDLAAGGKIESNLSKV 420	
QY 407 DKCFADSLQTNHKEKDSSESSNDTSPSTPEGIKORSGAVITCAPNPAATESIATNIF 466	
DB 421 DKCFADSLQTNHKEKDSSESSNDTSPSTPEGIKORSGAVITCAPNPAATESIATNIF 480	
QY 467 PLLDPTSENXTDKKIEBKAKQIVTEKNTSTKTSNPPFVAAQDSETDYVTTDNLTKYTE 526	
DB 481 PLLDPTSENXTDKKIEBKAKQIVTEKNTSTKTSNPPFVAAQDSETDYVTTDNLTKYTE 540	
QY 527 EVVANMPEGLTPDLVQACESELNEVTGKIAYETKMDLVQTSVMQESLYPAAQLCPSP 586	
DB 541 EVVANMPEGLTPDLVQACESELNEVTGKIAYETKMDLVQTSVMQESLYPAAQLCPSP 600	
QY 587 EBEATPSPVLPDIIVMEAPLNAVPSAGASVITQSSSPLEASSVNYESI KHEPENPPYE 646	
DB 601 EBEATPSPVLPDIIVMEAPLNAVPSAGASVITQSSSPLEASSVNYESI KHEPENPPYE 660	
QY 647 EAMSVSL-KVSGIKEEIKPENINAALQTEAPYISIACDLIKETKLSAEPAPDFS DYSE 705	
DB 661 EAMSVSLKVKSGIKEEIKPENINAALQTEAPYISIACDLIKETKLSAEPAPDFS DYSE 720	
QY 706 MAKVEQVPDHSSELVEDSPDVLPSDDSIPOVPQKQDETVMLVKESLTETSFESMI 765	
DB 721 MAKVEQVPDHSSELVEDSPDVLPSDDSIPOVPQKQDETVMLVKESLTETSFESMI 780	
QY 766 EYENKEKLSALPPEGKPYLESFKLSLONTKDTLLPDEVSTLSKKEKIPLOWEELSTAVY 825	
DB 781 EYENKEKLSALPPEGKPYLESFKLSLONTKDTLLPDEVSTLSKKEKIPLOWEELSTAVY 840	
QY 826 SNDDLFIKSAQIRIETETFSOSSPIEIIIDEPFTLISSTKTSFKLSAREYTDLEVSHKSEI 885	
DB 841 SNDDLFIKSAQIRIETETFSOSSPIEIIIDEPFTLISSTKTSFKLSAREYTDLEVSHKSEI 900	
QY 886 ANAPGAGSLPCTELPHDLSLKNIQPVKEEKISFSDDFSNGKSGATSCKVLLPPDVVSALGH 945	
DB 901 ANAPGAGSLPCTELPHDLSLKNIQPVKEEKISFSDDFSNGKSGATSCKVLLPPDVVSALA- 959	
QY 946 TQAEIESIVKPVLEKEKELPSDTEKEDRSPSAIFSA DLGKTSVVDLLLYWRDIIKKTGV 1005	
DB 960 TQAEIESIVKPVLEKEKELPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIIKKTGV 1019	
QY 1006 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAQKSDGHPFRAYLES 1065	



RESULT 8  
US-10-466-258-9  
; Sequence 9, Application US/10466258  
; Publication No. US20040132096A1  
; GENERAL INFORMATION:  
; APPLICANT: GLAXO GROUP LIMITED  
; TITLE OF INVENTION: ASSAY  
; FILE REFERENCE: P80966 GCW  
; CURRENT APPLICATION NUMBER: US/10/466,258  
; PRIOR FILING DATE: 2003-07-15  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-466-258-9  
Query Match 98.1%; Score 5810; DB 16; Length 1192;  
Best Local Similarity 97.2%; Pred. No. 5.9e-261;  
Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;  
Qy 1 MEDLDQSLVSSDSPRPQPAFKYQFVREPEDEEEDEDEDELEVLERKPA 60  
Db 1 MEDLDQSLVSSDSPRPQPAFKYQFVREPEDEEEDEDEDELEVLERKPA 60  
Qy 61 AGLSAAPVPTAPAGAPLMDFGNDVFPAPRGPLPAAPVAPERQSPWDPSPVSTVPAP 120  
Db 61 AGLSAAPVPTAPAGAPLMDFGNDVFPAPRGPLPAAPVAPERQSPWDPSPVSTVPAP 120  
Qy 121 SPLSAAAVSPSKLPEDDPAPRPAPPPASVSPQAEVPTWTPAPAPAPPTAPAPKBERG 180  
Db 121 SPLSAAVSPSKLPEDDPAPRPAPPPASVSPQAEVPTWTPAPAPAPPTAPAPKBERG 180  
Qy 181 SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAAXPSLSP 226  
Db 181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAAXPSLSP 240  
Qy 227 LSAAFKHEHYGNLSTVLTPTGTLQENVSEASKEVSEKAKTLTLDRLTFSELEYSEM 286  
Db 241 LSAAFKHEHYGNLSTVLTPTGTLQENVSEASKEVSEKAKTLTLDRLTFSELEYSEM 300  
Qy 287 GSSFSVSPKASSAVIVANPREIIVKNKDBEKLVSNNILHXQQLPTALTAKLVKEDVV 346  
Db 301 GSSFSVSPKASSAVIVANPREIIVKNKDBEKLVSNNILHXQQLPTALTAKLVKEDVV 360  
Qy 347 SSEKAKDSFNKRVAVAPREEVADFKPFRVMEVKDSKEDSDMLAAGGKIESNLSKV 406  
Db 361 SSEKAKDSFNKRVAVAPREEVADFKPFRVMEVKDSKEDSDMLAAGGKIESNLSKV 420  
Qy 407 DKCFADSLQTNHKKDSSENNDDTSFPSTPEGIKDRSGAVITCAPFNPAATESIATNIF 466  
Db 421 DKCFADSLQTNHKKDSSENNDDTSFPSTPEGIKDRSGAVITCAPFNPAATESIATNIF 480  
Qy 467 PLLDPTSENKTDKKIEKKAQIVTEKNTSTKTSNPFVAAQSDSETDYVTTDNLTKYTE 526  
Db 481 PLLDPTSENKTDKKIEKKAQIVTEKNTSTKTSNPFVAAQSDSETDYVTTDNLTKYTE 540  
Qy 527 EVVANMPGLTPDLVQEAACESELNEVTGKTIAYETKMDLVQTVSEVMQESLYPAAQLCPSP 586  
Db 541 EVVANMPGLTPDLVQEAACESELNEVTGKTIAYETKMDLVQTVSEVMQESLYPAAQLCPSP 600  
Qy 587 ESEATPSVPLPDIWMEAPLNSAVPSAGASVIQSSSPLEASSVNYSEIKHEPNPPPYE 646  
Db 601 ESEATPSVPLPDIWMEAPLNSAVPSAGASVIQSSSPLEASSVNYSEIKHEPNPPPYE 660  
Qy 647 EAMSVSL-KVSGIKKEEIKPENINAAOETAPYISACDLIKETKLSAEPAPDFSDYSE 705  
Db 661 EAMSVSLKKVSGIKKEEIKPENINAAOETAPYISACDLIKETKLSAEPAPDFSDYSE 720  
Qy 706 MAKVEQPVDPHSELVEDSSPDSEPVDLFSDDSIPDPVQKQDETVMLVKESLTETSFESMI 765

Db 721 MAKVEQPVDPHSELVEDSSPDSEPVDLFSDDSIPDPVQKQDETVMLVKESLTETSFESMI 780  
Qy 766 EYENKEKLSALPPGGKPYLESFKLSLNTKOTLLPDEVSTLSKKEKIPLOWEELSTAVY 825  
Db 781 EYENKEKLSALPPGGKPYLESFKLSLNTKOTLLPDEVSTLSKKEKIPLOWEELSTAVY 840  
Qy 826 SNDDLFTISKEAQIRETETFSOSSPIIIDEPTTIISSKTDSFKLAREYTDLEVSHKSEI 885  
Db 841 SNDDLFTISKEAQIRETETFSOSSPIIIDEPTTIISSKTDSFKLAREYTDLEVSHKSEI 900  
Qy 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDSFKNKSATSFKVLLLPDVSALGH 945  
Db 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDSFKNKSATSFKVLLLPDVSALGH 959  
Qy 946 TQAEIESIVPKVLEKEAEKKLPDTEKEDRSPSAISADLGKTSVVDLLYWRDIIKKTGV 1005  
Db 960 TQAEIESIVPKVLEKEAEKKLPDTEKEDRSPSAISADLGKTSVVDLLYWRDIIKKTGV 1019  
Qy 1006 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPPRAYLES 1065  
Db 1020 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPPRAYLES 1079  
Qy 1066 EVAISEELVQKYSNSALGHVNCCTIKELRRLFLVDLVDLSKFAVLMVFTVYGALFNGLT 1125  
Db 1080 EVAISEELVQKYSNSALGHVNCCTIKELRRLFLVDLVDLSKFAVLMVFTVYGALFNGLT 1139  
Qy 1126 LLLIALLSLFSVPVIYERHQAOIDHYGLANKNVKDMAKIOAKIPGLKRKAE 1178  
Db 1140 LLLIALLSLFSVPVIYERHQAOIDHYGLANKNVKDMAKIOAKIPGLKRKAE 1192

RESULT 9

US-10-810-653-23  
; Sequence 23, Application US/10810653  
; Publication No. US20040253218A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN Itun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONOGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SCHWARTZ-2A  
; CURRENT APPLICATION NUMBER: US/10/810,653  
; CURRENT FILING DATE: 2004-03-29  
; PRIOR APPLICATION NUMBER: US/09/893,348  
; PRIOR FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 23  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-810-653-23

Query Match 98.1%; Score 5810; DB 16; Length 1192;  
Best Local Similarity 97.2%; Pred. No. 5.9e-261;  
Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;  
Qy 1 MEDLDQSLVSSDSPRPQPAFKYQFVREPEDEEEDEDEDELEVLERKPA 60  
Db 1 MEDLDQSLVSSDSPRPQPAFKYQFVREPEDEEEDEDEDELEVLERKPA 60  
Qy 61 AGLSAAPVPTAPAGAPLMDFGNDVFPAPRGPLPAAPVAPERQSPWDPSPVSTVPAP 120



Db 661 EAMSVLKKVSGIKKEIKPENAINAALQTEAPYISACDLIKETKLSAEPAPDFSDYSE 720  
Qy 706 MAKVQOPVDHSELVEDSDPEVDLFSDDSI PDVPOKQDVTMLVKESLTETSFESMI 765  
Db 721 MAKVQOPVDHSELVEDSDPEVDLFSDDSI PDVPOKQDVTMLVKESLTETSFESMI 780  
Qy 766 EYENKEKLSALPPEGKPYLESFKLSLONTKDTLLPDEVSTLSKKEKIPLOMEELSTAVY 825  
Db 781 EYENKEKLSALPPEGKPYLESFKLSLONTKDTLLPDEVSTLSKKEKIPLOMEELSTAVY 840  
Qy 826 SNDDLFIKSEAQIRETETFSDDSPIIIDEFTLLISSKTDSPKSLAREYTDLEVSHKSEI 885  
Db 841 SNDDLFIKSEAQIRETETFSDDSPIIIDEFTLLISSKTDSPKSLAREYTDLEVSHKSEI 900  
Qy 886 ANAPDAGSLPCTELPHDLISLKNIOPKVEEKISFSDDFSKNGSATSKVLLPPDVSALGH 945  
Db 901 ANAPDAGSLPCTELPHDLISLKNIOPKVEEKISFSDDFSKNGSATSKVLLPPDVSALGH 959  
Qy 946 TOAEIESIVKPKVLEKEAKKLPSDTEKEDRSPSAIFSDADLGKTSVVDLLYWRDIKKTGV 1005  
Db 960 TOAEIESIVKPKVLEKEAKKLPSDTEKEDRSPSAIFSDADLGKTSVVDLLYWRDIKKTGV 1019  
Qy 1006 VEGASLFLLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIOAIQKSGDEGHPFAYLES 1065  
Db 1020 VEGASLFLLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIOAIQKSGDEGHPFAYLES 1079  
Qy 1066 EVAISEELVOKYSNLSALGHVNTIKELRRLFLVDLVDLSKFAVLMVFTYVYGALFNGIT 1125  
Db 1080 EVAISEELVOKYSNLSALGHVNTIKELRRLFLVDLVDLSKFAVLMVFTYVYGALFNGIT 1139  
Qy 1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKIPGLKRAE 1178  
Db 1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKIPGLKRAE 1192

RESULT 11  
US-09-893-348-18  
; Sequence 18, Application US/09893348  
; Patent No. US20020072493A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN, Irun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SCHWARTZ-2A  
; CURRENT APPLICATION NUMBER: US/09/893,348  
; PRIOR FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 18  
; LENGTH: 1163  
; TYPE: PR1  
; ORGANISM: Rattus norvegicus  
US-09-893-348-18

Query Match 72.5%; Score 4296.5; DB 9; Length 1163;  
Best Local Similarity 74.0%; Pred. No. 7.9e-191;  
Matches 885; Conservative 104; Mismatch 156; Indels 51; Gaps 19;  
Qy 1 MEDLQSPVLVSS-DSPPRPQAFKYQVREPEDEE-BEEEEDEDEDEDEDELEVLERK 58  
Db 1 MEDIQSSLVSSSTDSPPRPAPKYQVTEPEDEDEDEDEDEDEDELEVLERK 60

Qy 59 PAAGLSAAVPPTAPAGAPLMDFGNDVFPAPRGPPLPAAPVPAERQSPWSPSPSVSTVP 118  
Db 61 PAAGLSAAVP--PAAAAPLLDFSDSVPPAPRGPPLPAAPVPAERQSPWSPSPSVSTVP 115  
Qy 119 APSPLSAAVSPSKLPEDDEPPAPRPPPPPPASVSPQABPVMTPPAPAPAPSTPAAPKR 178  
Db 116 APSLPPAAVLPKLPEDDEPPAPRPPPPPPAGASPLAE-----PAAAPSTPAAPKR 166  
Qy 179 RGSAG-----AVVXXXKXKMDLKEOPGNTISAGOEFPSPVLLLETAASPSL 224  
Db 167 RGSAGVDTLTFALPAASEPVPSSGAELMDLMEQPGNTVSSGQEDFPVLLLETAASPSL 226  
Qy 225 SPLSAAAFKEHEYLGNLSTVLPTTECTLOENVSEAKSEKAKTLLIDRDITFESELEYS 284  
Db 227 SPLSTVSPKEHGYLGNLSAVSSSECTIETLNEASKELPERATNPFVNRDLAEFSELEYS 286  
Qy 285 EMGSSFSVSPKASAVIVANPREIIVKNDKEEKLVNNIILHXOQELPTALTULVKEDE 344  
Db 287 EMGSSFPGSPKESAILVENTKEEIVRSKDKED-LVCSAALHSPQESPVG-----KEDR 340  
Qy 345 VVSSEKAKDSFNEKXVAVEAPMRREYADFKPFRVWEVKDSKEDS-DMLAAGGKTESNLE 403  
Db 341 VVSPEKTMWIDIFNEMQMSVAVPRBEYADFKPFEQAWEVKDYEGSRDLAA-----RANVE 396  
Qy 404 SKVDKCCFADSLQTNHEKDSSESSNDTSPSTPEGIDKDRSGAYITTCAPFPAATESIAT 463  
Db 397 SKVDKCLDSLEQKSLGKDSSEGNEDASFSTPEPVKDSRAYITCASFT--SATESITA 455  
Qy 464 NIFPLEDPTSENKTDKKEIKKAKQIVTEKNTSTKTSNPPFFVAAQDSETDVVTDTNLT 523  
Db 456 NTFPLEDHTSENKTDKKEIKBERAKQIITEK-TSPKTSNPFVAVQDSEADYVTTDTLSK 514  
Qy 524 VTEEVANMPGLTPDLVQEAECESLNEVCTKATAYETKMDLVOTSEVMOESLYPAAOLC 583  
Db 515 VTEAAVSNMPEGLTPDLVQEAECESLNEATGKATAYETKMDLVQVQSEALYETAQULC 574  
Qy 584 PSFESEATPSVLPDIWMEAPLNSAVPSAGASVIQPSSSPLEA--SSVNYESIKHEPENP 642  
Db 575 PSFEAEATPSVLPDIWMEAPLNSLPSAGASVVQPSVPLEAPPPVYSIDSKLEPENP 634  
Qy 643 PPYEAMSVLSKVGIEKEIKPENINAAQETRAPYISACDLIKETKLSAEPAPDFSD 702  
Db 635 PPYEAMNVALKGTGEGIKPEPSFNAAVQETAPYISACDLIKETKLSPEPSDFSN 694  
Qy 703 YSEMAKVEQPPDHSSELVEDSSPEVDLFSDDSI PDVPOKQDVTMLVKESLTETSE 762  
Db 695 YSEIAKFEKSVPEHAELVEDSSPEVDLFSDDSIPEVPQTOBEAVMLKESLTVES-E 753  
Qy 763 SMIEYENKEKLSALPPEGKPYLESFKLSLONTKDTLLPDEVSTLSKKEKIPLOMEELST 822  
Db 754 TVAQHK-EERLSASFOELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQWEEFNT 811  
Qy 823 AVYNDLDFISKEAQIRETETFSDDSPIIIDEFTLLISSKTDSPKSLAREYTDLEVSHK 882  
Db 812 AIYSNDLILLSSKEDKIKESETFSDDSPIIIDEFTTFVSADKDS-PKLAKEYTDLEVSDK 870  
Qy 883 SEIANAPDAGSLPCTELPHDLISLKNIOPKVEEKISFSDDFSKNGSATSKVLLPPDVS 942  
Db 871 SEIANOSGADSLPCLLPCLSPFNKIPYK--DEVHVSDEFSENRSSVSKASISPSNVA 928  
Qy 943 LGHTQABIESIVKPKVLEKEAKKLPSDTEKEDRSPSAIFSDADLGKTSVVDLLYWRDIK 1002  
Db 929 L-EPQTEMGSIKSKSLTKAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK 987  
Qy 1003 TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIOAIQKSGDEGHPFAY 1062  
Db 988 TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIOAIQKSGDEGHPFAY 1047  
Qy 1063 LESEVAISEELVOKYSNLSALGHVNTIKELRRLFLVDLVDLSKFAVLMVFTYVYGALFN 1122  
Db 1048 LESEVAISEELVOKYSNLSALGHVNTIKELRRLFLVDLVDLSKFAVLMVFTYVYGALFN 1107  
Qy 1123 GLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKIPGLKRAE 1178







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Db      517 TEAVATMEGLTPDLVQACBSSELNEATGTKIAVETKVDLVQTSBAIQESIYPTAQLCP 576
Qy      585 SPEEAEATSPVLPDIWMEAPLNSAVPSAGASVIOFSSSPLEA--SSVNYESIKHEPENPP 643
Db      577 SPEEAEATSPVLPDIWMEAPLNSLPGTASVAQSPASPLEVSPVSDGKLEPENPP 636
Qy      644 PYEAMSVLKVSGIKKEIKKEPENINAALQETAPYISACDLIKETKLSABPADPDSY 703
Db      637 PYEAMSVALKTSKEDKMKESSETFSDSSPIEIIDFPFVSAKDDSD---PKEYTDLEVSNN 696
Qy      704 SEMAKVEQVPDHSSELVEDSSPDSEPVDFSDSDIPDPVKODETVMVKESITETSPES 763
Db      697 SEIAKFEKSVPHCELVDSSSESEPVDFSDSDIPDPVKODETVMVKESITETSPES 755
Qy      764 MIEYENKELKSALPPGEGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLOMBELSTA 823
Db      756 VTQHKHERLSASPOEVGKPYLESFQPNLHITKDA--ASNEIPTLTCKETISLQMEEFNTA 814
Qy      824 VYSNDDLFISKGAQIRETETFSDDSPPIEIIDFPFVSAKDDSD---PKEYTDLEVSNN 883
Db      815 IYSNDDLLSSKEDKMKESSETFSDSSPIEIIDFPFVSAKDDSD---PKEYTDLEVSNN 870
Qy      884 ETANAPDGAGSLPCTELPHDLISLKNIQKVEEKISFSDDFSKNGSATSKVLLPPDVSA 943
Db      871 ETANVQSGANSLPCSELPCDLSFKNTYPKDEAHV--SDEFKSRSSVSKVPULLPNVSA 928
Qy      944 GHTQAEIESIVKPKVLEKEAEKLPSTDEKEDRSPSAIFSDADLGKTSVVDLLYWRDIKKT 1003
Db      929 -ESQIEMGNIVKPKVLTKEAEKLPSTDEKEDRSLTAVLSAELNKTSSVVDLLYWRDIKKT 987
Qy      1004 GVYFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDSGHPFRAYL 1063
Db      988 GVYFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDSGHPFRAYL 1047
Qy      1064 ESEVAISELVOKYSNSALGHVNCITIKELRLFLVDLLVSLKFAVLMVFTYVGALENG 1123
Db      1048 ESEVAISELVOKYSNSALGHVNCITIKELRLFLVDLLVSLKFAVLMVFTYVGALENG 1107
Qy      1124 LTLILALISLFSVPVIYERHQAQIDHYGLANKNVKDMAKIOAIQKPLKRAE 1178
Db      1108 LTLILALISLFSVPVIYERHQAQIDHYGLANKNVKDMAKIOAIQKPLKRAE 1162

RESULT 15
US-10-267-502-431
; Sequence 431, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 431
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-267-502-431

Query Match      72.2%; Score 4277.5; DB 15; Length 1163;
Best Local Similarity 73.8%; Pred. No. 6e-190;
Matches 883; Conservative 108; Mismatches 154; Indels 51; Gaps 19;

Qy      1 MEDLDOSPLVSSS--DSPPRQPAFKYQFVREDEDEDEDEDEDEDELELEVLERKP 59
Db      1 MEDIDQSSLVSSADSPPPPPAFKYQFVTEPEDEDEDEDEDEDEDELELEVLERKP 60
Qy      60 AAGLSAAPTAPAAAGALMDFNDFVPPAPRGLPAAAPPAPEROPSPWDPSPVSTVPA 119
Db      61 AAGLSAVPVP--PAA--APLLDSSDSVPPAPRGLPAAAPTAPERQPSWERSPAAS--A 114

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Qy      120 PSLSAAAASVPSKLPEDDEPPARPPPPASVSPOAEVPVWTPPAPAPAPPPSTPAAPKRR 179
Db      115 PSLPAAAASVPSKLPEDDEPPAR--PPAPAGASPLAE-----PAAPPSTPAAPKRR 163
Qy      180 GSSG-----AVVXXXKIMDLKEOPGNTISAGOEDFPFVSLTETAASXPSLS 225
Db      164 GSGSVDETLFALPAASEPVPISSAEKIMDLKEOPGNTVSSGOEDFPFVLFETAASLPSLS 223
Qy      226 PLASAAAFKEHEHLYGNLSTVLPTEGLQENVSEASKEVSEKAKTLLTIDRLDTSESELEYE 285
Db      224 PLSTVSFKEHLYGNLNAVASTEGTIEETLNEASRELPERATNPFWNESAESFVLEYSE 283
Qy      286 MGSSFSVSPKASAVIVANPREIIIVKNKDBEKLVSNNILHXQELPTALTKLVKEDV 345
Db      284 MGSSFNFGSPKESAMLVENTKEEVIVRSKDKED-LVCSAALHNPOESPATLTKVVKEDGV 342
Qy      346 VSSEKAKDSFNEKRVAVAEAPMBEEYADFKPERVMEVKDSKEDS--DMLAAGGKIESNL 404
Db      343 MSPEKTMDFINEMKMSVAVPVEEYADFKPFQAVEVKDTEYEGSRDVLAA----RANMES 398
Qy      405 KVDKCFADSLFQTNHEKDSSENDDTSPSPTEGIDKDRSGAYITCAPENPAATSIATN 464
Db      399 KVDKCFEDSLQKSHGKDSERNENASFPSTPELVKDSRAYITCDST--SATESTAN 457
Qy      465 IPPLEDPTSENKTDKKEIEKKAQIVTEKNTSTKSNPFFVAAODSETDYVTTDNLTKV 524
Db      458 IPPVLEDHTSENKTDKKEIEKKAQIITEK--TSPKTSNPFLVAIHDSADYVTTDNLTKV 516
Qy      525 TEEVYANWPEGLTPDLVQACBSSELNEATGTKIAVETKMDLVQTSVMEVQESLYPAQALCP 584
Db      517 TEAVATMEGLTPDLVQACBSSELNEATGTKIAVETKMDLVQTSVMEVQESLYPAQALCP 576
Qy      585 SPEEAEATSPVLPDIWMEAPLNSAVPSAGASVIOFSSSPLEA--SSVNYESIKHEPENPP 643
Db      577 SPEEAEATSPVLPDIWMEAPLNSLPGTASVAQSPASPLEVSPVSDGKLEPENPP 636
Qy      644 PYEAMSVLKVSGIKKEIKKEPENINAALQETAPYISACDLIKETKLSABPADPDSY 703
Db      637 PYEAMSVALKTSKEDKMKESSETFSDSSPIEIIDFPFVSAKDDSD---PKEYTDLEVSNN 696
Qy      704 SEMAKVEQVPDHSSELVEDSSPDSEPVDFSDSDIPDPVKODETVMVKESITETSPES 763
Db      697 SEIAKFEKSVPHCELVDSSSESEPVDFSDSDIPDPVKODETVMVKESITETSPES 755
Qy      764 MIEYENKELKSALPPGEGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLOMBELSTA 823
Db      756 VTQHKHERLSASPOEVGKPYLESFQPNLHITKDA--ASNEIPTLTCKETISLQMEEFNTA 814
Qy      824 VYSNDDLFISKGAQIRETETFSDDSPPIEIIDFPFVSAKDDSD---PKEYTDLEVSNN 883
Db      815 IYSNDDLLSSKEDKMKESSETFSDSSPIEIIDFPFVSAKDDSD---PKEYTDLEVSNN 870
Qy      884 ETANAPDGAGSLPCTELPHDLISLKNIQKVEEKISFSDDFSKNGSATSKVLLPPDVSA 943
Db      871 ETANVQSGANSLPCSELPCDLSFKNTYPKDEAHV--SDEFKSRSSVSKVPULLPNVSA 928
Qy      944 GHTQAEIESIVKPKVLEKEAEKLPSTDEKEDRSPSAIFSDADLGKTSVVDLLYWRDIKKT 1003
Db      929 -ESQIEMGNIVKPKVLTKEAEKLPSTDEKEDRSLTAVLSAELNKTSSVVDLLYWRDIKKT 987
Qy      1004 GVYFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDSGHPFRAY 1063
Db      988 GVYFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDSGHPFRAY 1047
Qy      1063 LESEVAISELVOKYSNSALGHVNCITIKELRLFLVDLLVSLKFAVLMVFTYVGALENG 1122
Db      1048 LESEVAISELVOKYSNSALGHVNCITIKELRLFLVDLLVSLKFAVLMVFTYVGALENG 1107
Qy      1123 LTLILALISLFSVPVIYERHQAQIDHYGLANKNVKDMAKIOAIQKPLKRAE 1178
Db      1108 LTLILALISLFSVPVIYERHQAQIDHYGLANKNVKDMAKIOAIQKPLKRAE 1163

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Search completed: June 16, 2005, 13:04:04  
Job time : 158.811 secs

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Result No.	Score	Query Match	Length	DB	ID	Description	
1	787.5	13.3	776	2	A45583	neuroendocrine-spe	
2	688	11.6	208	2	I60904	neuroendocrine-spe	
3	671	11.3	267	2	A60021	tropomyosin-relate	
4	528	8.9	2484	2	T22216	hypothetical prote	
5	519.5	8.8	2607	2	T22215	hypothetical prote	
6	340.5	5.7	222	2	T22213	hypothetical prote	
7	331	5.6	7962	2	T18346	elastic titin - hu	
8	325.5	5.5	5337	2	T13564	microtubule-associ	
9	324.5	5.5	865	2	A47282	calcium-binding pr	
10	320.5	5.4	873	2	A47283	calphorin - fruit	
11	299.5	5.1	3488	2	T34418	hypothetical prote	
12	299	5.0	3924	2	S37431	ankyrin 2, neuro	
13	290.5	4.9	1274	2	T16251	hypothetical prote	
14	289	4.9	2364	2	A55577	microtubule-associ	
15	289	4.9	2464	1	QRNSP1	microtubule-associ	
16	287.5	4.9	971	2	T19431	hypothetical prote	
17	285.5	4.8	1621	2	A82255	hypothetical prote	
18	278	4.7	1948	2	S00485	gene 11-1 protein	
19	274	4.6	3507	2	T34513	hypothetical prote	
20	272.5	4.6	1829	2	T24583	hypothetical prote	
21	272.5	4.6	2361	2	T25752	hypothetical prote	
22	271	4.6	2187	2	T30826	nascent polypeptid	
23	270	4.6	1230	2	T22458	hypothetical prote	
24	267.5	4.5	1851	2	T19964	hypothetical prote	
25	263.5	4.4	2409	1	A60979	versican precursor	
26	262.5	4.4	6642	2	T29757	protein UNC-89 - C	
27	261	4.4	1558	2	B71603	RESA-H3 antigen p	
28	260.5	4.4	3381	2	T42389	versican precursor	
29	259.5	4.4	1828	2	A40115	microtubule-associ	

Db 404 SBAESGD-----SEIELVSEDPMAAEDALPSGYVSGHVGPPSP 444  
QY 869 -----KLAREYTDLEVSHKSEIANAPDAGSLPCTELPHDLISLKNIQPKVEEKISFSD 921  
Db 445 ASPIQOYSILREAREAELOSELLIESCDASSAS-----EESPKREQDSPPMKPSALD 496  
QY 922 DF-----SKNGSATSKVLL-----LPPDVSALGHTQAEISIVKP 956  
Db 497 AIREETGVRAERAPRRGLAEPGSLDYFSTPEPQGPBEPDGDGAL-----EPETPMLP 551  
QY 957 KVLKEAEKPLSDTEKEDEKSPSA-----LFSADLGKTSVDLLYWRDIK 1001  
Db 552 -----RKEEDSSSQSPARTKGPGLPGAPPPPLF---LNKQKADLLYWRDIK 599  
QY 1002 KTGWVGASLFLLSLTIVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSGDEGHPFRA 1061  
Db 600 QTGIVFGSFLLLLSLTQFSVSVVAYLALAALSATISFRIYKSVLQAVQKTDGHPFKA 659  
QY 1062 YLESEVAISELQKYSNLSALGHVNCITIKELRRLFLVDVLSLKPFAVLMMWFTYVYVGLP 1121  
Db 660 YLELEITLSQEQIKYTDCLQFYVNSTLKLRLFLVDVLSLKPFAVLMMWFTYVYVGLP 719  
QY 1122 NGTLTLLALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKIPGLKRAE 1178  
Db 720 NGTLTLLMAVSMFTLPVYVYKHQAQIDQYGLVLRTHINAVAKIOAKIPGAKRAE 776  
RESULT 2  
160904  
neuroendocrine-specific protein C - human  
C:Species: Homo sapiens (man)  
C>Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 09-Jul-2004  
C:Accession: I60904  
R:Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; V  
J. Biol. Chem. 268, 13439-13447, 1993  
A:Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spe  
A:Reference number: A46583; MUID:93233865; PMID:7685762  
A:Accession: I60904  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Cross-references: UNIPROT:Q16799; GB:L10335; NID:g307310; PIDN:AAA59952.1; PID:g307311  
C:Genetics:  
A:Gene: GDB:RTN1; NSP  
A:Map position: 14q21-14q22  
Query Match 11.6%; Score 688; DB 2: Length 208;  
Best Local Similarity 67.5%; Pred. No. 1.4e-21;  
Matches 129; Conservative 32; Mismatches 30; Indels 0; Gaps 0;  
QY 988 KTSVVDLLYWRDIKKTGVVFGASLFLLSLTIVFSIVSVTAYIALALLSVTISFRIYKGV 1047  
Db 18 KQAIDLLYWRDIKQTGIVFGSFLLLLSLTQFSVSVVAYLALAALSATISFRIYKSVL 77  
QY 1048 QAIQKSGDEGHPFRAYLESEVAISELQKYSNLSALGHVNCITIKELRRLFLVDVLSLKP 1107  
Db 78 QAVQKTDGHPFKAYLELEITLSQEQIKYTDCLQFYVNSTLKLRLFLVDVLSLKP 137  
QY 1108 AVLMMWFTYVYVGLFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIO 1167  
Db 138 AVLMMWFTYVYVGLFNGLTLLILALISLFSVPVIYERHQAQIDQYGLVLRTHINAVAKIO 197  
QY 1168 AKIPGLKRAE 1178  
Db 198 AKIPGAKRAE 208  
RESULT 3  
A60021  
tropomyosin-related protein, neuronal - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 05-Nov-1999

C:Accession: A60021  
R:Wieczorek, D.F.; Hughes, S.R.  
Brain Res. Mol. Brain Res. 10, 33-41, 1991  
A:Title: Developmentally regulated cDNA expressed exclusively in neural tissue.  
A:Reference number: A60021; MUID:91278684; PMID:1647480  
A:Accession: A60021  
A:Molecule type: mRNA  
A:Residues: 1-267 <WIE>  
A:Cross-references: EMBL:X52817; NID:g456549; PIDN:CAA37001.1; PID:g456550  
C:Comment: This neuronal-specific mRNA was identified by hybridization to an alpha-trop  
Query Match 11.3%; Score 671; DB 2: Length 267;  
Best Local Similarity 66.3%; Pred. No. 9.4e-21;  
Matches 124; Conservative 34; Mismatches 29; Indels 0; Gaps 0;  
QY 988 KTSVVDLLYWRDIKKTGVVFGASLFLLSLTIVFSIVSVTAYIALALLSVTISFRIYKGV 1047  
Db 9 KQAIDLLYWRDIKQTGIVFGSFLLLLSLTQFSVSVVAYLALAALSATISFRIYKSVL 68  
QY 1048 QAIQKSGDEGHPFRAYLESEVAISELQKYSNLSALGHVNCITIKELRRLFLVDVLSLKP 1107  
Db 69 QAVQKTDGHPFKAYLELEITLSQEQIKYTDCLQFYVNSTLKLRLFLVDVLSLKP 128  
QY 1108 AVLMMWFTYVYVGLFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIO 1167  
Db 129 AVLMMWFTYVYVGLFNGLTLLILALISLFSVPVIYERHQAQIDQYGLVLRTHINAVAKIO 188  
QY 1168 AKIPGLK 1174  
Db 189 AKIPGAR 195  
RESULT 4  
T26216  
hypothetical protein W06A7.3c - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T26216  
R:Ainscough, R.  
submitted to the EMBL Data Library, August 1996  
A:Reference number: Z20173  
A:Accession: T26216  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-2484 <WIL>  
A:Cross-references: UNIPROT:Q9U347; EMBL:Z78066; PIDN:CAB51467.1; GSPDB:GN00023; CESP:W  
A:Experimental source: clone W06A7  
C:Genetics:  
A:Gene: CESP:W06A7.3c  
A:Map position: 5  
A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2  
Query Match 8.9%; Score 528; DB 2: Length 2484;  
Best Local Similarity 20.9%; Pred. No. 1.3e-13;  
Matches 277; Conservative 186; Mismatches 461; Indels 402; Gaps 54;  
QY 1 MEDLQSPVUSSDSPPRPQPAFKYQFVREPDDEE-----BE 38  
Db 1397 LEKVEVQP--DLSONSPAPHKIIDLHF-NIPKDHEDYGNYPFGTSESEESQKADGNQE 1453  
QY 39 EREED-----EDEDLELEVLERKPA-----AGLSAAP----- 67  
Db 1454 NOREEDVVAELNPHPIRQWRDEDVLSLQSLKSLVAEVGCTIDVDASDVNEQDEESTLKIL 1513  
QY 68 --VPTAPAGAPLMDFGNDVFPAPRGPPLPAAPPVAP--ERQPSW----- 108  
Db 1514 KVPSEPSLLE--LDFTND--PKVIHVPIPLMEPATMYLEEMVWIIADAVKEVSEMEVV 1569  
QY 109 -----DPSPVSSSTVPAPSPLSAAAVSPSKLP-EDDEPPARPPPPPPASVSPQAPVW 159  
Db 1570 TESEISEMAPQVSESTCIPEPL-----ADLKLPEVDEDEKTEPEPEVVPVQVQVIRIPIE 1624  
QY 160 TTPAPA-PAAPPSTPAAPKRRGSSGAVVXXXKIMDLKEQPGNTISAGQEDFPSVL--LE 216

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Db      1625 VEQAPTIPQPRAP-----: : : : :KSELPKVAKPLD 1651
Qy      217 TAASXPSLSA-----ASKEHEYLGNLSTVLPTGCTQENVSEASKEVSEKATILL 270
Db      1652 DSKSRVAPLNIKGRVYSEQQKELVESLERPL-TIITOQKPEKPTEDIG--ALSPL 1708
Qy      271 IDRLDTEFSELEYSEMGSSFSVSPKAESAVIVANPREEIIIVKNDEEKLKVNILHQQ 330
Db      1709 SPNTLAEEVEVPMQM-----VHSPQE-----KQEEIEALSEII----- 1745
Qy      331 ELPTALTKLKVEDEVSSKAKDSNEKRVAVEAPMRBEYADPK---PFRVWVEKDSKE 387
Db      1746 EEPQAMKEKVEPE-SAPEKNESLEAPEI-INEPIRRVLVETKIMGPKGKSLNEDND 1803
Qy      388 D-SDMLAAGGKLESNKVDKCCADSLQTNHEKDSSESS---NDTSPSTPEGLKD 442
Db      1804 DQSECLDSIGDUS---ERTIQR--FNTSIDDPSIRDSFSSISSFGDRQKFRTAENIRQ 1858
Qy      443 RSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDEKKIEKKAQIVTEKNTSTKTSN 502
Db      1859 -----DLLPFOSSVSQVLRSSPNP-----SQQLVTN----- 1885
Qy      503 PFFVAQOSETVYTDNLTKVTEEVVANMPGLTPDLVQACESELNEVTGKIAYETK 562
Db      1886 ----LSMDSPSD--LSPNAPPVGFNTAQFLEKLOQE-DRPSAEGSIDSSGPEKVDHE-- 1936
Qy      563 MDLVQTSVMQESLPAQAQLCPSESEATPSVLPDIMEAPLNSAVPSAGASVIOQSS 622
Db      1937 -----GLDEFAAPP-----VHDPMQKSVFSGSLGSDDMKPGS 1967
Qy      623 SP-----LEASSVNYESIKEPENPPYEEAMSVSLKVSGIKEIKEPENIN-----AAL 672
Db      1968 QDDGFVFIERNAN-----EATLKKNQKSSHHNDVIEKNYFNDAPTAAL 2013
Qy      673 QETEPYISACDLIKETKLSABAPDFSDYSEMA-----KVEQPVDPHSEL 719
Db      2014 --LESPIABEARKLVQDAVESA-----SEYKQAVDSGEIGRELLDNVEQKIEQVKEP 2065
Qy      720 VEDSDPDEPDLFSDSDIPVQKQDETVMVLKESLITETSPESIEVENKEKLSALPPE 779
Db      2066 IVDLSL--HKAYDGVGDFVHETVPNAVDFVREAKQLPESPVPKEI-----TPE 2113
Qy      780 GGPYLEFSLDNTKOTL--LPDEVSTLSKKEKIPLOMEELSTAVYSNDDLFISKAQ 837
Db      2114 -----PLVDIHDTVKVHDEVNFLEREPTP-PFETDDVAPLSDDKPQCGNQTP 2161
Qy      838 IRETFTSDSPSIEIIDFPPTLISSKTSDFSKLAREYTDLEVSHKSEIANAPDGAAGSLPC 897
Db      2162 EDETTFRKGLPTIPEEVEKAAAQNDLD----DFDPLVTSNTGAAGAAVGAAGAAA-- 2215
Qy      898 TELPHDLKLNQPKVKEKISFSDDFSKNGSATSKVILLPPDVVSALGHQAEIESIVKPK 957
Db      2216 -----VESITTEEM-----FGH--QKFVTPRPP 2237
Qy      958 VLEKAEKLPDTEKEDRSPSAIFSADIG-----KT-- 989
Db      2238 T-----PPKDISDEVDKSTV---NLGSPSHSHSPSSPHHSILKHGDAWIDFKTVP 2286
Qy      990 --SVDDLKYRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQ 1048
Db      2287 PCVLVDIYWRDAKSAIVLSALLVFLVLAQYPLLVTVVTSLLSLLAALGAAGFRVPEKVEA 2346
Qy      1049 AIQKDEGHPPFRAYLESEVAISEELVQKYSNLSALGHVNTIKELRRLFLVDLVDLSKFA 1108
Db      2347 QIKKTDSEHPFSEIILAQDLTPQEKVHAQADVFEHATCIANKLKKLVFVESLPSIKFG 2406
Qy      1109 VLMVFTVYGALFNGLTLLIALLISLFSVPVIYERHQAQIDHYLGLANKNVKDAKMAKIOA 1168
Db      2407 LVLSLTTIASHWFSFTAILGLIGVFSVPKVBESNQEAIDPHLATISGHKLNQVNIIDE 2466
Qy      1169 KIPGLK 1174

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Db      2467 KLPLFLR 2472
RESULT 5
T26215
hypothetical protein W06A7.3a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26215
R:Ainscough, R.
submitted to the EMBL Data Library, August 1996
A:Reference number: Z20173
A:Accession: T26215
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2607 <WTL>
A:Cross-references: UNIPROT:Q23187; EMBL:Z78066; PIDN:CA01522.2; GSPDB:GN00023; CESP:W06A7
A:Experimental source: clone W06A7
C:Genetics:
A:Gene: CESP:W06A7.3a
A:Map position: 5
A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2; 2586/2
Query Match      8.8%; Score 519.5; DB 2; Length 2607;
Best Local Similarity 20.4%; Pred. No. 3e-13;
Matches 292; Conservative 175; Mismatches 474; Indels 491; Gaps 55;
Qy      1 MEDLDQSPLVSSSDSPRPQAPFKQVFRPEDEEE-----EE 38
Db      1397 LEKEVQV--DLSONSPAPHKIIDLHF-NIPKDHEDYDGYVVPFGTESSESQKADGNQE 1453
Qy      39 EEEED-----EEDLEELVLRKPA-----AGLSAAP----- 67
Db      1454 NQEEEDVVAELNFIPIRQWRDEDVISLQSLKSLVAEVCITDVSADVNEQDEESTLKIL 1513
Qy      68 --VPTAPAGAPLMDFGNDFVPPAPRGLPAPPVAP--ERQPSW----- 108
Db      1514 KVPSEPSLLE--LDFTND--PKVIHVPIPLMEPATMYLEEMVEWIIADAVKEVSEMEVV 1569
Qy      109 -----DPSVSTVTPAPSPLSAAAVSPSKLP-EDDEPPARPPPPPPASVPOAEPW 159
Db      1570 TESISMAPQVSESTCTPIEPL-----ADLKLPEVDEKTPPEPEPVVPGQVQERIIPTE 1624
Qy      160 TTPAPA-PAAPSTP-----AAPKRRGSGAVVXXXKKIMDKLKEQPGNTISAQGE-- 208
Db      1625 VEQAPTIPQPRAPKSELKPAKPLDSDKS-----RVRFAPLNILKGRVYSEQQKEL 1678
Qy      209 ----DFPSVLLETAASKP-----SLSPLSAASFKHEHY--LGNLSTVLPTGCTQEN 254
Db      1679 VESLERPLTII-TQKPEKPTEDIGALSPLSPNTLASVEEVPVMDMQSVPHSPQEKQEE 1737
Qy      255 VSEASKEVSEKATILLDRDLTEPSELEYSEMGSSFSVSPKAESAVIVANPREEIIIVK-- 312
Db      1738 I-EALSEITEEPQAM-----KEVEKPVESAPEKDNESLEAPEIINEPIRRLVETK 1787
Qy      313 -----NKDEEKLKVNILHQQOELPTALTCLVKEDEVVSSKAKDSFNEKRVAVEA 364
Db      1788 IMGPKGSLNEDNDSDGSECLDSIGDL-----SERTIQRN--TSIDD 1829
Qy      365 P--MREEYADPKPFRVWVEKDSKED--SDMLAAGGKLESNKVDKCCADSLQTNH 420
Db      1830 PSIRRDSPSSISSFGDRQKFRTAENIRQDLPLPQSSVSQVLRSSPNP--SQQLVTNL 1886
Qy      421 EKDESNDTSPSTPEGI-----KDRSGA--YITCAPFNPAATESIATNIF 466
Db      1887 SMDSPS---DLSPNAPPVGFNTAQFLEKLOQEDRPSAEGSIDSSGPEKVDHEGDEFAA 1943
Qy      467 PLLSDPTSEN-----XTDEKK-----IEEKAQIVTEKNTSTKTSNPFVVAQDS 511
Db      1944 PPHDHPQKSVFSGSLGSDDMKPGSQDDGDFVIERNEANEATLKKNQKSSHHNDVIEKNY 2003
Qy      512 ETDVYTTDNLTKVTEEVVANMPGLTPDLVQACESELNEV-TGTKIAYE----TKMDLV 566

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Db 2004 FNDNAPT---AALLESPIAEARKLVQDAVESASEYKKQAVDSGDGEIGRELLDNVEQKIE 2060
QY 567 QTSEVWQESLYPAQICPSEFESEATPSVLPDIVMEAPINSAPVAGASVIOQSSSPLE 626
Db 2061 QVKEPIVDSLHRAYDGVGFVH-ETVPNAV-DDFVREAE-----2097
QY 627 ASSVNTYESIKHPENPPPEEAMSVSLKVGIGKEEIKEPENINAALQETAPYISTACDL 686
Db 2098 -----KQLPESVVP-----EKIETPE-----PLVDIHDIV 2122
QY 687 IK-----ETKLSAEPAPDFSDYSEMAKVQEPVDHSELVEDSDSPDEPDLFSDSDIPDV 741
Db 2123 DKVHDEVDFNLREPTPE-----TDDVAPLSDDKPQFGNQI-----2160
QY 742 PQQDVTMLVKESLTFSTFESMIEYENKEKLSALPPEGKPYLESFKLSLONTKDTLLP 801
Db 2161 -PEDETTTDRKGPLT-----EKAAAAQNND-----IP 2177
QY 802 DEVSTLSKKEKIPLOMEELSTAVYSNDDLFIKSAQIRETETETSDSPSIEIIDEPFTLIS 861
Db 2178 EEV-----EKAAAAQNND-----LDDFPLVT 2199
QY 862 SKT-----DSFSKLAR-----EYTDLEVSHKSEIANAPD 890
Db 2200 SNTGAAFGAAGAAAVESLTEEMFGHQKFETVPRPTPKDISDEDVK-PSTVNLGFS 2258
QY 891 GAGSLPCTELPHD-----LSLKNIOPKVEEKIS-----FSDDFS 924
Db 2259 HHSHSPSS--PHHSILKHGDWDIDFKTPPCAQAFAFSGEIMFLLAFFVYLSCFASFSS 2316
QY 925 KNGSATSKVLL-----PPDVSALG-----944
Db 2317 KSLPLDNLGLSVVYLSILIHVKHRRFRMNEEQATMSKLGAVGGRGLYALIAFVNI 2376
QY 945 --HTQAEIESIVKPKVLEKEAEKPLSDTEKEDRSAPISADLGKTSVVDLLYWRDIKK 1002
Db 2377 VLRVGLNVALVGVASAEAYKLTGS-----SGVLRKKEVLVDIYWRDACK 2423
QY 1003 TGVVFGASIFLLLSLTVFSIVSVTAYIALALSVTISFRIYKGVIOAIQKSDGEGHFRAY 1062
Db 2424 SAIVLSLALLVPLAKYPLLTVTYSLIALGAAAGFRVKKVEAQIKKTDSEHPFSEI 2483
QY 1063 LSEVAISBELVQKYSNLSALGHVNCIYKELRLPLVDLVDLSLKEAVLMMVTVGALFN 1122
Db 2484 LAQDLTLPQEKHAQADVFEHATCIANKLKLVFVESPLESIKFGVLWLSLTIASWFS 2543
QY 1123 GLTLILALISLFSVPVIVYERHQAQIDHYIGLANKVNDAMAKIQAKIPGLK 1174
Db 2544 GFTLAILGLLVFSVPKVSQVYENQEAIDPHLATISGHLKNVQNIIDEKLPFLR 2595

RESULT 6
T26213
hypothetical protein W06A7.3b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26213
R:Ainscough, R.
submitted to the EMBL Data Library, August 1996
A:Reference number: Z20173
A:Accession: T26213
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-222 <WIL>
A:Cross-references: UNIPROT:Q23188; EMBL:Z78066; PIDN:CA801523.1; GSPDB:GN000023; CBSP:W0
A:Experimental source: clone W06A7
C:Genetics:
A:Gene: CBSP:W06A7.3b
A:Map position: 5
A:Introns: 27/1; 77/2; 201/2

Query Match 5.7%; Score 340.5; DB 2; Length 222;
Best Local Similarity 32.4%; Pred. No. 1.9e-07;
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Matches 66; Conservative 52; Mismatches 83; Indels 3; Gaps 2;
QY 972 EKEDRSPSAIFGADL-GKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYTA 1030
Db 9 KYSKQPTWVPATDFPGK--ILDVYWRDAKSAIVLSLALLVLFVLAKYPLLTVVVYSL 66
QY 1031 LALLSVTISFRIYKGVIOAIQKSDGEGHFRAYLESEVAISEELVQKYSNLSALGHVNCNTIK 1090
Db 67 LIALGAAAGFRVKKVEAQIKKTDSEHPFSEILAQDLTLPQEKHAQADVFEHATCIAN 126
QY 1091 ELRLPLVDLVDLSLKEAVLMMVTVGALFNGLTLILALISLFSVPVIVYERHQAQIDH 1150
Db 127 KLKLVFVESPLESIKFGVLWLSLTIASWFSFTLAILGLLVGFSVPKVSQVYENQEAIDP 186
QY 1151 YIGLANKVNDAMAKIQAKIPGLK 1174
Db 187 HLATISGHLKNVQNIIDEKLPFLR 210

RESULT 7
I38346
elastic titin - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I38346
R:Labeit, S.; Kolmerer, B.
Science 270, 293-296, 1995
A:Title: Titins: Giant proteins in charge of muscle ultrastructure and elasticity.
A:Reference number: A57430; MUID:96026330; PMID:7569978
A:Accession: I38346
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-7962 <RES>
A:Cross-references: UNIPROT:Q10465; EMBL:X90569; NID:g1017426; PIDN:CAAG2189.1; PID:g101
C:Genetics:
A:Gene: GDB:TTN
A:Cross-references: GDB:127867; OMIM:188840
A:Map position: 2q31-2q31

Query Match 5.6%; Score 331; DB 2; Length 7962;
Best Local Similarity 20.0%; Pred. No. 6.3e-05;
Matches 235; Conservative 144; Mismatches 404; Indels 392; Gaps 48;
QY 32 EDEEEEEEEDEDEDELE--VLERK--PAAGLSAAPV-----PTAPA 73
Db 6176 EBEREEEEAAVTEYEVMEEPPEYVVEEKLIISKVKEAPAEVTERQSKKIVLKEKIPA 6235
QY 74 AGAPLMDFGNDVFPAPRGPPLPAAP--PVAPERQPSMDPSVSVSTVPAPSLSAAYVSPSK 132
Db 6236 K-----IEBPPPAKVPAPKIVPEKK-----VPAPVP-KKEKVPVPPK 6272
QY 133 LPEDDEPPA---RPPP-----PPPASVS-----POAEPVWTPPAPAPAPPS-TPAA 175
Db 6273 VPPEPKVPPEKKVPKVPKIMBEPPLPAKVTEKHMQITQEEKVLAVTKKEAPPKARVPEE 6332
QY 176 PKRRGSGAVVXXXKIMDLK---EQPGNTISAGQEDF---PSVLETAASXPS-LSPL 227
Db 6333 PKR-----AVPEEKVLKPKREBEPKPAKVFTRKRVVVEEKVSIAPKREPQIKEV 6385
QY 228 SAASFKHEHYLGNLTVLPTEGLQEN--VSEASKVESEKAKTLLIDRLDTFSELYSEM 286
Db 6386 TIMEEKERAY-----TLEEAASVQREBEYEVE---EYDYKEFEYEPTEE 6429
QY 287 GSGFS-----VSPKAESAVIV--ANPREI 309
Db 6430 YDQYSEYERERYVEEHEEYITEPEKPIPVKVPPEEPVPTPKPAKPAKVLKAVPEEKV 6489
QY 310 IV-----KNKDEEEKLVSNILHXQQLPTALTKLKEDEVWSSEKAKDSFNEKRVAVEAP 365
Db 6490 FVPIPKLAPPPPKVPEEPKVFEEKIHSITK--REKQVTEPAKVPKPKRVVAEEK 6547
QY 366 MREEYADPKPFRVWVEVKDSKEDSMDLAAGGKIESNLESKVKDKCFCADSLQTNHKKOSE 425
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Db 6548 VVPRKKEVAPPVVRVPPVKELEPEV-----AFEEVVTHVE-EYLVEEEREEYIHEE-E 6600  
 Qy 426 SSNDTSPSTPEGIKORSGAVITCAPFNPAAATESIATNIPLLEDPTSENKTDKKEE 485  
 Db 6601 FITEEVVPIPVKPE-----VPRKVPDEKKVPVPPKKEAPPAKVPEVKKPEE 6652  
 Qy 486 KKAQIVTEKNTSTKTSNPF-----VAAQDSETDYVTTDNL----- 521  
 Db 6653 KVPVLPKKEKPPPAKVPEVPPKVPPEEKVPVPPKVEAPPAKVPEVPPKVPPEKVPV 6712  
 Qy 522 -----TKVTEEVANMEGLTDPDLVQACSESELNEVTGTKIATETKMDLVQTSSEV 571  
 Db 6713 PAPKVEAPPAKVPEVPPKGLIPEEKKTVPVPPKVEAPPKVPKKEPPVPVVALPQEEV 6772  
 Qy 572 M-QESLYPAAQLCPSESEATP----- 593  
 Db 6773 LFEEIIVPEEVLP-----EEEVLPPEEEVLPPEEEVLPPEEEVPPPEEVVPPEE 6830  
 Qy 594 -----SPVLPDIMEAPLNSAVPSAGASVQ-----PSSSPELEASSVNYESI- 635  
 Db 6831 EFPVEEVLPVPPKVPVPPAPVPEIKKVKTEKKVVPKKEBAPPAKVPEVPPKVEEKRII 6890  
 Qy 636 ---KHE-----PENPPYEEAMSVSLKVSIGIKKEI---KEPENIN 669  
 Db 6891 LPKEEVLVPEVTEPPEEPISEEEIPEEPPSIEV-----BEVAPPVPEVIK 6939  
 Qy 670 AALQTEAPYISACDLIKETKLSAEPAPDFSDYSEMAKVEOPVDPHSELVEDSSPDSEP 729  
 Db 6940 KAVPEAPTV-----PKVEAPP-----AKVSKKIPPEKVPVPPVQKKEAPP 6980  
 Qy 730 VDLFSDSDSIDVPQKQDETVMVKESLSTETSPESMIEYENKEKLSALPPEGKPYLESFK 789  
 Db 6981 A-----KVPEVPKVPPEKKVLV-----PKKEAVPPAKGR----- 7009  
 Qy 790 LSLDNTKDTLLPDEVSTLSKKEKIPLOMBELSTAVSYNDLDFISKEAQIRETETSDSSP 849  
 Db 7010 -----TVLEKVSVAFRQEVVVKERLELEVEARVEE--IPBEEFHEVEEYFERGE 7059  
 Qy 850 TEIIDEPFLISSKTDSPSKLAREYTDLEV--SHKSEIANAPDGAGSLPCTELPHDLSLK 907  
 Db 7060 FHEVEEPIKLEQHRVEEHRVKEVIEVFEAEVEVEFEPKAPPKGP-----EISEK 7113  
 Qy 908 NIQPK-----VEKISFSDDFKNGSATSQVLLPLPPDVSAL 943  
 Db 7114 LIPPKKPTKVPVPRKPPAKVPEVPPKIVVEEKVRPEE-----PRVPP----- 7157  
 Qy 944 GHTQAEIESIVKPKVLEKEAKKLPSDTEKEDRSP 978  
 Db 7158 ----TKVPEVLPPK--EVVPEKKVPVPPAKKPEAP 7186

## RESULT 8

Tl3564  
 microtubule-associated protein homolog - fruit fly (Drosophila melanogaster)  
 N:Alternate names: hypothetical protein EG:49E4.1  
 C:Species: Drosophila melanogaster  
 C:Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004  
 C:Accession: Tl3564  
 R:Spanos, L.; Papagiannakis, G.; Siden-Kiamos, I.; Louis, C.  
 submitted to the EMBL Data Library, April 1999  
 A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.  
 A:Reference number: Z17689  
 A:Accession: Tl3564  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-5327 <SPA>  
 A:Cross-references: UNIPROT:O76891; EMBL:AL031128; PIDN:CAA20006.1  
 C:Genetics:  
 A:Cross-references: FlyBae:FBgn0025392  
 A:Introns: 24/2; 52/3; 104/3; 179/1; 232/1; 1669/3; 2566/1; 4798/3; 5272/1  
 A>Note: EG:49E4.1  
 C:Superfamily: Drosophila 576K microtubule-associated protein homolog

Query Match 5.5%; Score 325.5; DB 2; Length 5327;  
 Best Local Similarity 23.6%; Pred. No. 6.1e-05;  
 Matches 275; Conservative 151; Mismatches 520; Indels 219; Gaps 53;  
 Qy 28 VREPEDEEBEEREE-----DEDELEEEVLERKPAAGLS-----AAPVPTAPAG 75  
 Db 1277 MEQVKDBEHEQKIESIGIITEKEAKKSASTPEEKETSDITSDELPAQLADPTTVPKSA 1336  
 Qy 76 APLMDFGNDFFPPA-----PRGPLPAAAPV-APERQPSWDPSPVSTVPAPSLAA 126  
 Db 1337 KDREDTGIESPTTIEAIEVEVQAKQEQAPVPAPEBAIKTEKSPLASK-ETSPESAT 1395  
 Qy 127 AVSPSKLPEDDEPPARPPPPASVSPQAEVPVTPPAPAPAPAPPTPA-----APK 177  
 Db 1396 ---GSVKEDTEQTKSKSPVSPSESAKKSPASGEASRPSEVAESVKDEAGKAB 1451  
 Qy 178 RRGSGAVVXXXKIMDLKEQPGNTISAGQE-----DPPSVLLETAAKXP-SLSPLSA 229  
 Db 1452 RRESIAKTHKDESSLIDKAKEQESRRSLAESIKPESGIDKESALASKEASRPESVTDKS- 1510  
 Qy 230 ASFKEHEVGLNLSVTLPTEGLQENVSEASEVSEKAKTLLIDRLTFESELEYSEMSS 289  
 Db 1511 ---KEPSRRRESIASLSKAEISTKDEKSAKSPGVSVDKDETERKSPSRRESIA 1567  
 Qy 290 FSVSPKAEASAVIVANPREIIVQNKDEBEKLVNN---ILHXQQELTALTALKVKEDEV 346  
 Db 1568 ESAKPPPIEFRE-VSRP-ESVIDGIKDESAKPESSRRDSPLASKEASRPESVLEKDEPIK 1625  
 Qy 347 SSEKAK-----DSFNEKKVAVE-APMREYADFPFERVWEVKOS--KEDSDMLAAGKI 398  
 Db 1626 STEKSRRESVAESFKADSTKDEKSPKTSKDIS-RPESAVENVMAPPKETSRRPESAVGSM 1684  
 Qy 399 ESNLESKVDKCFADSLQTNHE--KDESSNDTSP-STPEGIKORSGAVITCAPNP 455  
 Db 1685 KDEMSK-----EPSRRSVKGAASRSTRSPASVAESAKO--GADDLKELSRP 1732  
 Qy 456 AATE-----SIATNIIFLLEDPTS-----ENKTD--EKKIEKKAQIVTEKN--TSTK 499  
 Db 1733 ESTTQSKAGSIKDEKSPLEASEASRPASVAESVKDEAKESKEESRRSVAESKPLPKE 1792  
 Qy 500 TSNPFFVAAQDSEYDVTNDLTKVTEEVANMP-----EGLTDPDLVQACSESELNEVTGT 555  
 Db 1793 ASRPASVA--ESIIDEAKESKEESRRSVAESKPLPKEASRPASVAESI KDE-----AE 1845  
 Qy 556 KIAYETKMDLVQTSSEVM--QESLYPAAQLCPSESEATPSPVLPDIWE-APLNSAVPS 612  
 Db 1846 KSEESRRSVAESKPLPKEASRPASVAESI KDEAKESKEESRRSVAESKPLPKEAS 1905  
 Qy 613 AGASVIQFSSSPLEASSVNYESI KHEPENPPPYBEAMSVSLKVSIGIKKEI---KEPENIN 669  
 Db 1906 RPASVAESI KDEAKESKEESRRSVAESKPLPKEASRPASVAESI KDEAKESKEESRR 1965  
 Qy 670 AALQTEAPYISACDLIKETKLSAEPAPDFSDYSEMAKVEOPVDPHSELVEDSSPDSEP 729  
 Db 1966 SVAESKPLP-----SKEASRPASVAESI KDEAKESKEE-----SRRESVAESKP----- 2009  
 Qy 730 VDLFSDSDSIDVPQKQDETVMVKESLSTETSPESMIE--YENKEKLSALP-PEGKPY--Y 784  
 Db 2010 -----LPSKEASRPASVAESI KDEAKESKEESRRSVAESKPLPKEASRPASV 2058  
 Qy 785 LESFKLSIDNTKDTLLPDEVSTLSKKEKIPLOMBE-----LSTAVSYNDLDFISKEAQIRE 840  
 Db 2059 AESIKDEAKESK-----EESRRSAAKSPKPLPKEASRPASVAESVKDEADKESRR- 2112  
 Qy 841 TETFSDSPTIEII--DEFPPTLISKTSDFSKLAREYTDLEVSHKSEIANAPDGAGSLPCT 898  
 Db 2113 -ESMAESGKAQSIKGDQSPLEKVEVRPES---VAESVKDDDPYKSK-EFSRRRESVAGSVTAD 2167  
 Qy 899 ELPHDLISIKNIQPKVEEK-----ISFSDDFSKNGSATSQVLLPLPPDVSALGHTQAE 949  
 Db 2168 -----SARDQSPLESKGAASRPESVDSVKDEAKQES-----RRSK 2205  
 Qy 950 IESIVKPKVLEKEAKKL-----PSDTEKEDR-SPSAIFSDLGKTSVVDLLYV---RDI 1000







QY 722 DSSPDSEPPDLF-----SDSI-----PDVP 742  
Db 1199 KSTKESKSTVDEKPKKKVKKKTEKSDSIISQKSETSKTVVSESAGPSESETKQKVADAA 1258  
QY 743 QKQDET-----VMLVKESLTETSFESMIEYENKEKLSA-----LPP 778  
Db 1259 RKQKETDEKQKLBAEITAKKSADE---KSKLEAESKLKAAAEVAAKKEKKEDEQKLDOT 1315  
QY 779 EGKPKVLESPKSLDNTKOTLLPDEVSTLSK-----EKIPLOME 818  
Db 1316 EAASKAAAEKLELEKQSHIKKAAEVDVAVKKQLESEKQKORLESEATKKADAELKLEQ 1375  
QY 819 ELSTAVYS-----NDLFIKSEAQIRETETFS---DSSPIIIDEPP 857  
Db 1376 KKKAAEATLFEIQEQEKLAQESRLEDEAKKSAEKQKLESETKSKQTBEAPKESVDEKP 1435  
QY 858 --TLISKTDSPFKLAREYTDLEVSHKSEIANAP-DGAGSLPCTELPHDLISLKNIQKVE 914  
Db 1436 KKKVLKKKT-----EKSDSISQKSKSAKSTVDAAEETL-----ESDFNLVEKKTQKVE 1484  
QY 915 -----EKISFSDDFSXNGSATSKVLLLPDPVSGALGHTQAEIESIVK 955  
Db 1485 QSPDETSATIKRDPQAQTEIEISKQDGDGDKTTTGGPKPKPEDSEA----TPKRRVK 1539  
QY 956 PK-----VLEKEAEKLPDSTKEKEDRSPSAIFADLGKTSVVD 993  
Db 1540 KTKQKSDSVASDASLADSVKSLSDVVEKPKKVKLKKKTEKSDSVISETSSVDTIKPESVE 1599  
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Db 1600 I 1600

RESULT 12  
S37431  
N;ankyrin 2, neuronal long splice form - human  
N;Alternate names: ankyrin B, 440K splice form; ankyrin-B; brain ankyrin; non-erythroid  
N;Contains: ankyrin 2, short form  
C;Species: Homo sapiens (man)  
C;Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text change 09-Jul-2004  
C;Accession: S37431; B39643; A39643; A40334; A49462; S14533; S14569  
R;Chan, W.  
Submitted to the EMBL Data Library, September 1993  
A;Reference number: S37431  
A;Accession: S37431  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-3924 <CHA>  
A;Cross-references: UNIPROT:Q01484; EMBL:Z26634; NID:g406287; PIDN:CAA81397.1; PID:g406287  
R;Otto, E.; Kunimoto, M.; McLaughlin, T.; Bennett, V.  
J. Cell Biol. 114, 241-253, 1991  
A;Title: Isolation and characterization of cDNAs encoding human brain ankyrins reveal a  
A;Reference number: A39643; MUID:91302466; PMID:18330053  
A;Accession: A39643  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1443,3585-3924 <OTT>  
A;Cross-references: EMBL:X56958  
R;Tse, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux, S.E.; Ward, H.  
Genomics 10, 858-866, 1991  
A;Title: Isolation and chromosomal localization of a novel nonerythroid ankyrin gene.  
A;Reference number: A40334; MUID:92009921; PMID:18333308  
A;Accession: A40334  
A;Molecule type: DNA  
A;Residues: 463-474, 'PE', 477-495 <TSE>  
A;Cross-references: GB:M37123; NID:g178647; PIDN:AAA62828.1; PID:g178648  
R;Chan, W.; Kordeli, E.; Bennett, V.



Db 1507 EECPRMISIPDPSPKTKARTPVQDHRSEQSQSMISIEFCQSEPSHSLAMDFRSQSDHP 1566  
 Qy 612 SAGASVQ-----PSSSPLEASSVNTYESIKHE--PENPPPY-----EEAMSVS-LKVSQ 657  
 Db 1567 TVGAGMLHITENGPEVVDYSPSIQDSSLHKIPPTPEEPSYQDNDLSLISYSVQVEASP 1626  
 Qy 658 IKBEIKEPENINAAIQETE-----APYISIACDLIKE-----TKLSAEP----- 696  
 Db 1627 STSAAHTPSQIASPQLOEDTLSDVVPDRMSLYASLASEKVOSELEGEKLSPKSDISPLTPR 1686  
 Qy 697 -----APDFSDFSEMAK-----VEQPVDPHSSELVEDS----- 723  
 Db 1687 ESSPTYSFGFSDTSKAKESTAAYQTSSPPIDAAAAPYGFSSMLFDTMQHHLALSRD 1746  
 Qy 724 -----SPQSEPVDLFSD-----SIPDVP-----QKQD 746  
 Db 1747 LTTSSVEKONGGKTPGDFNAYQKPESTTSPDEEDYDYESHEKTIQAHDVGGVYVEKTE 1806  
 Qy 747 ETWML-----VKESLTETSPESMIEYENKEKLSALPPEGKPYLESFKLSLDNTKD 797  
 Db 1807 RTIKSPDCSGYSVETTEKTKTPEDGGYSCIEITEKTRTPEEGYSY-----EISEK 1858  
 Qy 798 TLLPDEYS--TLSSKKEKIPQMBELSTAVYSND-----LFTSKEA 836  
 Db 1859 TTRTPEVSGVTEKTERSRRLDDISNGYDDTDEGGHTLDCGSYSVETTEKITSFPESSE 1918  
 Qy 837 QIBETETFSDDP-----LEIDEPFLISSKTDGFSKLAREVT-----DL 877  
 Db 1919 YSVETTTKTRSPDTSAYCVETWEKITKTPQASYSYVETSDRCYTERKSPSEARQVDVL 1978  
 Qy 878 -----EVSH-KSEIANA--PDG-----AGSLPCTELPHDLSLKNIQ-----KV 913  
 Db 1979 CLVSSCEFKPKTELSPFNPNPLEWFACEEPTESERPLTQGGAPPSPGKGQGRQC 2038  
 Qy 914 EEKISFDDPSKNGSATSKVLLLPDVSALGHTQAEIESIVKPKVLEKEAEKK-LFSD-- 970  
 Db 2039 DETPPTSVSAPSQTDSV---PPETE-----ECPSTADANLDSDESETIPTDKT 2088  
 Qy 971 -----TEKEDRSPS-----AIFGADLGKTSVDVLLYWRDIKKTG 1004  
 Db 2089 VTYKHMPPAPMQDRSPSRHPDVSMDPEALAIQNGLKALKKDLKEKAKTKKPG 2145  
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 N: microtubule-associated protein MAP1B - mouse  
 N: Alternate names: microtubule-associated protein MAPI(X); microtubule-associated  
 C: Species: Mus musculus (house mouse)  
 C: Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text\_change 09-Jul-2004  
 C: Accession: S07549; S44387; A33645  
 R: Noble, M.; Lewis, S.A.; Cowan, N.J.  
 J. Cell Biol. 109, 3367-3376, 1989  
 A: Title: The microtubule binding domain of microtubule-associated protein MAP1B  
 A: Reference number: A33645; MUID: 50094539; PMID: 2480963  
 A: Accession: S07549  
 A: Molecule type: mRNA  
 A: Residues: 1-2464 <NO>  
 A: Cross-references: UNIPROT: P14873; EMBL: X51396; NID: g52999; PIDN: CAA35761.1; P  
 R: Sanchez, C.; Padilla, R.; Paciucci, R.; Zabala, J.C.; Avila, J.  
 Arch. Biochem. Biophys. 310, 428-432, 1994  
 A: Title: Binding of heat-shock protein 70 (hsp70) to tubulin.  
 A: Reference number: S44387; MUID: 94234720; PMID: 8179328  
 A: Accession: S44387  
 A: Status: preliminary  
 A: Molecule type: protein  
 A: Residues: 653-663, 'IC', <GAN>  
 C: Superfamily: microtubule-associated protein MAP1B  
 C: Keywords: microtubule binding; phosphoprotein; tandem repeat  
 F: S89-786/Domain: microtubule binding #status experimental <NB>  
 F: 589-592, 639-642, 649-652, 655-658, 660-663, 668-671, 674-677, 679-682, 683-686, 687-6  
 R-K-E/D-X)  
 F: 1861-2064/Region: 17-residue repeats  
 F: 91, 116, 351, 988, 1124, 1153, 1168, 1208, 1662, 1877, 1918, 2030, 2054, 2083/Binding

F:147,969,1336,1562,1563,1702,1708,1990,2057,2063,2419/Binding site: phosphate (Thr) (cd  
F:1953/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match  
Best Local Similarity 4.9%; Score 289; DB 1; Length 2464;  
Matches 262; Conservative 148; Mismatches 474; Indels 442; Gaps 55;

QY 32 EDEEEEEDEDEDL-EELEVLKPAAGLSAAPTAPAAAGAPLMDFGNDFVPPAP 90  
DB 1009 EAEQSEEEEDKAEADAREEGYEPDKTEADYVMAADKAAEAGVTEQYGY----- 1061

QY 91 RGLPLAAPV-APERQSPWDGPGVSTVPAPPLSAAAVSPSKLPEDDEPPAPPPPPA 149  
DB 1062 LGTSAKQPGIOGSPSREPA--SSIHDETLPGGSESEATA-----SDEENREDQPEEFTA 1112

QY 150 SVSPQAEPTVTPAPAPAPPTPAAPKRRGSGAVVXXXXKIMDLKEQPGNTISAGQED 209  
DB 1113 TSGYQSTIIEISSEPTMDENSTP-----RDVMSDETNNETSPSOEF 1156

QY 210 FPSVLLETAASPSLSPLSAASF-----EHEYLGNLSLTVLPTGCTLOENVSE 257  
DB 1157 VNITKVESLYSQEYKPAVASFNGLSEGSTDAIDGKYNASASTISPPSSWEDEKFSK 1216

QY 258 AS-----KEYSEK-----AKTLIDRLDTEFS 279  
DB 1217 SALRDAYCSEKELKASABLDIKDVSDERLSPAKSPSLSPSPSPTEKTPLGERSV-NFS 1275

QY 280 ----ELEYSEMSSFSVSPKASAVI---VANPRE---EIIIVKN----- 314  
DB 1276 LTPNEIKVSAEGEARSVPGVTOAVVEHCASPEKTLVWSPSOSVTSAGHTYYQSP 1335

QY 315 -DEEEKLVSNLTLHQELPTALTAKLVKEDEVSVSEKADSPNEKRVAVAPMREYADF 373  
DB 1336 TDEKSSHLPTVESENAQVPVSF-----EFSEAKOE-NER--ASLSPMDEFPVDS 1382

QY 374 K-PFERVWE-----VKDSKEDSDMLAAGKIESNLESKVKKCFADSLQETNHEKDE 425  
DB 1383 ESPVEKVLSPRLSPGLGSESPYEDFLSADSKVLGR-----RSESPFE 1425

QY 426 SNNDTSPSTPEGIKDRSGAVITCAPNPATESIATNIPLLLEDPTSENKT----- 478  
DB 1426 GKNGKQGPDRSPVSD-----LTSTGLYQDKQEEKSTGFIPKEDFGPEKTSVETMS 1480

QY 479 -----DEKKI-----EKKQAIQVTEKNTSTKTSNPPFFVAAQDSTD 514  
DB 1481 SOSALADERKLGVDVSTQIDVDSQFGFKEDTKMSISEGTVSDKASATP--VDEGVAEDT 1538

QY 515 YTTNLTAKVTEEVA--NMPEGLPDLVQEAASELNEVTGKIAETKMDLVQTSVM 572  
DB 1539 YSHMEGVASVSTASVATSGFPPEPTDD--VSPSLHAEVGSHPSTEVDDLSVSVVQTPTF 1597

QY 573 QBS-LYPAAQLCP-----SFESEATSPVLPDIVMEAPLNSAV-- 610  
DB 1598 QETEMSPSKEECPRMSPSPDFSPKTAKRTPVQDHRSEQSSMSIEFGQSSPEHSFAMD 1657

QY 611 -----PSGASVIQ-----PSSSPLEASSVNYESIKHE--PENPPPY-----EAM 649  
DB 1658 PSRQSPDHPTLGASVLHITENGTEVDYSPCDIQDSSLSHKIPPTPEEPSYTDNDLSLI 1717

QY 650 SVS-LKVGSIKEEIKPENINAAQETE-----APYISACDLIKE---TKLSAE 695  
DB 1718 SVSQVEASPSSTSAHTPSQIASPLQEDTLSDVPPPREMSLYASLASEKVQSLGSEKLSPK 1777

QY 696 P-----APDFSDYSEMAK-----VEQVPDPHSELVEDS- 723  
DB 1778 SDISPLTPRESSPLYSPGFSOSTSAKETAHAHQASSPPIDAATAEYGFRRSMLFDTM 1837

QY 724 -----SPDSEPVDLFSD-----DS 737  
DB 1838 OHHLALNRDLTSSVEKDSGGKTPGDFNYAYQKPENAAAGSPDEEDYDYESQEKTIETHDV 1897

QY 738 IPDVQKQDETVM-----VKESLTFESFESMIEYENKELASLPPEGKPYLESF 788

Search completed: June 16, 2005, 13:32:00  
Job time : 44.4224 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:33:51 ; Search time 159.813 Seconds  
(without alignments)  
3774.604 Million cell updates/sec

Title: US-09-830-972-29

Perfect score: 5923

Sequence: 1 MEDLDQSLVSSDSPRPQ.....VKDAMAKIQKIPGLKRAE 1178

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5815	98.2	1192	1 RTN4 HUMAN	Q9ncq3 homo sapien
2	4851	81.9	986	2 Q8IUA4	Q8Iua4 homo sapien
3	4296.5	72.5	1163	1 RTN4 RAT	Q9jkl1 rattus norv
4	4289	72.4	1162	2 Q8BGM9	Q8bqm9 mus musculu
5	4277.5	72.2	1163	2 Q8K3G8	Q8k3g8 mus musculu
6	3658.5	61.8	1046	2 Q8BGR7	Q8bgr7 mus musculu
7	2580.5	43.6	720	2 Q7TNB7	Q7tnb7 mus musculu
8	2527	42.7	639	2 Q8K290	Q8k290 mus musculu
9	2233	37.7	578	2 Q8OW95	Q8ow95 mus musculu
10	1735	29.3	658	2 Q6RSS8	Q6rss8 gallus gall
11	1534.5	25.9	1055	2 Q6JRV1	Q6jrv1 xenopus lae
12	1531	25.8	392	2 Q96B16	Q96b16 homo sapien
13	1518.5	25.6	1044	2 Q6JRV8	Q6jrv8 xenopus lae
14	1517.5	25.6	1043	2 Q6JRV0	Q6jrv0 xenopus lae
15	1510	25.5	1024	2 Q6JRV2	Q6jrv2 xenopus lae
16	1508.5	25.5	1032	2 Q6JRV7	Q6jrv7 xenopus lae
17	1492	25.2	1013	2 Q6JRV9	Q6jrv9 xenopus lae
18	1331.5	22.5	343	2 Q6IPN0	Q6ipn0 homo sapien
19	1201.5	20.3	375	2 Q8BHF5	Q8bhf5 mus musculu
20	1163	19.6	356	2 Q8BH78	Q8bh78 mus musculu
21	1152.5	19.5	357	2 Q8K3G7	Q8k3g7 mus musculu
22	992	16.7	250	2 Q6IG16	Q6igl6 sus scrofa
23	931	15.7	199	2 Q7YRW9	Q7yrw9 bos taurus
24	927	15.7	199	2 Q6IM70	Q6im70 sus scrofa
25	922	15.6	199	2 Q7PCJ7	Q7pcj7 macaca fasc
26	919	15.5	187	2 Q6IG15	Q6igl5 sus scrofa
27	915	15.4	199	1 RTN4 MOUSE	Q99p72 mus musculu
28	887	15.0	199	2 Q7T224	Q7t224 gallus gall
29	867	14.6	179	2 Q9GM33	Q9gm33 macaca fasc
30	804.5	13.6	315	2 Q6IFY4	Q6ify4 xenopus tro
31	792	13.4	311	2 Q6JRV3	Q6jrv3 xenopus lae

32	791	13.4	330	2	Q6JRV4	Q6jrv4 xenopus lae
33	791	13.4	777	1	RTN1 RAT	Q64548 rattus norv
34	790	13.3	193	2	Q6IFY5	Q6ify5 xenopus tro
35	788.5	13.3	760	2	Q90638	Q90638 gallus gall
36	787.5	13.3	776	1	RTN1 HUMAN	Q16799 homo sapien
37	787	13.3	1013	2	Q6T930	Q6t930 homo sapien
38	783	13.2	323	2	Q6JRW1	Q6jrw1 xenopus lae
39	781	13.2	199	2	Q6PB23	Q6pb23 xenopus lae
40	779	13.2	780	2	Q8K4S4	Q8k4s4 mus musculu
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42	778	13.1	780	2	Q8K0T0	Q8k0t0 mus musculu
43	776.5	13.1	316	2	Q6JRW2	Q6jrw2 xenopus lae
44	774.5	13.1	304	2	Q6JRW0	Q6jrw0 xenopus lae
45	755.5	12.8	214	2	Q7T222	Q7t222 carassius a

#### ALIGNMENTS

RESULT 1  
RTN4\_HUMAN  
ID RTN4\_HUMAN STANDARD; PRT: 1192 AA  
AC Q9NCQ3; Q94962; Q9BXG5; Q9H212; Q9H313; Q9U042; Q9Y293; Q9Y2Y7;  
AC Q9Y5U6;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foccen)  
DE (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific  
DE protein C homolog) (RTN-x) (Reticulon 5) (My043 protein).  
GN Name=RTN4; Synonyms=ASY, KIAA0886, NOGO;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RX MEDLINE=20129242; PubMed=10667780; DOI=10.1038/35000287;  
RA Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G.,  
RA Michalovich D., Simmons D.L., Walsh F.S.; "  
RT "Inhibitor of neurite outgrowth in humans."  
RL Nature 403:383-384(2000).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RC TISSUE=Brain;  
RX MEDLINE=21010696; PubMed=11126360; DOI=10.1038/sj.onc.1203948;  
RA Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;  
RT "A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on  
RT endoplasmic reticulum and reduces their anti-apoptotic activity."  
RL Oncogene 19:5736-5746(2000).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RX MEDLINE=20237542; PubMed=10773680;  
RA Yang J., Yu L., Bi A.D., Zhao S.-Y.;  
RT "Assignment of the human reticulon 4 gene (RTN4) to chromosome  
RT 2p14-->2p13 by radiation hybrid mapping";  
RL Cytogenet. Cell Genet. 88:101-102(2000).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 4).  
RX MEDLINE=20237542; PubMed=10773680;  
RA Jin W.-L., Ju G.;  
RT "Developmentally-regulated alternative splicing in a novel Nogo-A";  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).  
RC TISSUE=Placenta, and Skeletal muscle;  
RA Ito T., Schwartz S.M.;  
RT "Cloning of a member of the reticulon gene family in human";  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE=Fibroblast;  
RA Yutsudo M.;  
RT "Isolation of a cell death-inducing gene.";

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A. (ISOFORM 3).  
RC TISSUE=Pituitary;  
RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,  
RA Luo B., Hu R., Chen J.;  
RT "Human neuroendocrine-specific protein C (NSP) homolog gene.";  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
RN [8]  
RP SEQUENCE FROM N.A. (ISOFORM 3).  
RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,  
RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,  
RA Yu J., Han L.H.;  
RT "Novel human cDNA clones with function of inhibiting cancer cell  
RT growth.";  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
RN [9]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Brain;  
RX MEDLINE=99156230; PubMed=10048485;  
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirose M.,  
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. XII.  
RT The complete sequences of 100 new cDNA clones from brain which code  
RT for large proteins in vitro.";  
RL DNA Res. 5:355-364 (1998).  
RN [10]  
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).  
RC TISSUE=Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeng B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Tomshyuk S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [11]  
RP SEQUENCE FROM N.A. (ISOFORM 3).  
RC TISSUE=Umbilical cord blood;  
RX MEDLINE=2049367; PubMed=11042152; DOI=10.1101/gr.140200;  
RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,  
RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,  
RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;  
RT "Cloning and functional analysis of cDNAs with open reading frames for  
RT 300 previously undefined genes expressed in CD34+ hematopoietic  
RT stem/progenitor cells.";  
RL Genome Res. 10:1546-1560 (2000).  
RN [12]  
RP SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).  
RC TISSUE=Brain;  
RA Mao Y.M., Xie Y., Zheng Z.H.;  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
RN [13]  
RP SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1).  
RC TISSUE=Testis;  
RA Sha J.H., Zhou Z.M., Li J.M.;  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
RN [14]  
RP TOPOLOGY.

RC TISSUE=Brain;  
RX MEDLINE=20129259; PubMed=10667797; DOI=10.1038/35000226;  
RA GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.;  
RT "Identification of the Nogo inhibitor of axon regeneration as a  
RT Reticulon protein.";  
RL Nature 403:439-444 (2000).  
RN [15]  
RP FUNCTION.  
RC TISSUE=Brain;  
RX MEDLINE=21069055; PubMed=11201742; DOI=10.1038/35053072;  
RA Fournier A.E., GrandPre T., Strittmatter S.M.;  
RT "Identification of a receptor mediating Nogo-66 inhibition of axonal  
RT regeneration.";  
RL Nature 409:341-346 (2001).  
RN [16]  
RP REVIEW.  
RX MEDLINE=2188956; PubMed=11891768; DOI=10.1002/jnr.10134;  
RA Ng C.E.L., Tang B.L.;  
RT "Nogins and the Nogo-66 receptor: factors inhibiting CNS neuron  
RT regeneration.";  
RL J. Neurosci. Res. 67:559-565 (2002).  
CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help  
CC block the regeneration of the nervous central system in adults.  
CC Isoform 2 reduces the anti-apoptotic activity of Bcl-xL and Bcl-2.  
CC This is likely consecutive to their change in subcellular  
CC location, from the mitochondria to the endoplasmic reticulum,  
CC after binding and sequestration.  
CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xL and Bcl-2.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic  
CC reticulum. Anchored to the membrane of the endoplasmic reticulum  
CC through 2 putative transmembrane domains.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=4;  
CC Name=1; Synonyms=RTN 4A, Nogo-A, RTN-XL;  
CC IsoId=QNQC3-1; Sequence=Displayed;  
CC Name=2; Synonyms=RTN 4B, Nogo-B, RTN-XS, Foccen-M;  
CC IsoId=QNQC3-2; Sequence=VSP\_005655;  
CC Name=3; Synonyms=RTN 4C, Nogo-C, Foccen-S;  
CC IsoId=QNQC3-3; Sequence=VSP\_005652, VSP\_005653;  
CC Name=4;  
CC IsoId=QNQC3-4; Sequence=VSP\_005654;  
CC -!- TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain  
CC and testis and weakly in heart and skeletal muscle. Isoform 2 is  
CC widely expressed excepted for the liver. Isoform 3 is expressed in  
CC brain, skeletal muscle and adipocytes. Isoform 4 is testis-  
CC specific.  
CC -!- SIMILARITY: Contains 1 reticulon domain.  
CC -!- CAUTION: Ref.11 sequence differs from that shown due to  
CC frameshifts in positions 1149 and 1156.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AJ251383; CAB99248.1; -  
DR EMBL; AJ251384; CAB99249.1; -  
DR EMBL; AJ251385; CAB99250.1; -  
DR EMBL; AB040462; BAB18927.1; -  
DR EMBL; AB040463; BAB18928.1; -  
DR EMBL; AF148537; AAG12176.1; -  
DR EMBL; AF148538; AAG12177.1; -  
DR EMBL; AF087901; AAG12205.1; -  
DR EMBL; AF320999; AAG40878.1; -  
DR EMBL; AF132047; AAD31021.1; -  
DR EMBL; AF132048; AAD31022.1; -  
DR EMBL; AB015639; BAA83712.1; -  
DR EMBL; AF077050; AAD27783.1; -  
DR EMBL; AF177332; AAG17976.1; -  
DR EMBL; AB020693; BAA74909.2; ALT\_INIT.



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DR EMBL; BC001035; AAH01035.1; -.
DR EMBL; BC007109; AAH07109.1; -.

Query Match      98.2%; Score 5815; DB 1; Length 1192;
Best Local Similarity 97.2%; Pred. No. 7,3e-204;
Matches 1160; Conservative 4; Mismatches 13; Indels 16; Gaps 3;

Qy 1 MEDLQSPVLSGSSDPPRPQPAFKYQFVREPEDEDEDEDEDEDEDELEVLERKPA 60
Db MEDLQSPVLSGSSDPPRPQPAFKYQFVREPEDEDEDEDEDEDEDELEVLERKPA 60

Qy 61 AGLSAAPVPTAPAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQSPWDPSPVSTVPAP 120
Db AGLSAAPVPTAPAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQSPWDPSPVSTVPAP 120

Qy 121 SPLSAAAVSPKLPEDDPPAPPPPPASVSPQAEVWTPPAPAPAPPPSTPAAPKRG 180
Db SPLSAAAVSPKLPEDDPPAPPPPPPPASVSPQAEVWTPPAPAPAPPPSTPAAPKRG 180

Qy 181 SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP 226
Db SSGVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP 240

Qy 227 LSAASFKEHYLGNLSTVLPTGTLQENVSEASKEVSEKAKTLIDRLDTFSELEYSEM 286
Db LSAASFKEHYLGNLSTVLPTGTLQENVSEASKEVSEKAKTLIDRLDTFSELEYSEM 300

Qy 287 GSSFSVSPKASAVIVANPREIIVKNKDBREKLVNNILHXQQLPTALTCLKVEDRW 346
Db GSSFSVSPKASAVIVANPREIIVKNKDBREKLVNNILHXQQLPTALTCLKVEDRW 360

Qy 347 SSEKAKDFNEKRVAVEAPMEVEYADFKPFRVWEVKDSKEDSDMLAAGGKIESNLSKV 406
Db SSEKAKDFNEKRVAVEAPMEVEYADFKPFRVWEVKDSKEDSDMLAAGGKIESNLSKV 420

Qy 407 DKCKPADSLEQTNHEKDSSESSNDTSPFSTPEGIKDRSGAVITCAPFPNPAATESIATNIF 466
Db DKCKPADSLEQTNHEKDSSESSNDTSPFSTPEGIKDRSGAVITCAPFPNPAATESIATNIF 480

Qy 467 PLLDPTSENKTDKIEKKAQIVTEKNTSTKTSNPFVAAQSDSETDYVTTDLTKYTE 526
Db PLLDPTSENKTDKIEKKAQIVTEKNTSTKTSNPFVAAQSDSETDYVTTDLTKYTE 540

Qy 527 EVVANMPGLTPDLVOEACESELNEVTGKTAYETKMDLVOTSEVMQESLYPAQCLPSF 586
Db EVVANMPGLTPDLVOEACESELNEVTGKTAYETKMDLVOTSEVMQESLYPAQCLPSF 600

Qy 587 ESEATPSPVLPDIIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKEPENPPPYE 646
Db ESEATPSPVLPDIIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKEPENPPPYE 660

Qy 647 EAMSUSL-KVSGIKKEIKPENINNAALQETAPYISACDLIKETKLSAEPAPDFSDYSE 705
Db EAMSUSLKVSGIKKEIKPENINNAALQETAPYISACDLIKETKLSAEPAPDFSDYSE 720

Qy 706 MAKVEQPPVDSSELVEDSSPSEVDLPSDDSIDPVPQKQDETVMVKESLTETSFESMI 765
Db MAKVEQPPVDSSELVEDSSPSEVDLPSDDSIDPVPQKQDETVMVKESLTETSFESMI 780

Qy 766 EYENKEKLSALPPEGGKPYLESFKLSLNDNTKDTLLPDEVSTLSKKEKIPLOMBELSTAVY 825
Db EYENKEKLSALPPEGGKPYLESFKLSLNDNTKDTLLPDEVSTLSKKEKIPLOMBELSTAVY 840

Qy 826 SNDDLFIKSEAQIRETETFSOSSPIEIIDEPPTLISSKTDFSKLAREYTDLEVSHKSEI 885
Db SNDDLFIKSEAQIRETETFSOSSPIEIIDEPPTLISSKTDFSKLAREYTDLEVSHKSEI 900

Qy 886 ANAPDAGSLPCTELPHDLSLKNIOPKVEEKISPSDDDFSKNGSATSKVLLLPDVSALGH 945
Db ANAPDAGSLPCTELPHDLSLKNIOPKVEEKISPSDDDFSKNGSATSKVLLLPDVSALGH 959

Qy 946 TQAEIESIVKPKLVKEAEKKLPSPDTEKEDRSPSAIFGADLGKTSVVDLLYWRDIKKTGV 1005
Db TQAEIESIVKPKLVKEAEKKLPSPDTEKEDRSPSAIFGADLGKTSVVDLLYWRDIKKTGV 1005

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Db 960 TQAEIESIVKPKLVKEAEKKLPSPDTEKEDRSPSAIFGADLGKTSVVDLLYWRDIKKTGV 1019
Qy 1006 VFGASLFLLSLTVFSIVSVTAYTALALLSVTISFRIYKGVTOATOKSDEGHPFRAYLES 1065
Db 1020 VFGASLFLLSLTVFSIVSVTAYTALALLSVTISFRIYKGVTOATOKSDEGHPFRAYLES 1079
Qy 1066 EVAISEELVQKYSNSALGHVNCCTIKELRRLFLVDDLVDSLKFAVLMMVFTYVYVGFALFNGIT 1125
Db 1080 EVAISEELVQKYSNSALGHVNCCTIKELRRLFLVDDLVDSLKFAVLMMVFTYVYVGFALFNGIT 1139
Qy 1126 LLIILALISLSPVPIYERHQAIQIDHYLGLANKNVKQDAMAKIQAIPGLKRKAE 1178
Db 1140 LLIILALISLSPVPIYERHQAIQIDHYLGLANKNVKQDAMAKIQAIPGLKRKAE 1192

RESULT 2
QBIUA4
ID Q8IUUA4 PRELIMINARY; PRT; 986 AA.
AC Q8IUUA4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE RNT4 (RTN4 isoform Ab) (RTN4 isoform D) (RTN4 isoform E) (RTN4 isoform F) (RTN4 isoform G) (RTN4 isoform Aa).
GN Name=RTN4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
EX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT "Genomic structure and functional characterisation of the promoters of
  human and mouse nogo/rtn4.";
RL J. Mol. Biol. 325:299-323(2003).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Oertle T., Schwab M.E.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102285; AAM64244.1; -
DR EMBL; AY123246; AAM64250.1; -
DR EMBL; AY123247; AAM64251.1; -
DR EMBL; AY123248; AAM64252.1; -
DR EMBL; AY123249; AAM64253.1; -
DR EMBL; AY123250; AAM64254.1; -
DR EMBL; AY123245; AAM64249.1; -
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon.
DR PROSITE; PS0845; RETICULON.
SQ SEQUENCE 986 AA; 108449 MW; 0CDE8F647036415A CRC64;

Query Match      81.9%; Score 4851; DB 2; Length 986;
Best Local Similarity 98.9%; Pred. No. 7,3e-169;
Matches 976; Conservative 1; Mismatches 8; Indels 2; Gaps 2;

Qy 193 MDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAAAFKEHYLGNLSTVLPTGTLQ 252
Db MDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAAAFKEHYLGNLSTVLPTGTLQ 60

Qy 253 ENVSEASKEVSEKAKTLIDRLDTFSELEYSEMGSFSPKASAVIVANPREIIVK 312
Db ENVSEASKEVSEKAKTLIDRLDTFSELEYSEMGSFSPKASAVIVANPREIIVK 120

Qy 313 NKDEEKLVSNNILHXQQLPTALTCLKVEDVVSSEKAKDSFNEKRVAVEAPMREYAD 372

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Db 121 NDEBEKLVNNILNQQELPRLTKLVKDEDEVSEKADSNFKRVAVEAPMRREYAD 180
Qy 373 KXPFRVWEKDSKEDSMLAAGKIESNLEKVDKCCFADSLQTNHKKDSESSNDDTS 432
Db 181 KXPFRVWEKDSKEDSMLAAGKIESNLEKVDKCCFADSLQTNHKKDSESSNDDTS 240
Qy 433 FFSPTPEGIDKRGAYITCAPFPNPAATESIATNIFPILLGDPSTSENKTKDEKKIAQIVT 492
Db 241 FFSPTPEGIDKRGAYITCAPFPNPAATESIATNIFPILLGDPSTSENKTKDEKKIAQIVT 300
Qy 493 EKNTSTKTSNPPFVAQDSETDVTTDNLTKTVEEVVANNPEGLTLDVQECESSELNEV 552
Db 301 EKNTSTKTSNPPFVAQDSETDVTTDNLTKTVEEVVANNPEGLTLDVQECESSELNEV 360
Qy 553 TGTKIAYETKMDLVQTSVWQESLYPAAQLCPSFESEATPSPVLPDIWVEAPLNSAVPS 612
Db 361 TGTKIAYETKMDLVQTSVWQESLYPAAQLCPSFESEATPSPVLPDIWVEAPLNSAVPS 420
Qy 613 AGASVTPQSSPLEASVNESIKHEPENPPPYEEAMSVSL-KVSGIKKEIKEPENINAA 671
Db 421 AGASVTPQSSPLEASVNESIKHEPENPPPYEEAMSVSLKVSGIKKEIKEPENINAA 480
Qy 672 LQETEPAYISACDLIKETKLSAEPAPDFSDYSEMAKVQPPVDHSELVEDSSPSEPVD 731
Db 481 LQETEPAYISACDLIKETKLSAEPAPDFSDYSEMAKVQPPVDHSELVEDSSPSEPVD 540
Qy 732 LFSDDSIIPVPOKQDETVMVKESLTETSFESMIEYENKEKLSALPPEGKPYLESFKLS 791
Db 541 LFSDDSIIPVPOKQDETVMVKESLTETSFESMIEYENKEKLSALPPEGKPYLESFKLS 600
Qy 792 LONTKDTLLPDEVSTLSKKEKIPLOMBELSTAVYSNDDLFIKSAQIRTFETFSOSSPTE 851
Db 601 LONTKDTLLPDEVSTLSKKEKIPLOMBELSTAVYSNDDLFIKSAQIRTFETFSOSSPTE 660
Qy 852 IIDEFPTLLSSKTDSPSKLAREYTDLEVSHKSIANAPDAGSLPCTELPHDLSLKNIOF 911
Db 661 IIDEFPTLLSSKTDSPSKLAREYTDLEVSHKSIANAPDAGSLPCTELPHDLSLKNIOF 720
Qy 912 KVEEKISFDDFSKNGSATSQVLLLPDPVVSALGHQTOAEIESIVKPKVLKEAKKLPSPDT 971
Db 721 KVEEKISFDDFSKNGSATSQVLLLPDPVVSALA-TQAEIESIVKPKVLKEAKKLPSPDT 779
Qy 972 EKEDRSPSAIFSADLKTSTVDLLYWRDIKKTGVVFGASLFLLLSLTSTVSIYSTAYIAL 1031
Db 780 EKEDRSPSAIFSADLKTSTVDLLYWRDIKKTGVVFGASLFLLLSLTSTVSIYSTAYIAL 839
Qy 1032 ALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNCITKE 1091
Db 840 ALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNCITKE 899
Qy 1092 LRLFLVDDLVDLSLKFVLMWFTYVYGALFNGLTLLALISLFSVPVIYERHQADHY 1151
Db 900 LRLFLVDDLVDLSLKFVLMWFTYVYGALFNGLTLLALISLFSVPVIYERHQADHY 959
Qy 1152 LGLANKNVKDMAKIOAKIPGLKRKAE 1178
Db 960 LGLANKNVKDMAKIOAKIPGLKRKAE 986

RESULT 3
RTM4_RAT
ID RTM4_RAT STANDARD; PRT: 1163 AA.
AC Q9JKL1; Q9JKL10; Q9R0D9; Q9WUE9; Q9WUF0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foccen)
DE (Glut4 vesicle 20 kDa protein).
GN Names=Rtn4; Synonyms=Nogo;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
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OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Adipocyte;
RX MEDLINE=99249816; PubMed=10231557; DOI=10.1016/S0167-4889(99)00033-6;
RA Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lienhard G.E.;
RT "Cloning and characterization of a 22 kDa protein from rat adipocytes:
a new member of the reticulon family.";
RL Biochim. Biophys. Acta 1450:68-76(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=20129258; PubMed=10667796; DOI=10.1038/35000219;
RA Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,
Spillmann A., Christ F., Schwab M.E.;
RT "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an
antigen for monoclonal antibody IN-1.";
RL Nature 403:434-439(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).
RC STRAIN=Wistar Kyoto; TISSUE=vascular smooth muscle;
RA Ito T., Schwartz S.M.;
RT "Cloning of a member of the reticulon gene family in rat: one of two
minor splice variants.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBSJ databases.
RN [4]
RP FUNCTION.
RX MEDLINE=22033691; PubMed=12037567; DOI=10.1038/417547a;
RA GrandPre T., Li S., Strittmatter S.M.;
RT "Nogo-66 receptor antagonist peptide promotes axonal regeneration.";
RL Nature 417:547-551(2002).
CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
block the regeneration of the nervous central system in adults (By
similarity).
CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By
similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the
membrane of the endoplasmic reticulum through 2 putative
transmembrane domains (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1; Synonyms=Nogo-A, NI-220-250;
CC IsoId=Q9JKL1-1; Sequence=Displayed;
CC Name=2; Synonyms=Nogo-B, Foccen-M1;
CC IsoId=Q9JKL1-2; Sequence=VSP_005658;
CC Name=3; Synonyms=Nogo-C, VP20;
CC IsoId=Q9JKL1-3; Sequence=VSP_005656, VSP_005657;
CC Name=4; Synonyms=Foccen-M2;
CC IsoId=Q9JKL1-4; Sequence=VSP_005659;
CC -!- TISSUE SPECIFICITY: Isoforms 1_2 and 3 are present in optic
nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are
present in dorsal root ganglion, sciatic nerve and PC12 cells
after longer exposure. Isoforms 2 and 3 are detected in kidney,
cartilage, skin, lung and spleen. Isoform 3 is expressed at high
level in skeletal muscle. In adult animals isoform 1 is expressed
mainly in the nervous system.
CC -!- SIMILARITY: Contains 1 reticulon domain.
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF051335; AAF01564.1; -
CC EMBL; AJ242961; CAB71027.1; -
CC EMBL; AJ242962; CAB71028.1; -
CC EMBL; AJ242963; CAB71029.1; -
CC EMBL; AF132045; AAD31019.1; -
CC EMBL; AF132046; AAD31020.1; -
CC GO; GO:0030176; C:integral to endoplasmic reticulum membrane; IDA.
CC GO; GO:0005635; C:nuclear membrane; ISS.
CC
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DR GO: 0005515; F: protein binding; ISS.  
 DR GO: 0019987; P: negative regulation of anti-apoptosis; ISS.  
 DR GO: 0030517; P: negative regulation of axon extension; ISS.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS00845; RETICULON; 1.  
 KW Alternative splicing; Direct protein sequencing;  
 Endoplasmic reticulum; Transmembrane.  
 FT DOMAIN 1 989 Cytoplasmic (Potential).  
 FT TRANSMEM 990 1010 Potential.  
 FT DOMAIN 1011 1104 Lumenal (Potential).  
 FT TRANSMEM 1105 1125 Potential.  
 FT DOMAIN 1126 1163 Cytoplasmic (Potential).  
 FT DOMAIN 976 1163 Reticulon.  
 FT DOMAIN 33 46 Poly-Glu.  
 FT DOMAIN 73 76 Poly-Ala.  
 FT DOMAIN 140 145 Poly-Pro.  
 FT VARSPLIC 1 964 Missing (in isoform 3).  
 FT VARSPLIC 1 964 /FTid=VSP 005656.  
 FT VARSPLIC 965 975 AVLSAELSKTS -> MDGQKXHWKDK (in isoform 3).  
 FT VARSPLIC 173 975 /FTid=VSP 005657.  
 FT VARSPLIC 192 975 Missing (in isoform 2).  
 FT VARSPLIC 192 975 /FTid=VSP 005658.  
 FT VARSPLIC 192 975 Missing (in isoform 4).  
 FT VARSPLIC 192 975 /FTid=VSP 005659.  
 FT CONFLICT 1130 1131 Missing (in Ref. 3; AAD31020).  
 FT SEQUENCE 1163 AA; 126386 MW; 8CB894809B94F086 CRC64;  
 SQ  
 Query Match 72.5%; Score 4296.5; DB 1; Length 1163;  
 Best Local Similarity 74.0%; Pred. No. 1.4e-148;  
 Matches 885; Conservative 104; Mismatches 156; Indels 51; Gaps 19;  
 QY 1 MEDLDQSLVSS-DSPPROPAPKQYVPEDEE-BEEEEDEDEDEDELEVLERK 58  
 DB 1 MEDLDQSLVSSDSDPPPPAPKQYVPEDEE-BEEEEDEDEDEDELEVLERK 60  
 QY 59 PAAGLSAAPPVTPAAGAPLMDGNDVFPAPRGLPAAPVAPRQSPWDPSPVSSVTP 118  
 DB 61 PAAGLSAAPPVTPAAGAPLMDGNDVFPAPRGLPAAPVAPRQSPWDPSPVSSVTP 115  
 QY 119 APSPLSAAVSPKLPEDDEPPAPPPPPPPASVSPQAEPPVTPPAPAPAPPPTPAAPKR 178  
 DB 116 APSPLSAAVSPKLPEDDEPPAPPPPPPPAGAPLAE-----PAAPPSTPAAPKR 166  
 QY 179 RGSAG-----AVVXXXKIMDLKEQPGNTISAGQDFPSVLLETAASPSL 224  
 DB 167 RGSAGVDETLFALPAASEPVPSPSAEKIMDLMEQNTVSSGQDFPSVLLETAASPSL 226  
 QY 225 SPLSAASPKEHYLGNTSLVPTGTLQENVSEASKEVSEKAKTLILDRDLTEFSELEYS 284  
 DB 227 SPLSTVSPKEHYLGNTSLVPTGTLQENVSEASKEVSEKAKTLILDRDLTEFSELEYS 286  
 QY 285 EMGSFSPKSAEAVIVANPREIIVKNKDEEKLNSNTHXQQLPTALTATKLKVEDE 344  
 DB 287 EMGSFSPKSAEAVIVANPREIIVKNKDEEKLNSNTHXQQLPTALTATKLKVEDE 340  
 QY 345 VVSEKAKDSFNEKRAVAEMREYADFKPFRVWEVDSKEDS-DMLAGGKIESNLE 403  
 DB 341 VVSEKAKDSFNEKRAVAEMREYADFKPFRVWEVDSKEDS-DMLAGGKIESNLE 396  
 QY 404 SKVDKCPADSLQTNHSEKSSNDTSPSTPEGIKDRSGAVITCAPFPNPAATESIAT 463  
 DB 397 SKVDKCPADSLQTNHSEKSSNDTSPSTPEGIKDRSGAVITCAPFPNPAATESIAT 455  
 QY 464 NIPFLLEDPTSENKTDKIEKKAQIVTEKNTSTKTSNPFVAAQSDSETDYVTDNLTK 523  
 DB 456 NIPFLLEDPTSENKTDKIEKKAQIVTEKNTSTKTSNPFVAAQSDSETDYVTDNLTK 514  
 QY 524 VTEEVVAMPGLTPDLVQEAACESELNEVTGKTAETKMDLVQSEVMQESLTPAQLC 583  
 DB 515 VTEEVVAMPGLTPDLVQEAACESELNEVTGKTAETKMDLVQSEVMQESLTPAQLC 574

584 PSFESEATPSVLPDIWMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKEHPNP 642  
 DB PSFESEATPSVLPDIWMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKEHPNP 634  
 QY 643 PPEEAMSVSLKSGIKKEIKPENINAAQETAPYISIAACDLIKETKLSAEPAPDPSD 702  
 DB 635 PPEEAMSVSLKSGIKKEIKPENINAAQETAPYISIAACDLIKETKLSAEPAPDPSD 694  
 QY 703 YSEMAKVPQVPHSELVEOSSPDSEVDLPSDDSIIPVQKQDETVMVLESITETSPFE 762  
 DB 695 YSEMAKVPQVPHSELVEOSSPDSEVDLPSDDSIIPVQKQDETVMVLESITETSPFE 753  
 QY 763 SMIEYENKEKLSALPPGPGPYLESFKLSLNTKDTLLPDRVSTLSKKEKIPLOWEELST 822  
 DB 754 TVAGHK-EERLSASPOELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQWEEFNT 811  
 QY 823 AVYNDLDFISKEAQIRETETFSOSSPIEIDEPTLISSTKDSFKSLARYTDLVESHK 882  
 DB 812 AVYNDLDFISKEAQIRETETFSOSSPIEIDEPTLISSTKDSFKSLARYTDLVESHK 870  
 QY 883 SEIANAPDGAGSLPCTELPHDLISLKNQPKVEKISPSDDSKNGSATSKVLLPPDVSA 942  
 DB 871 SEIANAPDGAGSLPCTELPHDLISLKNQPKVEKISPSDDSKNGSATSKVLLPPDVSA 928  
 QY 943 LGHTQABIESIVKPKVLEKAEKLPSTDEKEDSPSAIFSDADLGKTSVVDLLYWRDIKK 1002  
 DB 929 L-EQPTMGSIIVKSKSLTKEAKLPSTDEKEDSPSAIFSDADLGKTSVVDLLYWRDIKK 987  
 QY 1003 TGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDGHPFRAY 1062  
 DB 988 TGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDGHPFRAY 1047  
 QY 1063 LESEVAISELVQKYSNLSALGHVNTKIKELRRLFLVDLVDLSLKFVLMVFTVYGALFN 1122  
 DB 1048 LESEVAISELVQKYSNLSALGHVNTKIKELRRLFLVDLVDLSLKFVLMVFTVYGALFN 1107  
 QY 1123 GLTLLIALLSLFSVPVIVYERHQAIIDHYLGANKNVKDMAKIQAIPGLKRAE 1178  
 DB 1108 GLTLLIALLSLFSVPVIVYERHQAIIDHYLGANKNVKDMAKIQAIPGLKRAE 1163

RESULT 4  
 Q8BGM9 PRELIMINARY; PRT; 1162 AA.  
 AC Q8BGM9  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE RTN4.  
 GN Name=Rtn4;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SvcJ7, and 129SvcJ7;  
 RX MEDLINE=22376540; Pubmed=12488097; DOI=10.1016/S0022-2836(02)01179-8;  
 RA Oertle T., Huber C., van der Putten H., Schwab M.E.;  
 RT "Genomic structure and functional characterisation of the promoters of  
 human and mouse nogo/rtn4.";  
 RL J. Mol. Biol. 325:299-323(2003).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SvcJ7;  
 RX Van der Putten H.;  
 RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129SVCJ7;  
 RX Van der Putten H., Mir A.;  
 RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AY102284; AAM73506.1; --.





Db 492 SVAQPSASPLEVPSVYDGKLEPENPPYBEAMSVALKTSKDEEIKPEPSFNAAQE 551  
 QY 675 TPAPYISACDLIKETKLSAEPAPDFSDYSEMAKVEQPPVDHSELVEDSSPSEPVDFLS 734  
 Db 552 AEAPYISACDLIKETKLSAEPAPDFSDYSEMAKVEQPPVDHSELVEDSSPSEPVDFLS 611  
 QY 735 DDISIPVQKQDETVMVKESLTETSFESMIEYENKEKLSALPPGEGKBYLESFKLSLDN 794  
 Db 612 DDISIEVPQTQBEAVMLMKESLTVS-ETVQHKHKLRLSASQVQKBYLESFQNLHI 670  
 QY 795 TKDTLLPDRSVTLSSKEKIPLOMEELSTAVYNSNDLFIKSEAQIRTEFTFSDSSPTEID 854  
 Db 671 TKDA-ASNEIPTLTKETLSLQMEENTAIYNSNDLFSKEDKMKSETFSDSSPTEID 729  
 QY 855 EPTTLISSKTDGSKLAREYTDLEVSHKSEIANAPDAGSLPCTELPHDLSLKNIQPKYE 914  
 Db 730 EPTTFVSAKDDSS---PKEYTDLVSNKSEIANVQSGANSLPCSELPCDLSFKNTYPKDE 785  
 QY 915 EKISFDDSKSGSATSKVLLPPDVSALGHTQAEISIVKPKLEKAEKLPDSTEKE 974  
 Db 786 AHV--SDEFSKRSKSVKPLLLPNVSAL-ESQIEMGNIVKPKVLTKEAEKLPDSTEKE 842  
 QY 975 DRSPSAIFSADLCKTSWDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALL 1034  
 Db 843 DRSLTAVLSAELNKTSSVLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALL 902  
 QY 1035 SVTISPRIYKGVIAQIOKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCITKELRR 1094  
 Db 903 SVTISPRIYKGVIAQIOKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCITKELRR 962  
 QY 1095 LFLVDDVLSLFAVLMWFTYVYGALFNGLTLLILALISLFSVPVIYERHQIDHYLGL 1154  
 Db 963 LFLVDDVLSLFAVLMWFTYVYGALFNGLTLLILALISLFSVPVIYERHQIDHYLGL 1022  
 QY 1155 ANKNVADAMAKIOAKIPGLKRAE 1178  
 Db 1023 ANKNVADAMAKIOAKIPGLKRAE 1046

RESULT 7  
 Q7TNB7  
 ID Q7TNB7 PRELIMINARY; PRT; 720 AA.  
 AC Q7TNB7  
 DT 01-OCT-2003 (TEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RP [2]  
 RC SEQUENCE FROM N.A.  
 RA STRAIN=C57BL/6; TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC056373; AAH56373.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 720 AA; 77435 MW; 80AB78728F16EAB2 CRC64;  
 Query Match 43.6%; Score 2580.5; DB 2; Length 720;  
 Best Local Similarity 70.8%; Pred. No. 2.4e-86;  
 Matches 527; Conservative 69; Mismatches 107; Indels 41; Gaps 13;  
 QY 1 MEDLQDSPLVSSS-DSPRPPOPAFYQVREPEDEEEDEDEDEDEDEDELEVLKRP 59  
 Db 1 MEDIQSSILVSSSADSPRPFPAPFYQVTEPEDEDEDEDEDEDEDELEVLKRP 60  
 QY 60 AAGLSAAPVPTAPAGAPLMDFGNDVFPAPRGPLPAPAPPVAPERQPSWDPSVSTVPA 119  
 Db 61 AAGLSAAPVP--PAA-APLLDFSSDVPAPRGPLPAPAPPVAPERQPSWERSPAAS--A 114  
 QY 120 PSLPSAAAVSPSKLPEDDEPPAPPPPPASVSPQAEVPTTPPAPAPAPPPSTPAAPKPR 179  
 Db 115 PSLPPAAAVLPSKLPEDDEPPAR--PPAPAGASPLAE-----PAPAPSTPAAPKPR 163  
 QY 180 GSGSG-----AVVXXXKIMDLKBPQNTISAGQEDFPFVLLETAASXPSSL 225  
 Db 164 GSGSVDETLFALPAASEPVPISSEAEKIMDLKBPQNTVSSGQEDFPFVLLETAASXPSSL 223  
 QY 226 PLASAASFHEHYGLNLSVLPTEGLQENVSASKEVSEKATLLIDRLDTFSELEYSE 285  
 Db 224 PLSTVTSFKHGYGLNLSVASTEGTIEETLNEASRELPERATNPFVNRSEAFSVLEYSE 283  
 QY 286 MGSSFSVSPKASAVIENPREIIVKKNDBEKLVSNNILHXQELPTALTAKLVKEDSV 345  
 Db 284 MGSSFNKSGPKGESAMLVNTEKEEIVVRKDKED-LVCSAALNHPQESPATLTKVVKEDGV 342  
 QY 346 VSSEKAKDSFNKRVAVAPMREEVADFKPFERVWEVSKDEDS-DMLAAGGKIESNLDS 404  
 Db 343 MSPEKTMDFINEMKMSVAVPREEVADFKPFQAEVVKDTEGSRDVLAA---RANMDS 398  
 QY 405 KVDKCFADSLQTNHKEKSSNDSTSPSPTEGIGKORSAYITCAPNPAATESIATN 464  
 Db 399 KYDKKCFEDSLQKGHGKDSERNENASFPPTPELVKDGSRAYITCDSFS-SATESTAA 457  
 QY 465 IPFLLEDPTSENKTDKKEIEKKAQIVTEKNTSTKTSNPPFFVAAQDSEYDVTNLTKV 524  
 Db 458 IPFVLEDHTSENKTDKKEIEKKAQIVTEK-TSPKTSNPPFLVAIHDSEADYVTTNLSKV 516  
 QY 525 TEEVVANMPEGLTPDLVQACSESELNVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLCP 584  
 Db 517 TEAVVATMPEGLTPDLVQACSESELNVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLCP 576  
 QY 585 SPEESEATPSVLPDIVMEAPLNSAVPNSAGASVIOFSSSPLAE-SSVNVYESIKHBPENDP 643  
 Db 577 SPEEAEATPSVLPDIVMEAPLNSLLPSTGASVAPQSPASPLEVPSVSDGKLBPENPP 636  
 QY 644 PYEEAMSVSLKVGSKIKEIKPENINAAALQETEAPEVSIACDLIKETKLSAEPAPDFSDY 703  
 Db 637 PYEEAMSVALKTSKDEEIKPEPSFNAAQAEAPYISACDLIKETKLSAEPDFSDY 696  
 QY 704 SEMAKVEQPPVDPHSELVEDSSPDS 727  
 Db 697 SEIAKFEKSVDPHSELVEDSSPES 720

RESULT 8  
 Q8K290  
 ID Q8K290 PRELIMINARY; PRT; 639 AA.  
 AC Q8K290;  
 DT 01-OCT-2002 (TEMBLrel. 22, Created)

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DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DE 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Rtn4 protein.
GN Name=Rtn4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;
RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Young A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032192; AAH3192.1; -.
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:cytoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS0845; RETICULON; 1.
SQ SEQUENCE 639 AA; 70312 MW; 309A19DA37603F11 CRC64;

Query Match 42.7%; Score 2527; DB 2; Length 639;
Best Local Similarity 79.5%; Pred. No. 1.8e-84;
Matches 515; Conservative 57; Mismatches 66; Indels 10; Gaps 6;

QY 532 MPEGLTPDLVQACSELNEVTGTXIAYETKMDLVQTSSEVQESLYPAAQLCPSPSESEA 591
DB 1 MPEGLTPDLVQACSELNEATGTXIAYETKVDLVQTSSEATQESLYPTAQLCPSEEA 60
QY 592 TSPVLPDIMEAPLNSAVPSAGASVIOQSSSPLA-SNVYSEIKHEPENPPPYEAMS 650
DB 61 TSPVLPDIMEAPLNSLTPSGASVQASPLEVPSVSDGKLPENPPPYEAMS 120
QY 651 VSLKSGIKKEETKEPENNAALQETEAPYISACDLIKETKLSAEPAPDFSDYSEMAKVE 710
DB 121 VALKTSDAKEEIKEPESFNAAQEAEPYISACDLIKETKLSPEFSFNYSIAKFE 180
QY 711 QVPVPSHSELVEDSPDSEPVDFSDSDSIPEVPOKQDETVMVKESLTSTFESMEYENK 770
DB 181 KSPVPHCELVDSSPESPEVDFSDSDSIPEVPOQTEAEAVLMKESLTVS-ETVTOHKH 239
QY 771 EKLALPPEGKPYLESFKLSLDNTKOTLLPDEVSTLSKKEKIPLOMEELSTAVYNSDDL 830
DB 240 ERLSASPQEVGPKPYLESFQPNLHITKDA-ASNEIPTLTCKETISLQMEEFNTAIVNSD 298
QY 831 FLSKAQIRETFTFSDSPSPEIIEIDFFPTLISKTDTSFKSLAREYTDLEVSHKSEIANAPD 890
DB 299 LSSKEDKMKESFTFSDSPSPEIIEIDFFPTFVSAKDDSDS----PKEYTDLEVSNKSEIANVQS 354

Query Match 37.7%; Score 2233; DB 2; Length 578;
Best Local Similarity 78.4%; Pred. No. 8.3e-74;
Matches 460; Conservative 52; Mismatches 65; Indels 10; Gaps 6;

QY 593 PSPVLPDIMEAPLNSAVPSAGASVIOQSSSPLA-SNVYSEIKHEPENPPPYEAMSV 651
DB 1 PSPVLPDIMEAPLNSLTPSGASVQASPLEVPSVSDGKLPENPPPYEAMSV 60
QY 652 SLKVSIGIKKEETKEPENNAALQETEAPYISACDLIKETKLSAEPAPDFSDYSEMAKVEQ 711
DB 61 ALKTSDAKEEIKEPESFNAAQEAEPYISACDLIKETKLSPEFSFNYSIAKFEK 120
QY 712 PVPDHSSELVEDSPDSEPVDFSDSDSIPEVPOKQDETVMVKESLTSTFESMEYENK 771
DB 121 SVPDHCCELVDSSPESPEVDFSDSDSIPEVPOQTEAEAVLMKESLTVS-ETVTOHKH 179
QY 772 KLSALPPEGKPYLESFKLSLDNTKOTLLPDEVSTLSKKEKIPLOMEELSTAVYNSDDL 831
DB 180 RLSASPOEVGPKPYLESFQPNLHITKDA-ASNEIPTLTCKETISLQMEEFNTAIVNSD 238
QY 832 ISKAQIRETFTFSDSPSPEIIEIDFFPTLISKTDTSFKSLAREYTDLEVSHKSEIANAPDG 891
DB 239 SSKEDKMKESFTFSDSPSPEIIEIDFFPTFVSAKDDSDS----PKEYTDLEVSNKSEIANVQS 294
QY 892 AGSLPCTELPHDLKLNQPKVBEKISFSDDFSKNGSATSKVLLPPDVSALGHTQABIE 951
DB 295 ANSLPSELPCDLSFKNTYPKDEAHV--SDEFSKRSRVSFVKVPLLPVNSAL-ESQIEMG 351

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QY 952 SIVKPKVLKEAEKKLPSTDEKEDRSPSAIFGADLGKTSVVDLLYWRDIKKTKGVVFGASL 1011
Db 352 NIVKPKVLTKAEAEKKLPSTDEKEDRSLTAVLSAELNKTSSVDLLYWRDIKKTKGVVFGASL 411
QY 1012 FLLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIOATOKSGDEGHPFRAYLESEVAISE 1071
Db 412 FLLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIOATOKSGDEGHPFRAYLESEVAISE 471
QY 1072 ELVQKYSNLSALGHVNTIKELRRLFLVDLVDLSKFAVLMWFTYVYGALFNGLTLLILAL 1131
Db 472 ELVQKYSNLSALGHVNTIKELRRLFLVDLVDLSKFAVLMWFTYVYGALFNGLTLLILAL 531
QY 1132 ISLFSVPVIYERHQAQIDHYLGLANKNVKDAKIAQKIPGLKRKAE 1178
Db 532 ISLFSVPVIYERHQAQIDHYLGLANKNVKDAKIAQKIPGLKRKAE 578

RESULT 10
Q6RS8
ID Q6RS8 PRELIMINARY; PRT; 658 AA.
AC Q6RS8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Neutrite outgrowth inhibitor NOGO-A (Fragment).
GN Name=NOGO;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Caltharp S.A., Pira C.U., McNeill D.S., Liwnicz B.H., Oberg K.C.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY494005; AAS18427.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
FT NON TER
SQ SEQUENCE 658 AA; 72075 MW; 14B7A000C5E8CDA5 CRC64;

Query Match 29.3%; Score 1735; DB 2; Length 658;
Best Local Similarity 58.0%; Pred. No. 1.3e-55;
Matches 388; Conservative 83; Mismatches 164; Indels 34; Gaps 15;

QY 533 PEGLTPLDVOEACESELNEVTGKIAYETMDLVQTSSEVMOESLYPAAQLCPSESEAT 592
Db 1 PEGLTPLDVOEACESEMHDACTKLAYETKIDLVQTSSEVMOESLYPAAQLCPSESEAT 60
QY 593 PSPVLDDIYNEAPLNSAVSAGASVLPQSSPLE--ASSVNYESIKHEPENPPVYEAMS 650
Db 61 PSPVLDDIYNEAPLNSAGASTVQLETSQGTFTTASTENVKAEKPLVQEAVN 120
QY 651 VSL-KVSGIKEEL---KEPENINAAQTEAPYISIACDLIKETKLSABPA-PDFSDYSE 705
Db 121 MPLTQAEAKEELTLKKADRESSTSPEDLETPIYISIACDLIKETKVSGESASPSLTDYST 180
QY 706 MAKVE---QVPDHSSELVEDSPDSEFVDFSDDSIPDPVQKQDETVMVLKESLSTETSE 762
Db 181 TPITEHLSQDSVEHKELAELKSPQFGKDLFRQVMPDFPGSESDQTLI---LNGKSVE 237
QY 763 SMIEYENKELKLSALPEEGKPKYLESPKSLDNTK-DTLLPDE--VSTLKKKIKIPLQWEE 819
Db 238 NIETDEQERLVDLSAATGKPYLESQDELDSKIVTQPSPTPAKIAKAEKIPLOWEE 297
QY 820 LSTAVYNSDDLFTSKAEQIRETETFTSDSPSIEIIDEFPTLISKTDTSFKLAREYDLEV 879
Db 298 LNALAYST-DVSVAMEPKGDSKGLSPSPSVSVEDDFVMLVDPKTC--TEFVAEVTDTRET 354
QY 880 SHKSE---IAN-APDGAAGSLPCTELPHDLSLKNIQKVEKISFSDPSFKNGSATS-K--- 932

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Db 355 VHKNESKDISNIRDEKQAPLTELPCDLSVRNVKTEDD---AHALKSKIQAIDREVP 411
QY 933 ---VLLLPDVSALGHQTAETESIVKPKVLEKAEKKLPSTDEKEDRSPSAIFGADLGKT 989
Db 412 EVSMVSLPATGTSPSTSEKEIVSVCKPEAFKEAERGASAKEKE--KPTAVFSKLVNYS 469
QY 990 SVVDLLYWRDIIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIOA 1049
Db 470 SVVDLLYWRDIIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISPRIYKGVIOA 529
QY 1050 IOKSGDEGHPFRAYLESEVAISELQKYSNLSALGHVNTIKELRRLFLVDLVDLSKFAV 1109
Db 530 IOKSGDEGHPFRAYLESDVAVSEELIQKYSVVVLGHNGTGVKELRRLFLVDLVDLSKFAV 589
QY 1110 LMWFTYVYGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAKIAQK 1169
Db 590 LMWFTYVYGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAKIAQK 649
QY 1170 IPGLKRKAE 1178
Db 650 IPGLKRKTE 658

RESULT 11
Q6JRV1
ID Q6JRV1 PRELIMINARY; PRT; 1055 AA.
AC Q6JRV1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE RTN4.1-A2.
GN Name=RTN4;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Wholemount embryos;
RX PubMed=15019938; DOI=10.1016/j.mcn.2003.09.021;
RA Klinger M., Diekmann H., Heinz D., Hirsch C., Hannbeck von Hanwehr S.,
RA Petrusch B., Oertle T., Schwab M.E., Stuermer C.A.;
RT "Identification of two NOGO/RTN4 genes and analysis of Nogo-A
RT expression in Xenopus laevis."
RL Mol. Cell. Neurosci. 25:205-216(2004).
DR EMBL; AY316196; RAQ82645.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 1055 AA; 115426 MW; F583A19F9BA51EDF CRC64;

Query Match 25.9%; Score 1534.5; DB 2; Length 1055;
Best Local Similarity 36.9%; Pred. No. 4.7e-48;
Matches 463; Conservative 157; Mismatches 353; Indels 281; Gaps 49;

QY 5 DOSPLVSSSDS-----PPRP-----OPAFKIQVVRPEDEE 35
Db 3 EESPDISSHSGDERREPAQGERKXPWDDLVDLDTGGAGQFQSFSGSHPARDIEEE 62
QY 36 EEEEEEEDEDELEVLKPAAGLSAAPV-PTAPAGAPLMDFGNDFVPPAPRGL 94
Db 63 EDEEERGAWKDLSLSPV-EPEPGSIDISVSPSPSPA-----V 101
QY 95 PAAPVAVERQSWDPSPSVSVTPAPSLAAVSPSKLPEDEPPARPPPPASVSQ 154
Db 102 PSAPMEERPP-----APCTAPSGSVATFLARLPEED----- 136
QY 155 AEPVMTVPAPAPAPPPSTPAAPKRGSGCAVVXXXKIMDLKEQPGNTISAGQEDPPSVL 214
Db 137 -ENLFTLPA-----ASAHLMHASADKIM---EPYSTVSTQGEERFASVL 175

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Qy 215 LETAASPLSLAAGSKEHYLGNLSTVLPTGTLQENVSEAKSEKAKTLLIDRD 274
Dy 176 LOSTASLSSPLSTDSKHAETVAFTGLAATEALQEPD----- 217
Qy 275 LTFSELEYSMGSGSFVSPKAGSAVIANPREIIVKNKDEEKLVSNNILHXQBLPT 334
Dy 218 ---NMYSVSRITSHLPLSLDNLSKAL-DQVKEBVFSEK-----YVVDHPT 260
Qy 335 ALTKLVKEDV-VSEKAKOSFNEKRVAVEAPMEE-----YADKPF-----E 377
Dy 261 SQQETISEEHAKLYSQAKEMFSGMLQSV-APPHEEFTDIKEVDYVPYDFKPFMSKSGD 319
Qy 378 RVMEVVKDSKSDMLAAGGKIESLKVDKCKFCADSLQTNHKKDESSNDTSPFSTP 437
Dy 320 VGYEVDVAEKFOVDV-GRLL-NLESVKHE-----EKSEMEWIDSLSDDIS-PLTP 368
Qy 438 EGIKDRGAYITCAPFNAATESIATNI-PLLEDPTSENKXTDBKKIEEKAQIVTSKNT 496
Dy 369 ELLPDST-----DYDMFAT--VEQNIPTFSFGGHRVAGNKTDEKKIEDIEAQ-----KT 414
Qy 497 S-----TKTSNPF-VAQODSETDYVTQNLTKVTEEVANMPEGLTDLVQACSESEL 549
Dy 415 SVGGLKVAIVNPNFNSAQSE--YVTHVATHVSTK-----PEGTPDILVQAYSEEA 467
Qy 550 NEVTGKIAYETKMDLVQT-SEVMQESLYPAAQLCPSESEATPSPVLPIVMEAPLNS 608
Dy 468 YDTGIPKQKYESNDLVQTAANSVQKVSPTAQAPARLEETDSVSSPVLPIVMEAPLAS 527
Qy 609 AVPSGASVIOPPSSPLEAS-SVNYEIKHEPNPPYEEAMSVLSKVGSIKEIKPEN 667
Dy 528 ALETV--ALKPDISPVGIKPARVEKTKABPEKPPSYEEAVT-----EVLQND 574
Qy 668 INAAL-----QTEAPVISTACDLIKETLSAEPADPDSYSEMAKVEQP--VPDH 716
Dy 575 LAAALGSKGAVVEETPTVISTACDLIKETLSA- --SGTFEFSKLKQNEFESQF 628
Qy 717 SELVEDSPSEPVDFLSDSDIPDVPQKQDVTMLVKESLT----ETSFESMIYENKEK 772
Dy 629 MEPSDESPOSE-----CSEPSYKQWDSVVQ--KEAFSIKTESVNAQSIIIPQKQV 679
Qy 773 LSALPPRG--GKPYLESFKLSLONTKDT--LLPDEVSTLSKKEKIPLOMBELSTAVYSND 828
Dy 680 FDQKSESSPSKSYLDSFQPEICVSKATSDLFAGLTLTLLQEK--PLQMBELDGL--SLE 736
Qy 829 DLFISKAQIRETTFSDSPIELIDFPTLISKTSDFSK--LAREYTDLEVSHKSEI 885
Dy 737 KIPCTKYSVSE-----SPEPRSPVPEDLSKLGDIQKEVLIAKQPEDKVKQKRSNL 789
Qy 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISPSDDFSKNGSATSKVLLLPDVSALGH 945
Dy 790 DFPVENIEFTPAVQKPDGSG-----KAVSDTFGLDITTKGSAVHEV----- 832
Qy 946 TQABIESIVRPKVLKEAE-KKLPDSTEKEDRSPSAIFSADLGKTSVVLDLYWRDIKKTG 1004
Dy 833 -----KVDPKPPSKEDDGSKLP-----KKESKASTVSSSDF-MNSVVDLYWRDIKRSK 881
Qy 1005 VVFGASIFLLISLTVFISVSVTAIALALISLTVISFRIYKGVIOAIQKSDGEGHPFRAYLE 1064
Dy 882 VVFGASIFLLISLTVFISVSVTAIALALISLTVISLRIYKGVIOAIQKSEEGHPFRILE 941
Qy 1065 SEVAISELVOKYNSALGHVNCITIKELRLFLVDLDVLSLKPAVLMWVFTYVGLFNGL 1124
Dy 942 SNLAVPEDLVOKYCNVALNHVNCITIKELRHLFLVEDLDVLSLKPAVLMWVFTYVGLFNGL 1001
Qy 1125 TLLIALISLFSVPVYERHOAQIDHYGLGNKVNKQAMAKIQKIPGLKRKAE 1178
Dy 1002 TLLIALISLFSIPVYERHQTQVDHYLALVNKLNKTSDDLILSKVPGLKRKAE 1055
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RESULT 12

Q96B16

ID Q96B16 PRELIMINARY; PRT; 392 AA.

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AC Q96B16;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Reticulon 4, isoform D (RTN4 isoform B2).
GN Name=RTN4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
RA Strausberg R.;
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT "Genomic structure and functional characterisation of the promoters of
RT human and mouse nogo/rt4.";
RL J. Mol. Biol. 325:299-323 (2003).
RN [4]
RP SEQUENCE FROM N.A.
RA Van der Putten H.;
RX Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC016165; AAH16165.1; -
DR EMBL; AY102278; AAM64247.1; -
DR EMBL; AY102285; AAM64242.1; -
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS00845; RETICULON; 1.
SQ SEQUENCE 392 AA; 42274 MW; D7B2AA5E839E58AD CRC64;

Query Match 25.8%; Score 1531; DB 2; Length 392;
Best Local Similarity 32.4%; Pred. No. 1.9e-48;
Matches 382; Conservative 7; Mismatches 3; Indels 786; Gaps 4;

Qy 1 MEDLDQSPVSSSDSPRPQPAFKYQVREPEDEEEDEDEDELEVLERKPA 60
Dy 1 MEDLDQSPVSSSDSPRPQPAFKYQVREPEDEEEDEDEDELEVLERKPA 60
Qy 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPRQPSWDSVSSSTVPAP 120
Dy 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPRQPSWDSVSSSTVPAP 120
Qy 121 SPLSAAAVSPSKLPEDDEPPARPPPPASVSQAEVPTTPAPAPAAPSTPAAPKRRG 180
Dy 121 SPLSAAAVSPSKLPEDDEPPARPPPPASVSQAEVPTTPAPAPAAPSTPAAPKRRG 180
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Db 121 SFLSAAAAPSFKLPEDDEPPARPPPPPPASVSQAEVWTPPAPAPAAPSTPAAPKRRG 180
Qy 181 SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPFVLLLETAASXPSLSPLSAASPKHEYLGN 240
    |||:|
Db 181 SSGSV----- 185
Qy 241 LSTVLPTEGTLOENVSEASKEVSEKAKTLLIDRLDTEFSELYSEMGSSFSVSPKAESAV 300
Db 186----- 185
Qy 301 IVANPREEEIIVKNKDEEKLVSNNILHXQQLPTALTCLVKEDEVVSSEKAKDSFNKRV 360
Db 186----- 185
Qy 361 AVEAPMREYADKPFERVMEVKDSKEDSDMLAAGKIEBNSLESKVDKCFADSLQTNH 420
Db 186----- 185
Qy 421 EKDSSENNDDTSPSTPEGIKDRSGAYITCAPNPAAETSIATNIFPLLEDPTSENXTDE 480
    |||:|
Db 186----- 190
Qy 481 KXIEEKKAIIVTEKNTKTSTNPNPFVAAQDSEYVTTDNLTKVTEEVVANMPEGITPDL 540
Db 191----- 190
Qy 541 VOEACESELNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLCPSESEATPSPVLPDI 600
Db 191----- 190
Qy 601 VMEAPLNSAVPAGASVIQPSPPLEASSVNYSEIKHEPENNPPVEEAMSVLSKVGIKE 660
Db 191----- 195
Qy 661 EIKEPENINAALQETAPYISACDLIKETKLSARPAPDFSDYSEMAKVEQVPDPHSELV 720
Db 196----- 195
Qy 721 EDSPPDSEPVDFSDDISPDVPQKQDETVMVKESLTETSFESMIEYENKEKLSALPPEG 780
    |||:|
Db 196----- 199
Qy 781 GRPYLESFKLSLNTKOTLLPDEVSTLSKKEKIPLOMBELSTAVYNNDDLFISKEAQIRE 840
Db 200----- 199
Qy 841 TETFSDDSPIEIIDBPPTLISSTKDSFKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL 900
Db 200----- 199
Qy 901 PHDLSLKNTPQVKEKISFSDDFSKNGSATSXVLLPPDVSALGHTQABIESIVKPKVLE 960
Db 200----- 199
Qy 961 KEAEKKLPDTEKEDRSPSAIFSA DLGKTSVVDLLYWRDIKKTGVVFGASFLLLSLTVF 1020
    :|||:|
Db 200----- 234
Qy 1021 SIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNS 1080
    |||:|
Db 235 SIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNS 294
Qy 1081 ALGHVNCTIKELRRFLVDDLVDSLKFAVLMMVFTYVVGALFNGLTLLILALISLSPVPI 1140
Db 295 ALGHVNCTIKELRRFLVDDLVDSLKFAVLMMVFTYVVGALFNGLTLLILALISLSPVPI 354
Qy 1141 YERHOAQIDHYLGLANKNVKDAWKIQAIPGLKRAE 1178
Db 355 YERHOAQIDHYLGLANKNVKDAWKIQAIPGLKRAE 392
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RESULT 13  
Q6JRV8

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ID Q6JRV8 PRELIMINARY; PRT; 1044 AA.
AC Q6JRV8;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE RTN4.2-A2.
GN Name=RTN4;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Wholemount embryos;
RC PubMed=15019938; DOI=10.1016/j.mcn.2003.09.021;
RA Klinger M., Diekmann H., Heinz D., Hirsch C., Hannbeck von Hanwehr S.,
RA Petrausch B., Oertle T., Schwab M.E., Stuermer C.A.;
RT "Identification of two NOGO/RTN4 genes and analysis of Nogo-A
RT expression in Xenopus laevis.";
RL Mol. Cell. Neurosci. 25:205-216(2004).
DR EMBL; AY316189; AAQ82638.1;
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 1044 AA; 115088 MW; 34PB48351A6C9888 CRC64;

Query Match 25.6%; Score 1518.5; DB 2; Length 1044;
Best Local Similarity 37.3%; Pred No. 1.8e-47;
Matches 459; Conservative 165; Mismatches 346; Indels 261; Gaps 52;

Qy 2 EDLQSPILVSSDSPRPQPAFKYQF-VREPEDEEEEEEEEDS---DEELELEVLER 57
    |||:|
Db 21 EDLDD-VLDLTGGAGQSPFPVSYPARHMEKEEENEDEDESKWSLEASPVLE- 77
    |||:|
Qy 58 KPAAGLSAAPTAPAGAPLMDGNDVFPAPRGPLPAAPVAPEROPSPWDPSVSTV 117
    |||:|
Db 78 DFGSTSGSSPTPHSP-----PEPSAPTEEPERP-----ATC 109
Qy 118 PAPSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSQAEVWTPPAPAPAAPSTPAAPK 177
    |||:|
Db 110 TAPSSSLAYTLAQLRKDE-----NLFLPAA----- 138
Qy 178 RRGSGAVVXXXXKIMDLKEQPGNTISAGQEDFPFVLLLETAASXPSLSPLSAASPKHEY 237
    |||:|
Db 139 ---SAHLMHLSADKIM---EPSSTVSTGQEDFASVLLQSTASLSLPSLSS---KEHVQ 188
Qy 238 LGNLSLTVLPTEGTLOE---NVSEASKEVSEKAKTLLIDRLDTEFSELYSEMGSSFSVSP 294
    |||:|
Db 189 TVAFSTGLAANEALQOEPTDNTYSASRLDITLETKALD---QF----- 228
Qy 295 KAESAVIVANPREEEIIVKNKDEEKLVSNNILHXQQLPTALTCLVKEDEV-VSSEKAKD 353
    |||:|
Db 229 -----KEEVI FSDKG-----YVVEHTSQOETISEEHAKLYSQSAKE 265
Qy 354 SFNEKRVAVEAPMRE-----EYADFKPF-----ERVVEVKDSKEDSDMLAAGK 398
Db 266 MFSGLMQVAPVAPHEEFTDIKEVDVQYVDFKPFIFSSNRDYGVEVMDVAEKLHV-----GRL 321
Qy 399 ESNLSKVDKCFADSLQTNHEKDSSENNDDTSPSTPEGIKDRSG--AYITCAPNPFA 456
    |||:|
Db 322 ---NLEST-----AKHEEKSSEKEEMDIS-DDIS-PLTPEVLSDTDYEMFATVBSHP- 370
Qy 457 ATESIATNIFPLLEDPTSENXTDEKKIEEKKAIIVTEKNTS-----TKTSNPF--VAQ 509
    |||:|
Db 371 -----FSLGSRVAGNKTDEKKIEDFAQ-----KTSVGFGCLKVATVNPFFYDESAQ 416
Qy 510 DSETDYVTTDNLTKVTEEVVANMPEGLTPDLVQEAACESELNEVTGTKIAYETMDLVQTS 569
    |||:|
Db 417 ESE--YVTTG---ATRVQVSTKAEGPTPDIVQEAYESAYDTGIGSLKNYEPNIDLQVTA 470
Qy 570 EV-MQESLYPAAQLCPSESEATPSPVLPDI VMEAPLNSAVPAGASVQPSPPLEAS 628
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Db 471 ATSMQKVSTQVPALEDS--VSSPVLVDVMEAPLASTIL-CLETWALKPDISPVRIE 527
Qy 629 -SVNYESIHEPENPPPEEAMSVSLKVSQ--IKEEIKPENINAAQOETEA----PYIS 681
Db 528 PARDEKTAEPKPEPSIEAEVTEVLQDGPAAADLGDQSKO-GAVVKEAEAPYISPYIS 586
Qy 682 IACDLIKETKLSAEPAPDSYSEMAKVQPVPHDS--ELVDSQSPDSPEVDLFDSDSIP 739
Db 587 IACDLIKGTQSA--SDTFESKFKQHEFDQFMPESSPDSE-----LS 631
Qy 740 DVPQKQDETVMVLKESLT-----ETSFESMIETENKEKLSALPPEG--GKPYLESFKLSUD 793
Db 632 EPSYQWDSVVYKRETFITIKTESAMAQSFVPEQKPGIDQKSEESSPKPYLASQPEIY 691
Qy 794 NTKDT-LLPDEVST-LSKKEKIPLOMEELSTAVYNSDDLFISKEAQIRETETFSSSPIE 851
Db 692 VSKATDLFAKGLDTISIPQERHLHMEEPDEGLYS--KLPGSKYSPVSESPEFRUS---- 746
Qy 852 IIDEPTLTISSKTSF-SKLAREYTDLVSHKSEITANAPDGAGSLPCTELPHDLSLKNIQ 910
Db 747 -----PEELTSKHEBIOTHIAGHPEDKLQKNDKLDLPE-----NIE 784
Qy 911 --PKVEKISFSDSKNGSATSQVLLPPDVVSALGHTQAEITESIVKPVLEKAE-KXL 967
Db 785 FTPIVQK---ADDFGKAASATHGGV---DTTAKGASVHEKVKTPPEPPSKDQVSKL 836
Qy 968 PSDTEKEDRSAPSAISADLGKTSVVDLLIYWRDIKKTGVVFGASLFLILSLTVFSIVSTA 1027
Db 837 P--KESKAPSTVPSSDFRNSVVDLIYWRDIKRSVGVFGASLFLILSLTVFSIVSLA 893
Qy 1028 YIALALLSVTISFRIYKGVIOAIQKSDGHPHPRAYLESEVALSEBELVOKYSNLSALGHVNC 1087
Db 894 YIALALLSVTISFRIYKGVIOAIQKSEGHPRFSLIESNLALPEDVQKHCTVALNQVR 953
Qy 1088 TIKELRRLFLVDLVDLSLKFAVLMVFTYVGLFNGLLILALISLFSVPVYERHOAQ 1147
Db 954 TVAEELRRLFLVDLVDLSLKFAVLMVFTYVGLFNGLLILALISLFSVPVYERHQTQ 1013
Qy 1148 IDHYLGLANKVNDKAMAKIQAIPGLKRAE 1178
Db 1014 VDHYLALINKNLKNTSDILAKVPLKRRKE 1044

RESULT 14
Q6JRV0 PRELIMINARY; PRT; 1043 AA.
AC Q6JRV0;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE RTN4.1-A1.
GN Name=RTN4;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Wholemount embryos;
RX PubMed=15019938; DOI=10.1016/j.mcn.2003.09.021;
RA Klingner M., Diekmann H., Heinz D., Hirsch C., Hannbeck von Hanwehr S.,
RA Petrausch B., Oertle T., Schwab M.E., Stuermer C.A.;
RT "Identification of two NOGO/RTN4 genes and analysis of Nogo-A
RL expression in Xenopus laevis.";
RL Mol. Cell. Neurosci. 25:205-216 (2004).
DR EMBL; AY316197; AAQ82646.1;
DR GO; GO:0005783; Cytoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS0845; RETICULON; 1.
SQ SEQUENCE 1043 AA; 113994 MW; 6AF170C14DD2CB1A CRC64;

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Query Match 25.6%; Score 1517.5; DB 2; Length 1043;
Best Local Similarity 36.6%; Pred No.1.9e-47;
Matches 459; Conservative 152; Mismatches 350; Indels 293; Gaps 48;

Qy 5 DQSPVSSSDS-----PPRP-----QPAFKYQVFRPEDEE 35
Db 3 EQSPDISSSHSGDERREPAQGERKPDWDDLDVLDLTGGAGQFSQPFSGSHPADIEEBE 62
Qy 36 EEEEEEDEDEDELEELVLERKPAAGLSAARV-PTAPAGAPLMDFGNDFVPPAPRGL 94
Db 63 EDEEBERGAWKDSLESPV-EEPGSIDSISEVSPHSPA-----VPSAPM--- 106
Qy 95 PAAPVAPERQSPWDPSPVSTVPAPSLAAAVSPKLPEDEDEPPAPPPPPASVSQ 154
Db 107 -----EPEPPAPCTAPSGSV 123
Qy 155 ABPVWTPAPAPAPPSTPAAPKRGSGAVVXXXXKIMDKQPGNTISAGQEPFVSL 214
Db 124 DENLFTLPA-----ASAHLMHASADKIM---EPYSTVSTQGEFASVL 163
Qy 215 LETASXPSLSPLSNAASPKHEHYLGNLSTVLPTEGLQENVSEASKEVSEKAKTLLIRD 274
Db 164 LQSTASLSLSLSLTDSSKHAETVAFTGLAATEALQEPD----- 205
Qy 275 LTFESELVSBMGSSFSVPKRAESAVIVANPREETIIVKNKDEEKLVSNNILHXQQLPT 334
Db 206 ----NWYSVSRIITSHLPUSDNLESKAL--DQVKEVIFSEK-----YVDHPT 248
Qy 335 ALTKLVKDEEV-VSEKAKDSFNKRVAVEAPMREE-----YADFKPF-----E 377
Db 249 SQOETISEEHAKLYSQSAKEMFGMLQSV-APPHSEFTDIKEVDPYVDFKPFMSKSGD 307
Qy 378 RVWEVKDSKSDMLAAGKLESNLSKVKKCPADSLSEQTNHEKXSSNDTDFPSTP 437
Db 308 VGYEVDVAEKQFQDVV--GRL--NLESVAKHE-----EKSEEMEISDSDIS-PLTP 356
Qy 438 EGIDORSQAYITCAPFNPAAETATNI-FPLEDPTSENXTDEKKEIKKAAQIVTEKNT 496
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Qy 497 S-----TKTSNPPF-VAAQDSETDYVTTDNLTKVTEEVVANMPGLTDLVQEAESL 549
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Qy 550 NEVTGKTIAETKMDLVOT-SEVMQESLYPAQALCPSESESEATPSVLPDIWMEAPLNS 608
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Qy 609 AVPSAGASVIOPISSSPLEAS-SVNYESIKHEPNPPPYEEAMSVSLKVGSIKEEIKPEN 667
Db 516 ALETV---ALAPDISPVGIKPPARVEKTKAPKPPSYEEAVT-----EVLQND 562
Qy 668 INAAL-----QTEAPYISACDLIKETKLSAEPAPDSYSEMAKVEQP--VPDH 716
Db 563 LAAALGGSQKQAVVEETETPVISACDLIKGTESVA-----SGTFESKLQNEFESQF 616
Qy 717 SELVEDSPDSEPVDLFSDDSIPDVQKQDETVMVLKESLT-----ETSFESMIETENKEK 772
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Qy 773 LSAALPPEG--CKPYLESFKLSLNDTKDT--LLPDEVSTLSKKEKIPLOMEELSTAVYNSD 828
Db 668 FDQKSESSPSKSLDSFQPEICVSKATSDLFAGKLTLLQEK--PLOMEELDEGL-SLE 724
Qy 829 DLFIKSEAQIRETETFSDDSSPIEIDEPPTLISSKTSDFSK---LAREYTDLVSHKSEI 885
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Qy 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEKISFSDSKNGSATSQVLLLPDVVSALGH 945
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DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
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OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Xenopodinae; Xenopus.
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RX PubMed=15019938; DOI=10.1016/j.mcn.2003.09.021;
RA Klinger M., Diekmann H., Heinz D., Hirsch C., Hannbeck von Hanwehr S.,
RA Petrasch B., Oertle T., Schwab M.E., Stuermer C.A.;
RT "Identification of two NOGO/RTN4 genes and analysis of Nogo-A
RL Mol. Cell. Neurosci. 25:205-216(2004).
DR EMBL; AV316195; AAQ82644.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon.
DR PROSITE; PS0845; RETICULON; 1.
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QY 221 XSLSPLSAASFKEHYLGNLSVTLPTGTLQENVSEASKESEKATLLIDRLDTERFE 280
Db 151 LSLPSLSTDSKSEAETVAFPPTGLAATEALQEPD-----NM 188
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2	931	100.0	2883	9	AF320999	Homo sapi
3	931	100.0	3491	9	AF333336	Homo sapi
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3402..3407

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Db 2870 AAGGAACCTCAGGCGCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAACCTTTGCAGTG 2929

Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140

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	DEFINITION	Sequence 5 from Patent WO03002602.				

RELEASED  
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 VERSION  
 AX766050.1  
 KEYWORDS  
 SOURCE  
 Homo sapiens (human)  
 GI:32260129

ORGANISM      HOMO SAPIENS  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo

REFERENCE  
I  
AUTHORS  
Eisenbach-Schwartz, M. and Hauben, E.  
Name and addresses of designated persons for all modified

**JOURNAL**  
neuroprotection  
Patent: WO 0302602-A 5 09-JAN-2003;

## YEDA RESEARCH AND DEVELOPMENT CO. LTD. (IL)

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Location/Qualifiers  
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exon  
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Score: 931.00 Matches: 189  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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LOCUS BD249446 3579 bp DNA linear PAT 17-JUL-2003  
DEFINITION Protein similar to neuroendocrine-specific protein, and encoding cDNA.

ACCESSION BD249446  
VERSION BD249446.1 GI:33059216  
KEYWORDS JP 2002522016-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 3579)  
AUTHORS Michalovich, D. and Prinjha, R. K.

TITLE  
JOURNAL

## COMMENT

Protein similar to neuroendocrine-specific protein, and encoding  
Patent: JP 2002522016-A 1 23-JUL-2002;  
SMITHKLINE BEECHAM PLC  
OS Homo sapiens (human)  
PN JP 2002522016-A/1  
PD 23-JUL-2002  
PF 21-JUL-1999 JP 2000561310  
PR 22-JUL-1998 GB 9816024.5 19-JUL-1999 GB 9916898.1 19  
DAVID MICHALOVICH, RABINDER KUMAR PRINJHA  
PC

C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ 10,  
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CC Protein similar to neuroendocrine-specific protein, and CC  
encoding cDNA

PH Key Location/Qualifiers  
FT source 1. .3579 /organism="Homo sapiens (human)".

FEATURES  
source

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## ORIGIN

Alignment Scores:  
Pred. No.: 9,38e-87 Length: 3579  
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Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BD249446 (1-3579)

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Db 3490 CATTATCTAGGACTTGCAATAAGAAATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAA 3549



Qy 181 IleProGlyLeuLysArgLysAlaGlu 189  
Db 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

RESULT 6  
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LOCUS Homo sapiens mRNA for Nogo-A protein (Nogo gene).  
DEFINITION  
ACCESSION AJ251383  
VERSION AJ251383.1 GI:9408095  
KEYWORDS Nogo gene; Nogo-A protein.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Prinjha, R., Moore, S.E., Vinson, M., Blake, S., Morrow, R.,  
Christie, G., Michalovich, D., Simmons, D.L. and Walsh, F.S.  
TITLE Inhibitor of neurite outgrowth in humans  
JOURNAL Nature 403 (6768), 383-384 (2000)  
MEDLINE 20129242  
PUBMED 10667780

REFERENCE 2 (bases 1 to 3579)  
AUTHORS Michalovich, D.  
TITLE Direct Submission  
JOURNAL Submitted (29-NOV-1999) Michalovich D., Bioinformatics, Smithkline  
Beecham, Third Avenue, Harlow, Essex, CM19 5AW, BOSNIA AND  
HERZEGOVINA

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ACCESSION CQ829486  
VERSION CQ829486.1 GI:49732808  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Barske, C., Mir, A.K., Oertle, T., Schnell, L., Schwab, M.E.,  
Vitaliti, A. and Zurini, M.  
TITLE Nogo a binding molecules and pharmaceutical use thereof  
JOURNAL Patent: WO 2004052932-A 4 24-JUN-2004;  
Novartis AG (CH)

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ACCESSION	AX195249			
VERSION	AX195249.1			
KEYWORDS	.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			

REFERENCE 1  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Hominidae; Homo.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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**AUTHORS** Strittmatter, S.M.  
**TITLE** Nogo receptor-mediated blockade of axonal growth  
**JOURNAL** Patent: WO 0151520-A 5 19-JUL-2001;

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LOCUS
DEFINITION Homo sapiens RTN4 isoform G (RTN4) mRNA, complete cds;
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VERSION AY123250.1 GI:26800589
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 4060)
Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.
Genomic structure and functional characterisation of the promoters
of human and mouse nogor/rtn4
J. Mol. Biol. 325 (2), 299-323 (2003)
JOURNAL
MEDLINE 22376540
PUBMED 12488097
REFERENCE
2 (bases 1 to 4060)
Van der Putten,H.
Direct Submission
Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basel, Switzerland
3 (bases 1 to 4060)
Oertle,T. and Schwab,M.E.
Direct Submission
Submitted (17-MAY-2002) Brain Research Institute, University of
Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
Switzerland
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DEFINITION alternatively spliced.
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VERSION AY123249.1 GI:26800586
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 4070)
Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.
Genomic structure and functional characterisation of the promoters
of human and mouse nogor/rtn4
J. Mol. Biol. 325 (2), 299-323 (2003)
JOURNAL
MEDLINE 22376540
PUBMED 12488097
REFERENCE
2 (bases 1 to 4070)
Van der Putten,H.
Direct Submission
Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basel, Switzerland
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VERSION AY123245.1 GI:26800574
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1 (bases 1 to 4102)
Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.
Genomic structure and functional characterisation of the promoters
of human and mouse nogo/rtn4
J. Mol. Biol. 325 (2), 299-323 (2003)
JOURNAL 22376540
MEDLINE 12488097
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AUTHORS Van der Putten,H.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basel, Switzerland
3 (bases 1 to 4102)
Oertle,T. and Schwab,M.E.
Direct Submission
JOURNAL Submitted (17-MAY-2002) Brain Research Institute, University of
Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
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 AUTHORS Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.  
 TITLE Genomic structure and functional characterisation of the promoters  
 of human and mouse nogo/rtn4  
 J. Mol. Biol. 325 (2), 299-323 (2003)  
 JOURNAL 22376540  
 MEDLINE 12488097  
 PUBMED  
 REFERENCE 2 (bases 1 to 4109)  
 AUTHORS Van der Putten,H.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma  
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 3 (bases 1 to 4109)  
 REFERENCE Oertle,T. and Schwab,M.E.  
 AUTHORS Direct Submission  
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 Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,  
 Switzerland

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		Oertle, T., Huber, C., van der Putten, H. and Schwab, M.E.	
JOURNAL		Genomic structure and functional characterisation of the promoters	
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PUBMED		J. Mol. Biol. 325 (2), 299-323 (2003)	
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TITLE		Oertle, T. and Schwab, M.E.	
JOURNAL		Direct Submission	
		Submitted (07-MAY-2002) Brain Research Institute, University of	
		Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,	
		Switzerland	
REFERENCE		3 (bases 1 to 4789)	
AUTHORS		Van der Putten, H.	
TITLE		Direct Submission	
JOURNAL		Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma	
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ACCESSION AR220865
VERSION AR220865.1 GI:23327742
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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4822)
AUTHORS Jones, K.A., Volkmut, W. and Walker, M.G.
TITLE Bone remodeling genes
JOURNAL Patent: US 6426186-A 106 30-JUL-2002;
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QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
DB 3505 TCTGAGGAGTTGGTTTCAGAAAGTACAGTAATTTCTGCTCTTGGTTCATGTGAACCTGCACGATA 3564
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
DB 3565 AAGAACTCAGGCGCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGAGTG 3624
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
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QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
DB 3685 GCTCTCATTTTCACTCTCTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 3744
QY 161 HisTyrLeuGlyLeuAlaLeuLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
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QY 181 IleProGlyLeuLysArgLysAlaGlu 189
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Db      3805 ATCCCTGGATTGAGCGCAAGCTGAA 3831
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BC016165      1784 bp      mRNA      linear      PRI 29-JUN-2004
LOCUS      Homo sapiens reticulon 4, transcript variant 4, mRNA (cDNA clone
DEFINITION      IMAGE:3505850), complete cds.
ACCESSION      BC016165
VERSION      BC016165.1 GI:16740575
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE
AUTHORS      Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schneitz, T.E., Brownstein, M.J., Usdin, T.B., Toshnyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Kzyvinski, M.I., Skalek, U., Smalish, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
human and mouse cDNA sequences
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED      12477932
2 (bases 1 to 1784)
Strausberg, R.
Direct Submission
Submitted (29-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: DCTD/DRP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Anara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
Duane Smalish, Jeff Stott, Miranda Teali, George Yang, Jacque
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 23 Row: d Column: 19
This clone has the following problem: The cds is short compared to
the longest cds in the locus.
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Alignment Scores:
Pred. No.: 8,2e-87 Length: 1784
Score: 928.00 Matches: 188
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.47% Mismatches: 0
Query Match: 99.68% Indels: 0
DB: 9 Gaps: 0
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Qy 1 SerValValAlaPheLeuLeuTyrTTPArgAspIleLysLysThrGlyValValPheGlyAla 20
Db 857 GCAGTTGTTGACCTCTCTGTTCTGGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGGTCC 916
Qy 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 917 AGCTATTCTCTGCTCTTTCATTGACAGATATTGAGCTTTGAGCGTAAACAGCCTACATT 976
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 977 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATATCAAGGGTGTGATCCAACT 1036
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 1037 ATCCAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAAATCTGAAGTTGCTATA 1096
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 1097 TCTGAGGAGTTGGTTTCAGAGTACAGTAATTTCTGCTCTTGTGTCATGTGAACCTGCACGATA 1156
Qy 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 1157 AAGAACTCAGAGGCCCTCTTCTTAGTTGATTTAGTTAGTTGATTTCTGAAGTTTGCAGTG 1216
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
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Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 1277 GCTCTCTTTCACCTTTCAGTGTCTCTGTTATTATTAAGACGCATCAGGCACAGATAGAT 1336
Qy 161 HistTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 1337 CATTATCTAGGACTTGCAAATGAAGATGTTAAAGATGCTATGGCTAAATCAAGCAAAA 1396

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ORIGIN

Alignment Scores:

Pred. No.: 2.73e-87 Length: 600

Score: 927.00 Matches: 188

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 99.57% Indels: 0

DB: 9 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x HSA251385 (1-600)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21

Db 34 GTTGTGGACCTCCTCTACTGGAGACATTAAGAAGACTGGAGTGGTGTGGTCCACG 93

Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

Db 94 CTATTCTCTGCTCTTTCATTGACAGTATTCAGCATTTGAGCGTGAACGCTACATTGCC 153

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

Db 154 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAAAGCTATC 213

Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81

Db 214 CAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGAATCTGGAAGTTGCTATATCT 273

Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101

Db 274 GAGGAGTTGGTTCAGAGTACAGTAATTCCTCTTGTGTCATGTGAACTGCAGATAAAG 333

Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121

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Db 394 ATGTGGGTATTTACCTATGTGGTGGCTGTGTTTAAATGCTGTGACACTACTGATTTGGCT 453

Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161

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Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

Db 514 TATCTAGGACTTGGCAATTAAGAATCTTAAAGATGCTATGGCTTAAATCCAAAGCAAAATC 573

Qy 182 ProGlyLeuLysArgLysAlaGlu 189

Db 574 CCTGGATTGAAGCGCAAAAGCTGAA 597

RESULT 25

AR028522

LOCUS

DEFINITION

ACCESSION

VERSION

AR028522.1 GI:5940495

AR028522

Sequence 2 from patent US 5858708.

AR028522

AR028522.1 GI:5940495

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 799)

AUTHORS Bandman,O., Au-Young,J., Goli,S.K. and Hillman,J.L.

TITLE Polynucleotides encoding two novel human neuroendocrine-specific proteins

JOURNAL Patent: US 5858708-A 2 12-JAN-1999;

FEATURES

source

1. .799

/organism="unknown"

/mol\_type="unassigned DNA"

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Pred. No.: 3.88e-87 Length: 799

Score: 927.00 Matches: 188

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 99.57% Indels: 0

DB: 6 Gaps: 0

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Db 108 GTTGTGGACCTCCTCTACTGGAGACATTAAGAAGACTGGAGTGGTGTGGTCCACG 167

Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

Db 168 CTATTCTCTGCTCTTTCATTGACAGTATTCAGCATTTGAGCGTGAACGCTACATTGCC 227

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

Db 228 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAAAGCTATC 287

Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81

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Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121

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Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141

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Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161

Db 528 CTCATTTACCTTCAGTGTTCCTGTTTATTTATGAACGGCATCAGGCGACAGATAGATCAT 587

Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

Db 588 TATCTAGGACTTGGCAATTAAGAATCTTAAAGATGCTATGGCTTAAATCCAAAGCAAAATC 647

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Db 648 CCTGGATTGAAGCGCAAAAGCTGAA 671

RESULT 26

BC007109

LOCUS

DEFINITION

ACCESSION

VERSION

BC007109.1 GI:13937989

BC007109

Homo sapiens reticulon 4, transcript variant 3, mRNA (CDNA clone IMAGE:429112?), complete cds.

BC007109

BC007109.1 GI:13937989

SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1079)  
REFERENCE  
AUTHORS  
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshuler S.F., Zerbach B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raja S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E., Jones S.J. and Marra M.A.  
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 1079)  
Strausberg R.  
Direct Submission  
Submitted (30-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapsb-remail.nih.gov](mailto:cgapsb-remail.nih.gov)  
Tissue Procurement: CLONTECH  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
Center Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson, Mark) [mcd@paxill.stanford.edu](mailto:mcd@paxill.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 21 Row: h Column: 12  
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein  
This clone has the following problem: The cds is short compared to the longest cds in the locus.  
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ORIGIN  
Alignment Scores:  
Pred. No.: 5,628-87 Length: 1079  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x BC007109 (1-1079)  
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
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Db 205 CTATTCTGCTGCTTTTCATTGACAGATTTCAGCAATGTGAGCGTAACAGCCATACATTGCC 264  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 265 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGATATACAGGGTGTGATCCAGCTATC 324  
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Db 325 CAGAAATCAGATGAAGGCCACCCATTAGGCGCATATCTGGAATCTGAAGTTGCTATATCT 384  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 385 GAGGAGTTGGTTTTCAGAGTACAGTAAATCTCTCTTGGTCACTGAACATGCAGATAAG 444  
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QY 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 685 CTGGGATTGAAGCGCAAGCTGAA 708  
RESULT 27  
BD249448  
LOCUS  
DEFINITION  
Protein similar to neuroendocrine-specific protein, and encoding cDNA.  
BD249448  
BD249448.1 GI:1393799218  
KEYWORDS  
JP 2002522016-A/3.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.



REFERENCE 1 (bases 1 to 1122)  
AUTHORS Michalovich, D. and Prinjha, R.K.  
TITLE Protein similar to neuroendocrine-specific protein, and encoding  
JOURNAL Patent: JP 200252016-A 3 23-JUL-2002;  
SMITHKLINE BEECHAM PLC  
COMMENT OS Homo sapiens (human)  
PN JP 200252016-A/3  
PD 23-JUL-2002  
PF 21-JUL-1999 JP 2000561310  
PR 22-JUL-1998 GB 9816024.5 19-JUL-1999 GB 9916898.1 PI  
DAVID MICHALOVICH, RABINDER KUMAR PRINJHA  
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC  
10, C12P21/02, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, PC  
G01N33/566//  
PC C12P21/08, C12N15/00, C12N5/00  
CC Protein similar to neuroendocrine-specific protein, and CC  
encoding cDNA  
FH Key Location/Qualifiers  
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FT /organism='Homo sapiens (human)'.  
FEATURES  
source  
Location/Qualifiers  
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Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 6 Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x BD249448 (1-1122)  
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DB 556 GTTGTGACCTCCTCTACTGGAGACATTAAGAAGCTGGAGTGGTGTGGTGGCCAGC 615  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 616 CTATTCTGCTGCTTTCATTGACATATTGACATTTGAGCTGTGAGCTAACGCTACATTGCC 675  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 676 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAGCTATC 735  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
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DB 796 GAGGAGTTGTTTCAGAGTACAGTAATCTGCTCTGTGCTGATGTAAGTGCAGATTAAG 855  
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DB 856 GAACTCAGCGCGCTCTTCTAGTCATGATTTAGTTGATTTCTCTCAAGTTGTCAGTGTG 915  
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LOCUS HSA251384 1122 bp mRNA linear PRI 22-JUL-2000  
DEFINITION Homo sapiens mRNA for Nogo-B protein (Nogo gene).  
ACCESSION AJ251384  
VERSION AJ251384.1 GI:9408097  
KEYWORDS Nogo gene; Nogo-B protein.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Prinjha, R., Moore, S.E., Vinson, M., Blake, S., Morrow, R.,  
Christie, G., Michalovich, D., Simmons, D.L. and Walsh, F.S.  
TITLE Inhibitor of neurite outgrowth in humans  
JOURNAL Nature 403 (6768), 383-384 (2000)  
MEDLINE 20129242  
PUBMED 10667780  
REFERENCE 2 (bases 1 to 1122)  
AUTHORS Michalovich, D.  
TITLE Direct Submission  
JOURNAL Submitted (29-NOV-1999) Michalovich D., Bioinformatics, Smithkline  
Beecham, Third Avenue, Harlow, Essex, CM19 5AW, BOSNIA AND  
HERZEGOVINA  
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DB 616 CTATTCTGCTGCTTTCATTGACATATTGACATTTGAGCTGTGAGCTAACGCTACATTGCC 675  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 676 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAGCTATC 735  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 736 CAGAAATCAGATGAAAGGCCACCCATTCAGGGCATATCTGGAATCTGGAATGTGTATATCT 795  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
DB 796 GAGGAGTTGTTTCAGAGTACAGTAATCTGCTCTGTGCTGATGTAAGTGCAGATTAAG 855  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 856 GAACTCAGCGCGCTCTTCTAGTCATGATTTAGTTGATTTCTCTCAAGTTGTCAGTGTG 915  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeuAla 141  
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QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
DB 976 CTCATTTTACCTCTTCTGAGTTCCTGTTATTTATGACGGCATCAGCAGATAGATCAT 1035  
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Qy	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer	81
Db	736	CAGAAATCAGATGAGGAGCCACCATTCAGGCATATCTGGATCTGAACTTGCATATCT	795
Qy	82	GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys	101
Db	796	GAGGAGTTGGTTCAGAAATACAGTAATCTCTCTTGGTCATGTCGAACTGCACGATAAAG	855
Qy	102	GluLeuArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu	121
Db	856	GAACTCAGCGGCTCTCTTAGTGTGATGATTTAGTTCTCTGAAGTTGCAGTGTG	915
Qy	122	MetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla	141
Db	916	ATGTGGGTATTTACCTATGTTGGTGGCTTGTGTTTAATGGTCTGACACTACTGATTTGGCT	975
Qy	142	LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis	161
Db	976	CTCATTTCACTCTTCAGTGTCTCTGTTATTTATTAACCGCATCAGGCACAGATAGATCAT	1035
Qy	162	TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle	181
Db	1036	TATCTAGGACTTGCAATTAAGATGTTAAGATGCTATGGCTAAATCCAGCAAAATC	1095
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Db	1096	CCTGGATTGAGCGCAAGCTGAA	1119
RESULT	29		
LOCUS	BC001035		
DEFINITION	Homo sapiens reticulon 4, transcript variant 3, mRNA (cdna clone IMAGE:3139770), complete cds.		
ACCESSION	BC001035		
VERSION	BC001035.2	GI:33975905	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 1151)		
	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Scapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Ussin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raja,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaby,S.J., Bosak,S.A., McSwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S.S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Munz,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallos,D.E., Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 1151)		
AUTHORS	Strausberg,R.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	On Aug 19, 2003 this sequence version replaced gi:12654418. Contact: MGC help desk Email: cgapbs@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL) Sequencing Center (NISC), Gaithersburg, Maryland; web site: http://www.nisc.nih.gov/ Contact: nisc.mgc@nih.gov Akter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,P.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsugeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 4 Row: c Column: 8 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5902015 This clone has the following problem: The cds is short compared to the longest cds in the locus. FEATURES Location/Qualifiers 1..1151 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:3139770" /tissue_type="placenta, choriocarcinoma" /clone_lib="NIH MGC_21" /lab_host="DH10B-R" /note="Vector: pOTB7" 1..1151 /gene="RTN4" /note="synonyms: NSP-CL, NOGO, ASY, NI220/250, NSP, RTN-X" /db_xref="LocusID:57142" /db_xref="MIM:604475" 186..785 /gene="RTN4" /codon_start=1 /product="reticulon 4, isoform C" /protein_id="AAH01035.1" /db_xref="GI:12654419" /db_xref="LocusID:57142" /db_xref="MIM:604475" /translation="MDGQKNWKDKVLLYWRDITKTGVFGASLFLLLSLTVFSIVSYTAYIALALSVTFISFRYKGIQAIQKSDGHPFRAYLESEVAISELVQKYSNALSCHVNTIKELRLFLVDLSLKFVLMVFTYVGVLFNGLLILALISLFSVPV IYERHQAIDHVLGLANKNVKDMAKIQAKIPLKRAE" ORIGIN Alignment Scores: Pred. No.: 6.08e-87 Length: 1151 Score: 927.00 Matches: 188 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 99.57% Indels: 0 DB: 9 Gaps: 0 US-09-830-972-29_COPY_990_1178 (1-189) x BC001035 (1-1151) Qy 2 ValValAspLeuLeuTyrTyrPheArgAspIleLysThrGlyValValPheGlyAlaSer 21 Db 219 GTTGTGACCTCTCTGCTGAGGACATTTAGAGACATGGAGTGTGTGGTGGCAGC 278 Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41		

Db 279 CTATTCCTGCTGCTTTTCATTGACAGTATTGACAGTATTGAGCGTAACAGCCCTACATTGCC 338  
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## RESULT 30

BD194907 1213 bp DNA linear PAT 17-JUL-2003  
LOCUS 86 human secreted proteins.  
DEFINITION BD194907  
ACCESSION BD194907.1 GI:33004658  
VERSION JP 2002514090-A/78.  
KEYWORDS unidentified  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 1213)  
AUTHORS Moore,P.A., Shi,Y., Rosen,C.A., Ruben,S.M., Lafleur,D.W.,  
Olson,H.S., Ebner,R., Brewer,L.A., Young,P., Greene,J.M.,  
Ferre,A.M., Yu,G.L., Ni,J. and Feng,P.  
TITLE 86 human secreted proteins  
JOURNAL Patent: JP 2002514090-A 78 14-MAY-2002;  
HUMAN GENOME SCIENCES INC  
COMMENT OS Unidentified  
PN JP 2002514090-A/78  
PD 14-MAY-2002  
PF 11-JUN-1998 JP 1999503203  
PR 13-JUN-1997 US 60/049547,13-JUN-1997 US 60/049548 PR  
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13-JUN-1997 US 60/049609,13-JUN-1997 US 60/049610 PR  
13-JUN-1997 US 60/049611,13-JUN-1997 US 60/050901 PR  
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18-AUG-1997 US 60/055984,12-SEP-1997 US 60/058665 PR  
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12-SEP-1997 US 60/058972,12-SEP-1997 US 60/058975 PR  
02-OCT-1997 US 60/060834,02-OCT-1997 US 60/060841 PR  
02-OCT-1997 US 60/060844,02-OCT-1997 US 60/060865 PR  
02-OCT-1997 US 60/061059,02-OCT-1997 US 60/061060 PI  
MOORE,YANGU SHI,CRAIG A ROSEN,STEVEN M RUBEN,DAVID W PI  
LAFLEUR,  
PI HENRIK S OLSEN,REINHARD EBNER,LAURIE A BREWER,PAUL YOUNG,JOHN  
PI M GREENE,

PI ANN M FERRIE,GUO LIANG YU,JIAN NI,PING FENG  
PC C07H21/02,C07H21/04,C12N5/00,C12N5/04,C12N5/06,C12N5/10 PC  
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Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 6 Gaps: 0  
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RESULT 31  
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DEFINITION Sequence 79 from Patent EP1439189.  
ACCESSION CQ855235  
VERSION CQ855235.1 GI:51510663

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KEYWORDS      Homo sapiens (human)
SOURCE
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS      Ruben, S.M., Ni, J., Rosen, C.A., Ebner, R., Young, P., Moore, P.A.,
Feng, P., Laflaur, D.W., Olsen, H.S., Yanggu, S., Brewer, L.A.,
Greene, J.M., Ferrie, A.M. and Yu, G.L.
86 Human Secreted Proteins
Patent: EP 1439189-A 79 21-JUL-2004;
Human Genome Sciences, Inc. (US)
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1172
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misc_feature
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/note="n equals a,t,g, or c"
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Pred. No.:      6,48e-87      Length:      1213
Score:          927.00      Matches:      188
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      99.57%      Indels:      0
DB:              6          Gaps:
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Db      788 CTGGATTGAAGCGCAAGCTGAA 811

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RESULT 32  
BC071848  
LOCUS

DEFINITION  
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ACCESSION  
BC071848

VERSION  
BC071848.1

KEYWORDS  
Homo sapiens (human)

SOURCE  
Homo sapiens

ORGANISM  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1 (bases 1 to 1466)

AUTHORS  
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uesdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Male, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Buttenberg, K., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Small, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

TITLE  
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBLISHED  
12477932

REFERENCE  
2 (bases 1 to 1466)

AUTHORS  
Strausberg, R.

TITLE  
Direct Submission

JOURNAL  
Submitted (01-JUN-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK  
NIH-MGC Project URL: http://mgc.nci.nih.gov

COMMENT  
Contact: MGC help desk  
Email: cgabbs@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: http://www.shgc.stanford.edu  
Contact: (Dickson, Mark) mcd@paxil.stanford.edu  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

FEATURES  
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gene

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Series: IRAL Place: 58 Row: d Column: 23

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24431932

This clone has the following problem: The cds is short compared to the longest cds in the locus.

Location/Qualifiers



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PPAPAPPSPPAPKRRSGSVVLDLYWRDKTKTGVFGSLFLLSLTSPVSI  
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## CDS

DEFINITION  
ACCESSION AK130812  
VERSION AK130812.1 GI:34527696  
KEYWORDS oligo capping; fis (full insert sequence).  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Homo sapiens cDNA FLJ27302 fis, clone TMS04776.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS

1 Suzuki, O., Sasaki, N., Matsutaka, S., Shoji, T., Ichihara, T.,  
Shiohata, N., Matsumoto, K., Hirano, M., Sano, S., Nomura, R.,  
Yoshikawa, Y., Matsumura, Y., Moriya, S., Chiba, E., Momiyama, H.,  
Onogawa, S., Kaeriyama, S., Sato, N., Matsunawa, H., Takahashi, E.,  
Kataoka, R., Kuga, N., Kuroda, A., Satoh, I., Kamata, K., Takami, S.,  
Terashima, Y., Watanabe, M., Suzuki, Y., Hata, H., Nakagawa, K.,  
Mizuno, S., Morinaga, M., Kawamura, M., Sugiyama, T., Irie, R.,  
Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, A., Kawakami, B.,  
Nagai, K., Isogai, T. and Sugano, S.  
NEDO human cDNA sequencing project

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

2 (bases 1 to 1525)  
Sugano, S. and Suzuki, Y.  
Direct Submission  
Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science,  
University of Tokyo, Laboratory of Genome Structure, Human Genome  
Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan  
(E-mail: flicdn@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,  
Fax:81-3-5449-5416)  
NEDO human cDNA sequencing project supported by Ministry of  
Economy, Trade and Industry of Japan; cDNA full insert sequencing:  
Research Association for Biotechnology (RAB); cDNA library  
construction and 5'-end one pass sequencing: Institute of Medical  
Science, University of Tokyo, Laboratory of Genome Structure, Human  
Genome Center; 3'-end one pass sequencing: RAB; clone selection for  
full insert sequencing: RAB and Helix Research Institute.

## COMMENT

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FEATURES  
source

Alignment Scores:  
Pred. No.: 8,598-87 Length: 1525  
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Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: Gaps: 0

## ORIGIN

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Db 615 GTTGTGACCTCCTCTGCTGACCATCAGTTTACAGATATACAGGGTGTGTTGGTGCACG 674  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerLeuValSerValThrAlaValLeuAla 41  
Db 675 CTATTCTGCTGCTCTTCATTGACGATTTACGATTGTGAGCGGTACAGCCTACATTGCC 734  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 735 TTGGCCCTGCTCTCTGTGACCATCAGTTTACGATATACAGGGTGTGATCCAGCTATC 794  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 795 CAGAAATCAGATGAAGGCCACCACCAATTCAGGGCATATCTGGAATCTGGAATCTGATATCT 854  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101

## ORIGIN

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Best Local Similarity: 100.00% Mismatches: 0  
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DB: Gaps: 0

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Db 561 GTTGTGACCTCCTGCTGACCATCAGTTTACAGATATACAGGGTGTGTTGGTGCACG 620  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValLeuAla 41  
Db 621 CTATTCTGCTGCTCTTCATTGACGATTTACGATTGTGAGCGGTACAGCCTACATTGCC 680  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
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QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
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QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 801 GAGGAGTTGGTTCAGAGTACAGTAATTCCTGCTTGGTCACTGTAAGTGCAGTAAG 860  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 861 GAACCTCAGCGGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTGCAGTGTG 920  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
Db 921 ATGTGGGATTTATACCTATGTTGGTGCCTTTTAAATGGTCTGACACTACTGATTTGGCT 980  
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
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QY 162 TyrLeuGlyLeuAlaSerValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 1041 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGCTTAAATCCAAAGCAAAATC 1100  
QY 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 1101 CCTGGATTGAAGCGCAAGCTGAA 1124  
RESULT 34  
AK130812  
LOCUS AK130812 1525 bp mRNA linear PRI 10-SEP-2003

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 Db 915 GAATTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 974  
 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 975 ATGTGGTATTACCTATGTTGGTCCCTGTTTAAATGCTGACACTACTGATTTGGCT 1034  
 Qy 142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
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 Qy 162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
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## RESULT 35

CQ769577  
 LOCUS CQ769577 1599 bp DNA linear PAT 04-MAR-2004  
 DEFINITION Sequence 303 from Patent WO2003058021.  
 ACCESSION CQ769577  
 VERSION CQ769577.1 GI:45113880

KEYWORDS  
 SOURCE Homo sapiens (human)

ORGANISM  
 Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
 1 Koenig-Hoffman, K., Kazinski, M., Schaefer, R. and Kesper, B.

TITLE Novel apoptosis-inducing dna sequences  
 JOURNAL Patent: WO 2003058021-A 303 17-JUL-2003;

Xantos Biomedicine AG (DE)

FEATURES  
 source Location/Qualifiers

1..1599 /organism="Homo sapiens"  
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## ORIGIN

Alignment Scores:  
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 Score: 927.00 Matches: 188  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.57% Indels: 0  
 DB: 6 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CQ769577 (1-1599)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
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 Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 731 CTATTCTCTGCTGCTTTTCATTGACAGTATTCAGCATTTGAGCGTAACAGCTACATTGCC 790  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 791 TTGGCCCTGCTCTCTGCTGACCATCAGCTTTAGGATATACAAAGGGTGTGATCCAAGCTATC 850  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 851 CAGAAATCAGATGAAGGGCCACCCATTTCAGGGCATATCTGGAATCTGGAATGTGCTATATCT 910  
 Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCyseThrIleLys 101

Db 911 GAGGAGTTGGTTTCAGAACTACAGTAATTCCTGCTCTTGGTCAATGTGAACCTGCACGATAAAG 970  
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 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 1031 ATGTGGTATTACCTATGTTGGTCCCTGTTTAAATGCTGACACTACTGATTTGGCT 1090  
 Qy 142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 1091 CTCATTTCACCTTCAGTGTCTCTGTTATTTATGAACGCGCATCAGGCACAGATAGATCAT 1150  
 Qy 162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 1151 TATCTAGGACTTGCATAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAGCAAAATC 1210  
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## RESULT 36

BD231889  
 LOCUS BD231889 1610 bp DNA linear PAT 17-JUL-2003  
 DEFINITION Bone marrow secreted proteins and polynucleotides.  
 ACCESSION BD231889  
 VERSION BD231889.1 GI:33041659  
 KEYWORDS JP 2002511231-A/3.  
 SOURCE Homo sapiens (human)

ORGANISM  
 Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 1 (Bases 1 to 1610)  
 AUTHORS Lin, H. and Cao, L.  
 TITLE Bone marrow secreted proteins and polynucleotides  
 JOURNAL Patent: JP 2002511231-A 3 16-APR-2002;

CHIRON CORP

OS Homo sapiens (human)  
 PN JP 2002511231-A/3  
 PD 16-APR-2002

PF 18-DEC-1998 JP 2000526635  
 PR 30-DEC-1997 US 60/068958,24-SEP-1998 US 60/101603 PR  
 30-SEP-1998 US 60/102540

PI HAISHAN LIN, LI CAO  
 PC C12N15/09,A61K38/00,A61P43/00,C07K14/47,C07K16/18,C12N5/10, PC  
 C12Q1/68,

PC C12N15/00,A61K37/02,C12N5/00  
 CC Bone marrow secreted proteins and polynucleotides PH Key

FT source Location/Qualifiers  
 FT 1..1610 /organism="Homo sapiens (human)".

FEATURES  
 source Location/Qualifiers

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## ORIGIN

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 Query Match: 99.57% Indels: 0  
 DB: 6 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BD231889 (1-1610)

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RESULT 37  
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DEFINITION AF087901  
ACCESSION AF087901  
VERSION AF087901.1 GI:10039642  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 1617)  
Yang, J., Yu, L., Bi, A. D. and Zhao, S. Y.  
Assignment of the human reticulon 4 gene (RTN4) to chromosome  
2p14-->2p13 by radiation hybrid mapping  
Cytogenet. Cell Genet. 88 (1-2), 101-102 (2000)  
JOURNAL 20237542  
MEDLINE 10773680  
PubMed  
REFERENCE 2 (bases 1 to 1617)  
Yang, J., Yu, L., Dai, F. Y., Cui, W. C., Zheng, L. H. and Zhao, S. Y.  
Direct Submission  
Submitted (27-AUG-1998) Lab of Human Gene Research, Institute of  
Genetics, Fudan University, No. 220 Handan Rd., Shanghai 200433,  
P.R.China

FEATURES  
source  
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Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 9 Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x AF087901 (1-1617)  
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 139 GTTGTGTGACCTCTCTGTCTGAGAGACATTAAGAAGACTGGAGTGTGTTGGTCCAGC 198  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 199 CTATTCCTGCTGCTTTTCATTGACAGTATTTCAGCATTTGTGAGCGTAAACAGCCTACATTCGC 258  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 259 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGCTGTGTATCAAGCTATC 318  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 319 CAGAAATCAGATGAGCGCCACCCATTCAGGCGCATATCTGGAATCTGGAATCTGTAATCT 378  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 379 GAGGAGTTGGTTCAGAGTACAGTAATTTCTGCTCTTGGTCTGATGAACTGCACGATAAAG 438  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 439 GAATCAGCGCGCTCTCTCTTAGTGTATGATTTAGTTGATTTCTCTGAAGTTTCAGGTGTTG 498  
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Db 559 CTCAATTCACCTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 618  
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 619 TATCTAGGACTTGCAAAATAGAAATGTTAAAGATGCTATGCTGCTGCTGCTGCTGCTGCTGCT 678  
QY 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 679 CCTGGATTGAGCGCAAGCTGAA 702  
RESULT 38  
AK129806 1619 bp mRNA linear PRI 10-SEP-2003  
LOCUS Homo sapiens cDNA FLJ26295 fis, clone DMC07157.  
DEFINITION AK129806  
ACCESSION AK129806  
VERSION AK129806.1 GI:34526422  
KEYWORDS oligo capping; fis (full insert sequence).  
SOURCE Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1  
Ota, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H., Suzuki, Y.,  
Hata, H., Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M.,  
Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Nishikawa, T.,  
Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and Sugano, S.



TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

NEDO human cDNA sequencing project  
2 (bases 1 to 1619)  
Sugano, S. and Suzuki, Y.  
Direct Submission  
Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science,  
University of Tokyo, Laboratory of Genome Structure, Human Genome  
Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan  
(E-mail: flicdn@ims.u-tokyo.ac.jp, Tel: 81-3-5449-5286,  
Fax: 81-3-5449-5416)

NEDO human cDNA sequencing project supported by Ministry of  
Economy, Trade and Industry of Japan; cDNA full insert sequencing:  
Research Association for Biotechnology (RAB); cDNA library  
construction and 5'-end one pass sequencing; Institute of Medical  
Science, University of Tokyo, Laboratory of Genome Structure, Human  
Genome Center; 3'-end one pass sequencing: RAB; clone selection for  
full insert sequencing: RAB and Helix Research Institute.

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/clone="DMC071157"  
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ORIGIN

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Score: 927.00 Matches: 188  
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 9 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AK129806 (1-1619)

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DB 713 GTTGTTGACCTCTCTGCTGAGAGACATTAGAGACTGGAGTGGTGTGGTCCAGC 772

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 773 CTATTCTCTGCTCTTTCATTGACAGTATTTCAGCATTTGAGGCTAACAGCCTACATGCC 832

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
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QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 893 CAGAAATCAGATGAGAGCCACCATTTCAGGGCATATCTGGAAATCTGGAAGTTCGTATATCT 952

QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
DB 953 GAGGAGTGGTTTCAGAGTACAGTAACTCTGCTCTTGGTCACTGACAGTCAAGTAAG 1012

QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 1013 GAACCTCAGCGGCTCTCTCTAGTATGATGATTTAGTTGATCTCTCAAGTTCAGTGTG 1072

QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuIleAla 141  
DB 1073 ATGTGGGTATTTACCTATGTTGGTCTGTTTAAATGGTCTGACACTACTGATTTGGCT 1132

QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
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QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
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RESULT 39  
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

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IMAGE:4082756), complete cds.  
BC012619.1 GI:15214977  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1654)  
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
Scheetz, T.E., Brownstein, M.J., Uedin, T.B., Toshiyuki, S.,  
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,  
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S.,  
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shvchenko, Y.,  
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smalley, D.E.,  
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 1654)  
Direct Submission  
Straussberg, R.  
Submitted (15-AUG-2001) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbio.org>  
contact: [amadn@systemsbiology.org](mailto:amadn@systemsbiology.org)  
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha  
Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 19 Row: d Column: 8  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 24431932  
This clone has the following problem: The cds is short compared to  
the longest cds in the locus.  
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FEATURES  
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ORIGIN
Alignment Scores:
Pred. No.: 9,49e-87 Length: 1654
Score: 927.00 Matches: 188
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.57% Indels: 0
DB: 9 Gaps: 0
US-09-830-972-29_COPY_990_1178 (1-189) x BC012619 (1-1654)
QY 2 ValValAspLeuLeuThrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 711 GTGTGTGACCTCTGTACTGGAGAGACATTAAAGACATGGAGTGTGTGTGGCCAGC 770
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValIleAla 41
Db 771 CTATTCTGCTGCTTTCATTGACAGTATTACAGCATTTGAGCGTAAACAGCTACATGCC 830
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleThrLysGlyValIleGlnAlaIle 61
Db 831 TTGGCCCTGCTCTCTGTGACCATCTAGGATATACAAAGGTGTGTATCCAGCTATC 890
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaThrLeuGluSerGluValAlaIleSer 81
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QY 82 GluGluLeuValGlnLysThrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db 951 GAGGAGTTGGTTTCAGAGTACAGTAATTCCTGCTCTTGTCTGTCATGTAACGACGATAAG 1010
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QY 122 MetTrpValPheThrTrpValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
Db 1071 ATGTGGGTATTTACCTATGTTGGTGGCTTGTATATGCTGTGACACTACGATTTGGCT 1130
QY 142 LeuIleSerLeuPheSerValProValIleThrGluArgHisGlnAlaGlnIleAspHis 161
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QY 162 TyrLeuGlyLeuAlaIleAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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Db 1251 CTGTGATTCAAGCGCAAGCTGAA 1274

RESULT 40  
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LOCUS  
DEFINITION  
Homo sapiens reticulon 4, transcript variant 2, mRNA (cDNA clone IMAGE:3862911), complete cds.  
ACCESSION  
BC026788  
VERSION  
BC026788.1 GI:20070661  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 1658)  
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altshul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J., McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettner, M., Madan, A., Rodrigues, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, U., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 1658)  
Straussberg, R.  
Direct Submission  
Submitted (04-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)  
Tissue Procurement: DCTD/DTF  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center  
Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [ang@bcm.tmc.edu](mailto:ang@bcm.tmc.edu)  
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulsges, H., Kowals, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 21 Row: h Column: 13  
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, similarity but not identity to protein  
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FEATURES  
Source

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Score: 927.00 Matches: 188
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.57% Indels: 0
Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x BC026788 (1-1668)

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Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 862 TTGGCCCTGCTCTCTGAGCATTACAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 921
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ACCESSION AFI32048
VERSION AFI32048.1 GI:4838518
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ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1691)
AUTHORS Ito, T. and Schwartz, S.M.
TITLE Cloning of a member of the reticulon gene family in human: skeletal muscle type
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1691)
AUTHORS Ito, T. and Schwartz, S.M.
TITLE Direct Submission
JOURNAL Submitted (27-FEB-1999) Pathology, University of Washington, 1959 Pacific NE, Seattle, WA 98195, USA
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ORIGIN
Alignment Scores:
Pred. No.: 9,75e-87 Length: 1691
Score: 927.00 Matches: 188
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.57% Indels: 0
Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x AFI32048 (1-1691)

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Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
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142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161

574 CTCATTTCATCTCTCAGTGTCTCTGTTATTATTAAGACGGCATCAGGCACAGATAGATCAT 633

162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

634 TATCTAGGACTTGCATTAAGATGTTAAAGATGCTATGCTGCTAAATCCAGCAAAATC 693

182 ProGlyLeuLysArgLysAlaGlu 189

694 CCTGGATTGAGCGCAAGCTGAA 717

BC014366 1698 bp mRNA linear PRI 29-JUN-2004

LOCUS Homo sapiens reticulon 4, transcript variant 3, mRNA (cdna clone IMAGE:3933041), complete cds.

ACCESSION BC014366

VERSION BC014366.1 GI:15680080

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE

AUTHORS

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Donaldson,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carrinci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalish,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

human and mouse cdna sequences

Generation and initial analysis of more than 15,000 full-length human and mouse cdna sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 1698)

Strausberg,R.

Direct Submission

Submitted (17-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)

Tissue Procurement: CLONTECH

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>

Contact: [amadansystemsbiology.org](mailto:amadansystemsbiology.org)

Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 31 Row: 9 Column: 2

This clone has the following problem: The cds is short compared to the longest cds in the locus.

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ORIGIN

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Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 99.57% Indels: 0

DB: 9 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BC014366 (1-1698)

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Db 145 GTTGTGACCTCTCTGCTGAGACATTAAGAAGCTGGAGTGGTGTGTTGGTCCAGC 204

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ACCESSION AF177332
VERSION AF177332.1 GI:10503960
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SOURCE
ORGANISM Homo sapiens (human)
REFERENCE 1 (bases 1 to 1700)
AUTHORS Gu,J.R., Wan,D.F., Zhao,X.T., Zhou,X.M., Jiang,H.Q., Zhang,P.P.,
Qin,W.X., Huang,Y., Qiu,X.K., Qian,L.F., He,L.P., Li,H.N., Yu,Y.,
Yu,J. and Han,L.H.
TITLE Novel human cDNA clone with function of inhibiting cancer cell
growth
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1700)
AUTHORS Gu,J.R., Wan,D.F., Zhao,X.T., Zhou,X.M., Jiang,H.Q., Zhang,P.P.,
Qin,W.X., Huang,Y., Qiu,X.K., Qian,L.F., He,L.P., Li,H.N., Yu,Y.,
Yu,J. and Han,L.H.
TITLE Direct Submission
JOURNAL Submitted (08-AUG-1999) National Laboratory For Oncogenes & Related
Genes, Shanghai Cancer Institute, 25/Ln 2200 Xie Tu Road, Shanghai
200032, P.R. China
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CDS
Alignment Scores:
Pred. No.: 9,828-87 Length: 1700
Score: 927.00 Matches: 188
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.57% Indels: 0
DB: 9 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x AF177332 (1-1700)

Qy 2 ValValAspLeuLeuTrrArgAspLleLysLysThrGlyValValPheGlyAlaSer 21
Db 153 GTTGTGACCTCTCTACTGAGAGACATTAAAGACTGGAGTGGTGTGGTGGCCAGC 212
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Qy 42 LeuAlaLeuSerValThrLleSerPheArgLleTrrLysGlyValLleGlnAlaIle 61
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DEFINITION AB040463
ACCESSION AB040463
VERSION AB040463.1 GI:11610576
KEYWORDS reticulon.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Tagami,S., Eguchi,Y., Kinoshita,M., Takeda,M. and Tsujimoto,Y.
TITLE A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on
endoplasmic reticulum and reduces their anti-apoptotic activity
JOURNAL Oncogene 19 (50), 5736-5746 (2000)
MEDLINE 21010696
PUBMED 11126360
REFERENCE 2 (bases 1 to 1709)
AUTHORS Eguchi,Y., Tagami,S. and Tsujimoto,Y.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-2000) Yutaka Eguchi, Osaka University Graduate
School of Medicine, Biomedical Research Center, Department of
Medical Genetics, Yamadaoka 2-2, Suita, Osaka 567-0871, Japan
(E-mail: eguchi@gene.med.osaka-u.ac.jp, Tel:+81-6-6879-3363,
Fax:+81-6-6879-3369)
FEATURES
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## RESULT 46

BC068991

LOCUS

DEFINITION

Homo sapiens reticulon 4, transcript variant 2, mRNA (cDNA clone

IMAGE:4634289), complete cds.

ACCESSION

BC068991

VERSION

BC068991.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 1728)  
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
 Altschul, S.F., Zeeberg, K.H., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
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 Stattenkon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
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 Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,  
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E.,  
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 12477932  
 2 (bases 1 to 1728)  
 Strausberg, R.  
 Direct Submission  
 Submitted (05-APR-2004) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue procurement: ATCC  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA sequencing by: Genome Sequence Centre,  
 BC Cancer Agency, Vancouver, BC, Canada  
 info@bcgsc.bc.ca  
 Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,  
 Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth  
 Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,  
 Kim MacDonald, Anara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,  
 Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prabhu,  
 Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,

Duane Smalus, Jeff Stott, Miranda Tsai, George Yang, Jacquie  
 Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAL Plate: 54 Row: C Column: 22  
 This clone was selected for full length sequencing because it  
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gene

CDS

## ORIGIN

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Best Local Similarity:	100.00%	Mismatches:	0
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DB:	9	Gaps:	0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BC068991 (1-1728)

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SOURCE Homo sapiens
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REFERENCE 1 (bases 1 to 1800)
AUTHORS Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.
TITLE Genomic structure and functional characterisation of the promoters
of human and mouse nogo/rtn4
JOURNAL J. Mol. Biol. 325 (2), 299-323 (2003)
MEDLINE 22376540
PUBMED 12488097
REFERENCE 2 (bases 1 to 1800)
AUTHORS Oertle,T. and Schwab,M.E.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Brain Research Institute, University of
Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
Switzerland
REFERENCE 3 (bases 1 to 1800)
AUTHORS Van der Putten,H.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basel, Switzerland
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Percent Similarity: 100.00%    Conservatives: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:     99.57%       Indels:      0
DB:              9           Gaps:        0

US-09-830-972-29_COPY_990_1178 (1-189) x AY102276 (1-1800)

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Db      628 ATGTGGGTATTTACCTATGTTGGTGGCTTGTTTAAATGGTCTGACACTACTGATTTGGCT 687
QY      142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db      688 CTCATTTCACCTCTCAGTGTCTCTGTTATTTAAGACGGCATCAGGCACAGATAGATCAT 747
QY      162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      748 TATCTAGGACTTGCAAAATAAGAAATGTTAAAGATGCTATGGCTAAATCCAGCAAAATC 807
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RESULT 48
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LOCUS Homo sapiens ASY mRNA, complete cds.
DEFINITION AB015639
ACCESSION AB015639
VERSION AB015639.1 GI:5821139
KEYWORDS ASY.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2052)
AUTHORS Yutsudo,M.
TITLE Isolation of a cell death-inducing gene
JOURNAL Published Only in DataBase (1999)
REFERENCE 2 (bases 1 to 2052)
AUTHORS Yutsudo,M.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-1998) Masuo Yutsudo, Osaka University, Dept. of

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565-0871, Japan [E-mail:yuteudo@biken.osaka-u.ac.jp,  
Tel.81-6-879-8313, Fax:81-6-879-8315]

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    QY      22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThAlaTyrIleAla 41
    Db      682 CTATTCTCTGCTCTTCTATGACAGTATTACAGATTGTGAGCGTAACAGCCTACATTGCC 741

    QY      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
    Db      742 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 801

    QY      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
    Db      802 CAGAAATCAGATGAAGGCCACCCATTTCAGGCGATATCTGGAATCTGGAAGTTGCTATATCT 861

    QY      82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
    Db      862 GAGGAGTTGGTTTCAGAAAGTACAGTAACTCTGCTCTTGGTTCATGTGAACTGCACGATAAG 921

    QY      102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
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    QY      142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
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    QY      182 ProGlyLeuLysArgLysAlaGlu 189
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Db      1162 CCTGGATTGAAGCGCAAAAGCTGAA 1185

RESULT 49
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DEFINITION Homo sapiens reticulon 4b mRNA, complete cds.
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VERSION    AF148538.1
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SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 2235)
AUTHORS    Yang,J., Yu,L., Bi,A.D. and Zhao,S.Y.
TITLE       Assignment of the human reticulon 4 gene (RTN4) to chromosome
            2p14--2p13 by radiation hybrid mapping
JOURNAL     Cytogenet. Cell Genet. 88 (1-2), 101-102 (2000)
MEDLINE     20237542
PUBMED      10773680
REFERENCE  2 (bases 1 to 2235)
AUTHORS    Zhou,Y., Yu,L. and Zhao,S.Y.
TITLE       Direct Submission
JOURNAL     Submitted (05-MAY-1999) Lab of Human Gene Research, Institute of
            Genetics, Fudan University, No. 220 Handan Rd., Shanghai 200433,
            P.R.China
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    Pred. No.:      1,37e-86      Length:      2235
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    Percent Similarity: 100.00%      Conservative: 0
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    QY      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
    Db      877 CAGAAATCAGATGAAGGCCACCCATTTCAGGCGATATCTGGAATCTGGAAGTTGCTATATCT 936

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QY	82	GluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAenCysThrIleLys	101	DB:	
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QY	102	GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu	121	QY	2
DB	997	GAACTCAGCGGCTCTTCTAGTGTAGTATGATTTAGTTGATTTCTGAAAGTTTGAGTGTG	1056	DB	735
QY	122	MetTrpValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuLysAla	141	QY	22
DB	1057	ATGTGGGTATTTACCTATGTTGGTGGCTGTTTAAATGGTCTGACACTACTGATTTGGCT	1116	DB	795
QY	142	LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis	161	QY	42
DB	1117	CTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT	1176	DB	855
QY	162	TyrLeuGlyLeuAlaAenLysAenValLysAspAlaMetAlaLysIleGlnAlaValIle	181	DB	855
DB	1177	TATCTAGGACTTGCAATTAAGATGTTAAAGATGCTATGGCTAAATAATCCAGCAAAAATC	1236	QY	62
QY	182	ProGlyLeuLysArgLysAlaGlu	189	DB	915
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AUTHORS					182
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AUTHORS					AY102277
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AUTHORS					Homo sapiens RTN4 isoform B1 (RTN4) mRNA, complete cds;
TITLE					alternatively spliced.
JOURNAL					AY102277
AUTHORS					AY102277.1
TITLE					GI:26800561
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AUTHORS					Homo sapiens
TITLE					Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL					Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS					1 (bases 1 to 2276)
TITLE					Oertle, T., and Schwab, S.M.
JOURNAL					Cloning of a member of the reticulon gene family in human:
AUTHORS					ubiquitous type
TITLE					Unpublished
JOURNAL					2 (bases 1 to 2276)
AUTHORS					Ito, T. and Schwartz, S.M.
TITLE					Direct Submission
JOURNAL					Submitted (27-FEB-1999) Pathology, University of Washington, 1959
AUTHORS					Pacific NE, Seattle, WA 98195, USA
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Qy	22	LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db	860	CTATTCTGCTGCTTTCTATTGACAGTATTTCAGCAATTGTGAGCGTAACAGCTTACATTGCC 919
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VERSION		
CQ783030.1		
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Homo sapiens (human)		
ORGANISM		
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE		
AUTHORS		
Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.,		
Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and		
Koga, H.		
TITLE		
Primers for synthesizing full length cDNA clones and their use		
JOURNAL		
Patent: EP 1396543-A 3170 10-MAR-2004;		
Research Association for Biotechnology (JP)		
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Qy	22	LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db	848	CTATTCTGCTGCTTTTCATTGACAGTATTTCAGCAATTGTGAGCGTAACAGCTTACATTGCC 907
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Db	908	TGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 967
Qy	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db	968	CAGAAATCAGATGAAGGCCACCCATTTCAGGCAATCTGGAATCTGGAATCTGCTATATCT 1027
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Db	1088	GAACTCAGCGCCTCTTTCTTGGTATGATTTAGTTGATTTCTGAAATTTGACGATTTG		1147
Qy	122	MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla		141
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LOCUS	BD127437			
DEFINITION	BD127437	1694 bp DNA linear	PAT 18-SEP-2002	
ACCESSION	BD127437	Primer for synthesizing full-length cDNA and use thereof.		
VERSION	BD127437.1	GI:23222382		
KEYWORDS	JP 2002017375-A/2868.			
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and Koga, H.			
TITLE	Primer for synthesizing full-length cDNA and use thereof			
JOURNAL	Patent: JP 2002017375-A 2868 22-JAN-2002;			
COMMENT	HELIX RESEARCH INSTITUTE			
	OS Homo sapiens (human)			
	PN JP 2002017375-A/2868			
	PD 22-JAN-2002			
	PF 07-JUL-2000 JP 2000253172			
	PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO ISHII,			
	PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI SHINICHI KOJIMA,			
	PI TETSUOI OTSUKI, HISASHI KOGA			
	PC			
	C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, PC C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC			
	Primer for synthesizing full-length cDNA and use thereof FH Key			
	Location/Qualifiers			
FT	CDS	(479).. (1351).		
FEATURES	Location/Qualifiers			
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ORIGIN				
Alignment Scores:				
Pred. No.:	2,556-86	Length:	1694	
Score:	923.00	Matches:	187	
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Best Local Similarity:	99.47%	Mismatches:	1	
Query Match:	99.14%	Indels:	0	
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US-09-830-972-29_COPY_990_1178 (1-189) x BD127437 (1-1694)				

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Db	788	GTGTGTTGACCTCCTGTAAGAGACATTAAGAGAGCTGGAGTGGTGTGTGGTGTCAGC	847
Qy	22	LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla	41
Db	848	CTATTTCCTGCTGCTTTCAATGACAGTATTGAGCAATGTGAGCGTAACAGCCTACATTGCC	907
Qy	42	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle	61
Db	908	TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGTGTGATCCAAAGCTATC	967
Qy	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer	81
Db	968	CAGAAATCAGATGAAGGCCACCCATTCTAGGCATATCTGGAATCTGAAGTTGCTATATCT	1027
Qy	82	GlulLeuLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValLeuLysThrIleLys	101
Db	1028	GAGGAGTTGGTTTCAGAAAGTACAGTAATTTCTGCTCTTGGTCTATGTAACATCCAGATAAG	1087
Qy	102	GlulLeuArgLysLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu	121
Db	1088	GAACTCAGCGCCTCTTCTTAGTTGATGATTTAGTTGATTTCTGGAAGTTTTCAGTGTTC	1147
Qy	122	MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla	141
Db	1148	ATGTGGGTATTTTACCTATGTTGGTGGCTTGTTTAAATGCTGACACTACTGATTTTGGCT	1207
Qy	142	LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis	161
Db	1208	CTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT	1267
Qy	162	TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle	181
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DEFINITION	Homo sapiens cDNA FLJ90558 fis, clone OVARC1001030.		
ACCESSION	AK075039		
VERSION	AK075039.1	GI:22760874	
KEYWORDS	oligo capping; fis (full insert sequence).		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		
AUTHORS	Isogai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T., Sugiyama, T., Suzuki, Y., Sato, H., Nagai, K., Sugano, S., Ishii, S., Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Kojima, S., Nagahari, K., Masuho, Y., Ono, T., Okano, K., Yoshikawa, Y., Aotsuka, S., Sakaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and Ninomiya, K.		
TITLE	NEDO human cDNA sequencing project		
JOURNAL	Unpublished		
AUTHORS	2 (bases 1 to 1694)		
TITLE	Isogai, T. and Otsuki, T.		
JOURNAL	Direct Submission		
COMMENT	Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)		
	Economy, Trade and Industry of Japan; cDNA full insert sequencing: NEDO human cDNA sequencing project supported by Ministry of Research, Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.)		

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## ORIGIN

Alignment Scores:  
Pred. No.: 2,558-86 Length: 1694  
Score: 923.00 Matches: 187  
Percent Similarity: 99.47% Conservativeness: 0  
Best Local Similarity: 99.47% Mismatches: 1  
Query Match: 99.14% Indels: 0  
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US-09-830-972-29\_COPY\_990\_1178 (1-189) x AK075039 (1-1694)

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Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db CTATTCTCGCTGCTTTCATTCACAGTATTGACGATTGTGAGCGTAAACAGCCTACATTGCC 907  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGATCCAGCTATC 967  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
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Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
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Db GAACCTCAGCGCGCTCTCTTAGTTGATGATTAGTTGATTCCTGAAAGTTGCGAGTGTG 1147  
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Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db CTCATTTCTACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATGATCAT 1267  
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## RESULT 55

BD083733

## LOCUS

BD083733 1980 bp DNA linear PAT 27-AUG-2002  
Nucleic acid sequence characterized in that expression is  
potentiated in human neuroblastoma with good prognosis, in  
comparison between human neuroblastoma with good prognosis and human  
neuroblastoma with bad prognosis.

## ACCESSION

BD083733

## VERSION

BD083733.1 GI:22629343

KEYWORDS  
SOURCE

JP 2001321175-A/22.  
Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 1980)

## AUTHORS

Nakagawara, A.

## TITLE

Nucleic acid sequence characterized in that expression is

potentiated in human neuroblastoma with good prognosis, in

comparison between human neuroblastoma with good prognosis and human

neuroblastoma with bad prognosis

Patent: JP 2001321175-A 22 20-NOV-2001;

CHIBA PREF,HISAMITSU PHARMACEUTICAL CO INC

OS Homo sapiens (human)

PN JP 2001321175-A/22

PD 20-NOV-2001

PF 12-MAY-2000 JP 2000140387

PI AKIRA NAKAGAWARA

PC C12N15/09,C12Q1/02,C12Q1/68,G01N33/50,C12N15/00 CC Nucleic

acid sequence characterized in that expression is CC

potentiated in

CC human neuroblastoma with good prognosis, in comparison between

CC human

CC neuroblastoma with good prognosis and human

neuroblastoma with

CC bad

CC prognosis

PH Key

FT source

FT Location/Qualifiers

1..1980

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## ORIGIN

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Qy 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
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Db ATCCAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGAATCTGAAGTTGCTATA 1245  
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
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Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
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Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140





896 GAACACTCAGGGCCCTCTTCTTAGTGANGATTAGTTGATTCTCTGACGTTTGCAGTGTG 955

122 MetTrrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141

956 ATGTGGGTATTTACCTATGTTGGTGGCTTGTGTTTAAATGGTCTGACGCTACTGATTTTGGCT 1015

142 LeuIleSerIeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161

1016 CTCAATTTCACTCTTCACTAGTCTTCTGTTATTTATGAACGGCATTCAGGCACACATAGATCAT 1075

162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaValIleGlnAlaLysIle 181

1076 TATCTAGGACTTGCAATTAAGAAATGTTAAAGATGCTATGCTTAAATCCAGCGAATATC 1135

182 ProGlyLeuLysArgLysAlaGlu 189

1136 CCTGGATTGAAGCGCAAGCTGAA 1159

RESULT 59

AB073672

LOCUS

DEFINITION

AB073672

ACCESSION

VERSION

AB073672.1

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1

Tozaki,H. and Hirata,T.

The partial sequence of mouse nogo-A cDNA clone#4109

Unpublished

2 (bases 1 to 1738)

Tozaki,H. and Hirata,T.

Direct Submission

Submitted (29-OCT-2001) Hirokazu Tozaki, Division of Brain Function, National Institute of Genetics; Yata 1111, Mishima, Shizuoka 411-8540, Japan (E-mail:h.tozaki@lab.nig.ac.jp).

URL: <http://www.nig.ac.jp/home-j.html>, Tel:81-55-981-6721(ex. 6721), Fax:81-55-981-6722)

Location/Qualifiers

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Alignment Scores:

Pred. No.: 1.79e-85

Score: 915.00

Percent Similarity: 99.47%

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Query Match: 98.28%

ORIGIN

Length: 1738

Matches: 186

Conservative: 2

Mismatches: 1

Indels: 0

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US-09-830-972-29\_COPY\_990\_1178 (1-189) x AB073672 (1-1738)

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QY 121 LeuMetTrrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140

Db 1529 TTGATGTGGTATTTACTTACCTTACGTTGGTGGCTTGTTCATGTTTGCACACTACTGATTTTA 1588

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QY 161 HistTyrLeuGlyLeuAlaAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180

Db 1649 CATTATCTAGGACTTTGCAACAGAGTGTTAAGGATGCCATGCGCAAAATCCAAAGCAAAA 1708

QY 181 IleProGlyLeuLysArgLysAlaGlu 189

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RESULT 60

LOCUS

DEFINITION

BC032192

Mus musculus reticulon 4, mRNA (cdna clone MGC:38204

IMAGE:5323152), complete cds.

ACCESSION

BC032192

VERSION

BC032192.1

KEYWORDS

GI:21618980

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.

1 (bases 1 to 2958)

REFERENCE

1 Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altshuler,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Haieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldi,M.F., Casavant,T.L., Scheet,T.E., Brownstein,M.J., Uedin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,



TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
JOURNAL  
REMARK  
COMMENT

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalilus, D.E.,  
Schnercher, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
2388257  
12477932  
2 (bases 1 to 2958)  
Direct Submission  
Straussberg, R.  
Submitted (06-JUN-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)  
Tissue Procurement: Jeffrey Green M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc\\_mgc@hghri.nih.gov](mailto:nisc_mgc@hghri.nih.gov)  
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,  
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Maduro, O.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,  
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,  
Tsurgou, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,  
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LILNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 56 Row: k Column: 2.

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## gene

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ORIGIN  
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Query Match: 98.28% Indels: 0  
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RESULT 61  
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LOCUS BC032272 3815 bp mRNA linear ROD 16-APR-2003  
DEFINITION Mus musculus reticulon 4, mRNA (cDNA clone IMAGE:536860), partial  
cde.  
ACCESSION BC032272  
VERSION BC032272.1 GI:22749634  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE	1 (bases 1 to 3815)	Best Local Similarity: 98.41%	Mismatches: 1
AUTHORS	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L.H., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diachenko,L., Marudani,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,J.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalls,D.E., Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.	98.28%	Indels: 0
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	DB: 10	Gaps: 0
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	US-09-830-972-29_COPY_990_1178 (1-189) x BC032272 (1-3815)	
MEDLINE	22398257		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 3815)		
AUTHORS	Strausberg,R.		
TITLE	Direct Submission		
JOURNAL	Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>		
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgabs-remail.nih.gov">cgabs-remail.nih.gov</a> Tissue Procurement: The Cepko Laboratory cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: <a href="http://www.nisc.nih.gov/">http://www.nisc.nih.gov/</a> Contact: nisc.mgc@nih.gov Akhter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsourgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.		
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DEFINITION	Mus musculus RTN4 (Rtn4)	mRNA, complete cds, alternatively spliced.	
ACCESSION	AY102280		
VERSION	AY102280.1	GI:23379808	
KEYWORDS			
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	1 (bases 1 to 4063)		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.		
JOURNAL	Genomic Structure and Functional Characterisation of the Promoters of Human and Mouse nogo/rtn4		
MEDLINE	J. Mol. Biol. 325 (2), 299-323 (2003)		
PUBMED	22376540		
REFERENCE	2 (bases 1 to 4063)		
AUTHORS	Oertle,T. and Schwab,M.E.		
TITLE	Direct Submission		
JOURNAL	Submitted (07-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057, Switzerland		
REFERENCE	3 (bases 1 to 4063)		
AUTHORS	Van der Putten,H.		
TITLE	Direct Submission		

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DEFINITION		Mus musculus cDNA clone MGC:73436 IMAGE:6847916, complete cds.	
ACCESSION		BC056373	
VERSION		BC056373.1 GI:33604147	
KEYWORDS		MGC.	
SOURCE		Mus musculus (house mouse)	
ORGANISM		Mus musculus	
REFERENCE			
AUTHORS			
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		Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klauener,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altshuler,S.F., Zeeberg,K.H., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Ditzchenko,L., Marusina,K., Farmer,A.C., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schetz,T.E., Brownstein,M.J., Udwin,T.B., Toshiyuki,S., Carninci,P., Frange,C., Raja,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalls,D.E., Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.	
TITLE		Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
MEDLINE		22388257	
PUBMED		12477932	
REFERENCE		2 (bases 1 to 4518)	
AUTHORS		Strausberg,R.	
TITLE		Direct Submission	
JOURNAL		Submitted (11-AUG-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
REMARK		NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>	
COMMENT		Contact: MGC help desk Email: <a href="mailto:cgabbs-r@mail.nih.gov">cgabbs-r@mail.nih.gov</a> Tissue Procurement: Dr. Jim Lin, University of Iowa cDNA Library Preparation: M. Bento Soares, University of Iowa cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) cDNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr. Thomas L. Casavant. Web site: <a href="http://genome.uiowa.edu">http://genome.uiowa.edu</a>	

Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu  
 Ronaldo, M.F., Akabogu, I., Bair, T., Bair, J., Crouch, K., Davis, A.,  
 Fishler, K., Koppel, C., Kucaba, T., Lebeck, M., Melo, A., Schaefer, K.,  
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 Casavant, T., Soares, M.B.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: Plate: Row: Column: 0.

## FEATURES

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## ORIGIN

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Score:          915.00      Matches:      186
Percent Similarity: 99.47%      Conservative: 2
Best Local Similarity: 98.41%      Mismatches: 1
Query Match:      98.28%      Indels: 0
DB:              10      Gaps: 0

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DEFINITION AY102284
ACCESSION AY102284
VERSION AY102284.1 GI:23379816
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 4627)
AUTHORS Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.
TITLE Genomic Structure and Functional Characterisation of the Promoters
of Human and Mouse nogo/rtn4
JOURNAL J. Mol. Biol. 325 (2), 299-323 (2003)
MEDLINE 22376540
PUBMED 12488097
REFERENCE 2 (bases 1 to 4627)
AUTHORS Oertle,T. and Schwab,M.E.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Brain Research Institute, University of
Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
Switzerland
REFERENCE 3 (bases 1 to 4627)
AUTHORS Van der Putten,H.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
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ORIGIN

Alignment Scores:  
Pred. No.: 5,95e-85 Length: 4627  
Score: 915.00 Matches: 186  
Percent Similarity: 99.47% Conservative: 2  
Best Local Similarity: 98.41% Mismatches: 1  
Query Match: 98.28% Indels: 0  
DB: 10 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AY102284 (1-4627)

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ACCESSION AR379837  
VERSION AR379837.1 GI:40087471

KEYWORDS

SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2610)  
AUTHORS Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.  
TITLE Compositions for the detection of blood cell and immunological  
composition gene expression  
JOURNAL Patent: US 6607879-A 382 19-AUG-2003;  
FEATURES Location/Qualifiers  
1..2610  
/organism="unknown"  
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DB 1311 GTTGTGTACCTCTGTGACTTGGAGAGACATTAAGAAGATGGAGTGGTGTGGTGCACG 1370  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAl 41  
DB 1371 CTATTCCTGCTGCTTTCATTGCACAGTATTCAGCATTTGAGCGGTAAACAGCTTACA 1430  
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 1431 CTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATATAAGAGCTGGATCCAAAGCTAT 1490  
QY 61 eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 81  
DB 1491 CCAGAAATCAGATGAAAGCCACCCATTCAGGCGCATATCTGGAACTGGAAGTTGCTATATC 1550  
QY 81 rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIlely 101  
DB 1551 TGAGGAGTTGGTTCAGAAAGTACAGTAATCTCTGCTTCTGCTCATGTGAACCTGCACGATAA 1610  
QY 101 sGluLeuArgArgPheLeuValAspLeuValAspSerLeuLysPheAlaValle 121  
DB 1611 GGAACCTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCCTGAAAGTTTGCAGTGT 1670  
QY 121 uMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAl 141  
DB 1671 GATGTGGGTATTTACCTATGTTGGTGGCTTGTGTTAATGCTTGACACACTGATGATTTGGC 1730  
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHi 161  
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QY 161 sTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIl 181  
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QY 181 eProGlyLeuLysArgLysAlaGlu 189  
DB 1851 CCTTGGGTTGAAGCGCAAGCTGAA 1875

RESULT 66

AY102282  
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DEFINITION Mus musculus RTN4 (Rtn4) mRNA, complete cds, alternatively spliced.  
ACCESSION AY102282  
VERSION AY102282.1 GI:23379812  
KEYWORDS Mus musculus (house mouse)  
SOURCE



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Db	160 TTATTCCTCGCTGCTCTGCACAGTTCAGCATTTGTCAGTGTAAACGGCTACATTCGC 219		
QY	42 LeuAlaLeuLeuSerValThrIleSerPheargileTyrylysGlyValIleGlnAlaIle 61		
Db	220 TTTGGCCCTGCTCTGTGACTATCACTAGCTTTTAGGATATATAAGGGTGTGATCCAAGCTATC 279		
QY	62 GlnLySerAspGluGlyHisProPheArgAlaTyrlauGluSerGluValAlaIleSer 81		
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Db	580 TATCTAGGACTTGCACAAACAGAGTGTAAAGATGCCATGCCCAAATCCCAAGCAAAAAATC 639		
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Db	640 CCTGGATTGAAGCGCAAGCAGAA 663		
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DEFINITION	AY102283		
ACCESSION	AY102283.1 GI:23379814		
VERSION			
KEYWORDS			
SOURCE	Mus musculus (house mouse)		
ORGANISM			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.		
JOURNAL	Genomic Structure and Functional Characterisation of the Promoters		
MEDLINE	of Human and Mouse nogo/rtn4		
PUBMED	J. Mol. Biol. 325 (2), 299-323 (2003)		
REFERENCE	2 (bases 1 to 1769)		
AUTHORS	Oertle,T. and Schwab,M.E.		
TITLE	Direct Submission		
JOURNAL	Submitted (07-MAY-2002) Brain Research Institute, University of		
REFERENCE	Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,		
AUTHORS	Switzerland		
TITLE	3 (bases 1 to 1769)		
JOURNAL	Van der Putten,H.		
REFERENCE	Direct Submission		
AUTHORS	Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma		
TITLE	Inc., Basel, Switzerland		
JOURNAL			

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Qy 182 ProGlyLeuIysArgLysAlaGlu 189
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RESULT 69
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LOCUS Mus musculus RTN4 (Rtn4) mRNA, complete cds, alternatively spliced.
DEFINITION AY102281
ACCESSION AY102281
VERSION AY102281.1 GI:23379810
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.
Genomic Structure and Functional Characterisation of the Promoters
of Human and Mouse nogo/rtn4
J. Mol. Biol. 325 (2), 299-323 (2003)
PUBMED 12488097
REFERENCE 2 (bases 1 to 2209)
AUTHORS Oertle,T. and Schwab,M.E.
DIRECT SUBMISSION
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Brain Research Institute, University of
Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
Switzerland
REFERENCE 3 (bases 1 to 2209)
AUTHORS Van der Putten,H.
DIRECT SUBMISSION
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basel, Winterthurerstr.190, Zuerich 8057,
Switzerland
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exon
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Best Local Similarity: 98.40% Mismatches: 1
Query Match: 97.85% Indels: 0
DB: 10 Gaps: 0

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Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 61
Db 873 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAGGGTGTGATCCAGCTATC 932

Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
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Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
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Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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Qy 182 ProGlyLeuLysArgLysAlaGlu 189
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LOCUS AX766046
DEFINITION Sequence 1 from Patent WO03002602.
ACCESSION AX766046
VERSION AX766046.1 GI:32260128
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1
AUTHORS Eisenbach-Schwartz,M. and Hauben,E.
TITLE Nogo and nogo receptor derived peptides for t-cell mediated
neuroprotection
JOURNAL Patent: WO 03002602-A 1 09-JAN-2003;
YEDA RESEARCH AND DEVELOPMENT CO. LTD. (IL)
FEATURES
source
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ORIGIN
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exon
ORIGIN
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Score: 908.00 Matches: 184
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Best Local Similarity: 97.35% Mismatches: 2
Query Match: 97.53% Indels: 0
DB: 6 Gaps: 0

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US-09-830-972-29\_COPY\_990\_1178 (1-189) x AX766046 (1-3489)

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Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 3043 GCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAGGGCGTGCATCCAGGCT 3102

Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
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Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
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Qy 161 HisTyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLys 180  
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LOCUS CQ829507 3492 bp DNA linear PAT 05-JUL-2004  
DEFINITION Sequence 25 from Patent WO2004052932.  
ACCESSION CQ829507  
VERSION CQ829507.1 GI:49732820

KEYWORDS Rattus norvegicus (Norway rat)  
SOURCE Rattus norvegicus  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1 Barske, C., Mir, A. K., Oertle, T., Schnell, L., Schwab, M. E.,  
Vitaliti, A. and Zurini, M.  
Nogo a binding molecules and pharmaceutical use thereof  
Patent: WO 2004052932-A 25 24-JUN-2004;  
Novartis AG (CH)

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Alignment Scores:  
Pred. No.: 2,25e-84 Length: 3492  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 97.53% Indels: 0  
DB: 6 Gaps: 0

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Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 2983 AGCTTATTCCTGCTGCTCTCTGACAGTGTTCAGCATTTGTCAGTGAACGGCTACATT 3042

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Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 3163 TCAGAGGAATGGTTTCAGAAATACAGTAATTTCTGCTCTTGTTCATGTGAACAGCACATA 3222

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Db 3343 GCTCTGATCTACTCTTCAGTATTCCTGTTATTTATGAAAGCGCATCAGTGCAGATAGAT 3402

Qy 161 HisTyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3403 CATTATCTAGGACTTGCAACAAAGAGTGTAAAGATGCCATGGCCAAATCCAAAGCAAA 3462

Qy 181 IleProGlyLeuLysArgLysAlaGlu 189  
Db 3463 ATCCCTGGATTGAAGCGCAAGCAGAT 3489

RESULT 72  
RNO242961

LOCUS RNO242961 4684 bp mRNA linear ROD 28-JAN-2000  
DEFINITION Rattus norvegicus mRNA for Nogo-A protein.  
ACCESSION AJ242961  
VERSION AJ242961.1 GI:6822246  
KEYWORDS Nogo-A protein.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1  
AUTHORS Chen, M.S., Huber, A.B., van der Haar, M.E., Frank, M., Schnell, L.,  
Spillmann, A.A., Christ, F. and Schwab, M.E.  
TITLE Nogo-A is a myelin-associated neurite outgrowth inhibitor and an  
antigen for monoclonal antibody IN-1  
JOURNAL Nature 403 (6768), 434-439 (2000)  
MEDLINE 20129258  
PUBMED 10667796  
REFERENCE 2 (bases 1 to 4684):  
AUTHORS Van der Haar, M.E.  
TITLE Direct Submission  
JOURNAL Submitted (14-JUN-1999) Van der Haar M.E., Department of  
Neuromorphology, Brain Research Institute, University of Zurich,  
Winterthurerstrasse 190, Zurich, CH-8057, SWITZERLAND  
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QY 161 HistTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180	
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AX700396 2782 bp DNA linear PAT 03-APR-2003  
LOCUS AX700396  
DEFINITION Sequence 165 from Patent EP1284297.  
ACCESSION AX700396  
VERSION .AX700396.1 GI:29536204  
KEYWORDS Rattus norvegicus (Norway rat)  
SOURCE Rattus norvegicus  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1  
AUTHORS Brooksbank, R.A., Dixon, A.K., Lee, K. and Pinnock, R.D.  
TITLE Identification and use of molecules implicated in pain  
JOURNAL Patent: EP 1284297-A 165 19-FEB-2003;  
WARNER-LAMBERT COMPANY (US)  
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1. .2782  
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US-09-830-972-29\_COPY\_990\_1178 (1-189) x RNO242961 (1-4684)



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DEFINITION	Rattus norvegicus foocen-m2 mRNA, alternate splice product, complete cds.				
ACCESSION	AF132045				
VERSION	AF132045.1	GI:4838512			
KEYWORDS	Rattus norvegicus (Norway rat)				
SOURCE	Rattus norvegicus				
ORGANISM	Rattus norvegicus				
REFERENCE	1 (bases 1 to 2782)				
AUTHORS	Ito,T. and Schwartz,S.M.				
TITLE	Cloning of a member of the reticulum gene family in rat: One of two minor spliced variants				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 2782)				
AUTHORS	Ito,T. and Schwartz,S.M.				
TITLE	Direct Submission				
JOURNAL	Submitted NE, Seattle, WA 98195, USA				
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QY	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40		
Db	1331	AGCTTATTCTGCTGCTGCTCTGACAGTGTTCAGCATTTGTACAGTCGCGCTACATT	1390		
QY	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60		
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LOCUS	AY114152	3821 bp	mRNA	linear	ROD 17-JUL-2002
DEFINITION	Mus musculus nogo-A mRNA, complete cds.				
ACCESSION	AY114152				
VERSION	AY114152.1	GI:21898576			
KEYWORDS	Mus musculus (house mouse)				
SOURCE	Mus musculus				
ORGANISM	Mus musculus				
REFERENCE	1 (bases 1 to 3821)				
AUTHORS	Jin,W., Long,M., Li,R. and Ju,G.				
TITLE	Cloning and expression of the mouse Nogo-A protein				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 3821)				
AUTHORS	Jin,W., Long,M., Li,R. and Ju,G.				
TITLE	Direct Submission				
JOURNAL	Submitted (17-MAY-2002) Institute of Neurosciences, 17 Chang Le Xi Road, Xi'an, Shaanxi 710032, China				
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CDS					



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 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
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 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 DB 570 TATCTAGGACTTGCAACAAGAGTGTTAAGGATGCCCAAAATCCAAGCAAAATC 629  
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RESULT 78  
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 DEFINITION AJ242963  
 ACCESSION AJ242963.1 GI:6822250  
 VERSION Nogo-C protein.  
 KEYWORDS Rattus norvegicus (Norway rat)  
 SOURCE Rattus norvegicus  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 REFERENCE 1  
 AUTHORS Chen, M.S., Huber, A.B., van der Haar, M.E., Frank, M., Schnell, L., Spillmann, A., Christ, F. and Schwab, M.E.  
 TITLE Nogo-A is a myelin-associated neurite outgrowth inhibitor and an antigen for monoclonal antibody IN-1  
 JOURNAL Nature 403 (6768), 434-439 (2000)  
 MEDLINE 20129258  
 PUBMED 10667796  
 REFERENCE 2 (bases 1 to 1568)  
 AUTHORS Van der Haar, M.E.  
 TITLE Direct Submission  
 JOURNAL Submitted (14-JUN-1999) Van der Haar M.E., Department of Neuromorphology, Brain Research Institute, University of Zurich, Winterthurerstrasse 190, Zurich, CH-8057, SWITZERLAND  
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 REFERENCE 1 (bases 1 to 2156)  
 AUTHORS Oertle, T., Klinger, M., Stuermer, C.A. and Schwab, M.E.  
 TITLE A reticular rhapsody: phylogenetic evolution and nomenclature of the RTN/Nogo gene family  
 JOURNAL PNAS 100 (10), 1238-1247 (2003)  
 PUBMED 12832288  
 REFERENCE 2 (bases 1 to 2156)  
 AUTHORS Oertle, T. and Schwab, M.E.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-OCT-2002) Brain Research Institute and Department Biology, University of Zurich and ETH Zurich, Winterthurerstr.190,

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Zurich 8057, Switzerland
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DEFINITION Rattus norvegicus mRNA for Nogo-B protein.
ACCESSION AJ242962
VERSION AJ242962.1 GI:6822248
KEYWORDS Nogo-B protein.
SOURCE Rattus norvegicus (Norway rat)
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Rattus.
REFERENCE
1 Chen, M.S., Huber, A.B., van der Haar, M.E., Frank, M., Schnell, L.,
Spillmann, A.A., Christ, F. and Schwab, M.E.
Nogo-A is a myelin-associated neurite outgrowth inhibitor and an
antigen for monoclonal antibody IN-1
Nature 403 (6768), 434-439 (2000)
JOURNAL Nature 403 (6768), 434-439 (2000)
MEDLINE 20129258
PUBMED 10667796
REFERENCE
2 (bases 1 to 2156)
Van der Haar, M.E.
Direct Submission
Submitted (14-JUN-1999) Van der Haar M.E., Department of
Neuromorphology, Brain Research Institute, University of Zurich,
Winterthurerstrasse 190, Zurich, CH-8057, SWITZERLAND
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ORIGIN
Alignment Scores:
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VDDIADSLKFAVLMMVFTYTGALFNGLTLLILALISLFSIPVIYERHQAOIDHVLGA
NKSVKDAMAKIQAKIPGLKRAE"

ORIGIN
Alignment Scores:
Pred. No.: 3,95e-84 Length: 1276
Score: 900.50 Matches: 185
Percent Similarity: 98.94% Conservative: 2
Best Local Similarity: 97.88% Mismatches: 1
Query Match: 96.72% Indels: 1
DB: 10 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x AY114153 (1-1276)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 1276
Db 624 GTTGTGACCTCTCTGCTGAGAGACATTAGAGAGACTGGAGTGGTGTATTTGGTGCC 683
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 684 AGCTTATTCCTGCTGCTCTCTCACAGTGTTCAGCATTGTTCAGTAAACGCGCTACATT 743
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 744 GCCTTGGCCCTGCTCTCTGCTGACTATCAGCTTTAGGATATATAGGGTGTGATCCAAGCT 803
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 804 ATCCAGAAATCAGATGAAGGCCACCATTCAGGCGATATTTGGAACTCTGAAGTTGCCATA 863
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 864 TCAGAGGAATTTGGTTTCAGAAATATAGTAATTCCTCTCTGCTCATGTGAACAGCACAATA 923
QY 101 LysGluLeuArgLeuPheLeuValAspIleValAspSerLeuLysPheAlaVal 120
Db 924 AAAGAATTTGAGCGCTCTCTCTTAGTTAGTATTTAGTTAGTATTCCTCGAAGTTTGCAGTG 983
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 984 TTGATGTGGGTATTTACTTACGTTGGTGGCTTGTTCATGTTTGCACACTACTGATTTTA 1043
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 1044 GCTCTGATCTCACCTCTTCAGTATTTCTGTTATATATGAACGCGCATCAGCGCAGATAGAT 1103
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 1104 CATTATCTAGGACTTGCACAAACAGAGCGTTAAGGATGTCATGGCCAAATCCAAAGCAAAA 1163
QY 181 IleProGlyLeuLysArgLysAlaGlu 189
Db 1164 ATCCCTGATTTGAAGCGCAAGACGAGAA 1190

RESULT 83
BD190738
LOCUS BD190738 2386 bp DNA linear PAT 17-JUL-2003
DEFINITION Secreted proteins and polynucleotides encoding them,,
ACCESSION BD190738
VERSION BD190738.1 GI:33000477
KEYWORDS JP 2002515751-A/5.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2386)
AUTHORS Jacobs,K., Mccoy,J.M., Lavallie,B.R., Racie,L.A., Merberg,D.,
Treacy,M., Spaulding,V. and Agostino,M.J.

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QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 890 GTTGTGACCTCTCTCTGAGAGACATTAGAGAGCTGGAGTGGTGTGGTGCCAGC 949
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 950 TTATTCCTGCTGCTCTGACAGTGTTCAGCATTGTTCAGTAAACGCGCTACATTGCC 1009
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 1010 TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAGGGCGTGCATCCAGGCTATC 1069
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 1070 CAGAATTCAGATGAAGGCCACCATTCAGGCGATATTTAGAAATCTGAAGTTGCTATATCA 1129
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db 1130 GAGGAATTTGGTTTCAGAAATACAGTAATTCCTGCTCTTGGTTCATGTGAACAGCACAATAAAA 1189
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 1190 GAACCTGAGCGCGCTTTCTTCTAGTTGATTTAGTTGATTCCTCGAAGTTTGCAGTGTG 1249
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
Db 1250 ATGTGGGTGTTTACTATGTGTGGTGGCTTGTTCATAGTGTGACACTACTGATTTTAGCT 1309
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 1310 CTGATCTCACCTTCAGTATTCCTGTTATTTATGAACGCGCATCAGTGCAGATAGATCAT 1369
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 1370 TATCTAGGACTTGCACAAACAGAGTGTAAAGATGTCATGGCCAAATCCAAAGCAAAAATC 1429
QY 182 ProGlyLeuLysArgLysAlaGlu 189
Db 1430 CTGGATTTGAAGCGCAAGACGAT 1453

RESULT 82
AY114153
LOCUS AY114153 1276 bp mRNA linear ROD 17-JUL-2002
DEFINITION Mus musculus nogo-B mRNA, complete cds.
ACCESSION AY114153
VERSION AY114153.1 GI:21898578
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1276)
AUTHORS Jin,W., Li,R., Long,M., Shen,J. and Ju,G.
TITLE Cloning and expression of the mouse Nogo-B protein
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1276)
AUTHORS Jin,W., Li,R., Long,M., Shen,J. and Ju,G.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-2002) Institute of Neurosciences, 17 Chang Le Xi
Road, Xi'an, Shaanxi 710032, China
FEATURES
SOURCE
1..1276
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
120..1193
/note="RTN4; foocen"
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/product="nogo-B"
/protein_id="AAM77069.1"
/db_xref="GI:21898579"
CDS

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TITLE JOURNAL  
 COMMENT Secreted proteins and polynucleotides encoding them  
 Patent: JP 2002515751-A 5 28-MAY-2002;  
 GENETICS INSTITUTE INC  
 PN JP 2002515751-A/5  
 PD 28-MAY-2002  
 PF 24-OCT-1997 JP 1998519738  
 PR 25-OCT-1996 US 08/740274  
 PI KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI  
 DAVID MERBERG,  
 PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC  
 C12N15/12, C12N5/10, C07K14/47, C12Q1/68, A61K38/17 CC Strandedness:  
 Double:  
 CC Topology: Linear;  
 FH Key Location/Qualifiers.

FEATURES  
 source  
 1. .2386  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"

ORIGIN

Alignment Scores:  
 Pred. No.: 3.58e-83 Length: 2386  
 Score: 894.50 Matches: 184  
 Percent Similarity: 97.35% Conservative: 0  
 Best Local Similarity: 97.35% Mismatches: 0  
 Query Match: 96.08% Indels: 5  
 DB: 6 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BD190738 (1-2386)  
 QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
 Db 1476 TCAGTTGTTGACCTCTGCTACTGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGC 1535  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 1536 AGCCTATTCTGCTGCTTTCATTGACAGTATTCAGCATTTGAGCGTAAACAGCTACAT 1595  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAla 60  
 Db 1596 GCCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAAGCT 1655  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 1656 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGG-----GAAGTTGCTATA 1700  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 Db 1701 TCTGAGGAGTTGGTTCAGAAGTACAGTAATTCCTGCTCTTGGTCATGTGAACGACGATA 1760  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 1761 AAGAACTCAGGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTCAGTG 1820  
 QY 121 LeuMetTrpValPheThrTrpValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 Db 1821 TTGATGGGTATTTACCTATGTTGGTGGCTTGTAAATGGTCTGACACTACTGATTTTG 1880  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 Db 1881 GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTTATGACGGCATCAGGCACAGATAGAT 1940  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 1941 CATTATCTAGGACTTGCAAAATAGATGTTAAAGATGCTATGCTAAATATCCAAAGCAAAA 2000  
 QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
 Db 2001 ATCCCTGGATTGAAGCGCAAAAGCTGAA 2027

RESULT 84  
 AX099401

LOCUS AX099401 2386 bp DNA linear PAT 02-APR-2001  
 DEFINITION Sequence 41 from Patent WO0119988.  
 ACCESSION AX099401  
 VERSION AX099401.1 GI:13538524  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1  
 AUTHORS Jacobs, K., McCoy, J.M., Lavallie, E.R., Collins-Racie, L.A., Evans, C.,  
 Merberg, D., Treacy, M., Bowman, M.R., Spaulding, V. and Agostino, M.J.  
 TITLE Secreted proteins and polynucleotides encoding them  
 JOURNAL Patent: WO 0119988-A 41 22-MAR-2001;  
 FEATURES Location/Qualifiers  
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 1. .2386  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

ORIGIN

Alignment Scores:  
 Pred. No.: 3.58e-83 Length: 2386  
 Score: 894.50 Matches: 184  
 Percent Similarity: 97.35% Conservative: 0  
 Best Local Similarity: 97.35% Mismatches: 0  
 Query Match: 96.08% Indels: 5  
 DB: 6 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AX099401 (1-2386)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
 Db 1476 TCAGTTGTTGACCTCTGCTACTGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGC 1535  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 1536 AGCCTATTCTGCTGCTTTCATTGACAGTATTCAGCATTTGAGCGTAAACAGCTACAT 1595  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAla 60  
 Db 1596 GCCTTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAAGCT 1655  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 1656 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGG-----GAAGTTGCTATA 1700  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 Db 1701 TCTGAGGAGTTGGTTCAGAAGTACAGTAATTCCTGCTCTTGGTCATGTGAACGACGATA 1760  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 1761 AAGAACTCAGGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTCAGTG 1820  
 QY 121 LeuMetTrpValPheThrTrpValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 Db 1821 TTGATGGGTATTTACCTATGTTGGTGGCTTGTAAATGGTCTGACACTACTGATTTTG 1880  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 Db 1881 GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTTATGACGGCATCAGGCACAGATAGAT 1940  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 1941 CATTATCTAGGACTTGCAAAATAGATGTTAAAGATGCTATGCTAAATATCCAAAGCAAAA 2000  
 QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
 Db 2001 ATCCCTGGATTGAAGCGCAAAAGCTGAA 2027

RESULT 85

**EX934715**  
**LOCUS**  
**DEFINITION** Gallus gallus finished cDNA, clone CHEST117m23.  
**ACCESSION** BX934715  
**VERSION** BX934715.1 GI:41635243  
**KEYWORDS**  
**SOURCE** Gallus gallus (chicken)  
**ORGANISM** Gallus gallus  
**REFERENCE**  
**AUTHORS** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
1 (bases 1 to 1591)  
Boardman,P.E., Bonfield,J.K., Brown,W.R.A., Carder,C., Chalk,S.E., Croning,M.D.R., Davies,R.M., Francis,M.D., Grafham,D.V., Hubbard,S.J., Humphray,S.J., Hunt,P.J., Maddison,M., McLaren,S.R., Niblett,D., Overton,I.M., Rogers,J., Scott,C.E., Taylor,R.G., Tickle,C. and Wilson,S.A.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (02-FEB-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: chickest@hms.umbist.ac.uk  
**COMMENT** BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA sequencing project.  
This sequence is from the BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection, from a library constructed by Elizabeth Bosch. cDNA was prepared from RNA extracted from brain, and poly A-trimmed. EcoRI-NotI cut cDNA was then ligated into the vector. Vector: pBluescript II KS(+); Site\_1: EcoRI; Site\_2: NotI  
Host: Escherichia coli DH10B.  
Location/Qualifiers  
1..1591  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="White Leghorn, HiseX"  
/db\_xref="taxon:9031"  
/clone="CHEST117m23"  
/clone\_lib="CSEQCML24"  
/dev\_stage="16 days"  
**ORIGIN**  
Alignment Scores:  
Pred. No.: 8,14e-83 Length: 1591  
Score: 889.00 Matches: 178  
Percent Similarity: 97.35% Conservative: 6  
Best Local Similarity: 94.18% Mismatches: 5  
Query Match: 95.49% Indels: 0  
DB: 5 Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x BX934715 (1-1591)  
Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLeuLysThrGlyValValPheGlyValA 20  
Db 185 TCAGTTGTTGACCTCTTTACTGCGAGACATTAAAGAAGACAGAGTGGTTTGGTGCC 244  
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 245 AGCTTGTTCCTGCTCTCTATTAAACAGTGTTCAGCATCGTGAGCGGTGACAGCTTACATT 304  
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 305 GCCTTGCCCTCGCTTCTCTGTGACCATCAGCTTTAGGATATACAAAGGAGTTATCCAGGCA 364  
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 365 ATCCAAAGTCCGATGAAGGCCATCCATTATAGGCTTACTTGGAGTCTGATGAGCTGTG 424  
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValenCysThrIle 100  
Db 425 TCTGAAGAGCTGATTCAAGAATAACAGAGTGTGTGCTGCTCATCAACAGGCACAGTC 484  
Qy 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
Db 485 AAGAGAGCTGAGAGCCCTCTCTCGTTGATGACTTGGTTCATCTCTGAAGTTTCAGTG 544



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Db      1288 CCTGGATTGAAGCGCAAGCAGAT 1311
RESULT 88
BX933922
LOCUS   BX933922      1363 bp      mRNA      linear      VRT 02-FEB-2004
DEFINITION Gallus gallus finished cDNA, clone CHEST1198.
ACCESSION BX933922
VERSION   BX933922.1 GI:41634450
KEYWORDS . Gallus gallus (chicken)
SOURCE    Gallus gallus
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
          Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 1363)
AUTHORS Boardman,P.E., Bonfield,J.K., Brown,W.R.A., Carder,C., Chalk,S.E.,
          Croning,M.D.R., Davies,R.M., Francis,M.D., Graham,D.V.,
          Hubbard,S.J., Humphray,S.J., Hunt,P.J., Maddison,M., McLaren,S.R.,
          Niblett,D., Overton,I.M., Rogers,J., Scott,C.E., Taylor,R.G.,
          Tickle,C. and Wilson,S.A.
DIRECT SUBMISSION
Submitted (02-FEB-2004) Sanger Institute, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: chickest@bms.unist.ac.uk
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
sequencing project.
This sequence is from the
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection,
from a library constructed by Elizabeth Bosch. cDNA was prepared
from RNA extracted from cerebrum, and poly A-trimmed. EcoRI-NotI
cut cDNA was then ligated into the vector. Vector: pBluescript II
KS(+); Site 1: EcoRI; Site 2: NotI Host: Escherichia coli DH10B.
FEATURES             Location/Qualifiers
     source            1..1363
                        /organism="Gallus gallus"
                        /mol_type="mRNA"
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                        /db_xref="taxon:9031"
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ORIGIN
Alignment Scores:
Pred. No.:      1.76e-82      Length:      1363
Score:          885.00      Matches:    177
Percent Similarity: 97.34%      Conservative: 6
Best Local Similarity: 94.15%      Mismatches: 5
Query Match:    95.06%      Indels:     0
DB:              .5          Gaps:       0

US-09-830-972-29_COPY_990_1178 (1-189) x BX933922 (1-1363)

Qy      2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db      177 GTTGTGTACCTCCTTACTGCGAGACATTAAAGACAGAGGTGGTCTTGGTGCCAGC 236
Qy      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db      237 TTGTTCTCGCTGCTCTCAATTAACAGTGTTCAGCATCGTGAGCGTACAGCTTACATGCC 296
Qy      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db      297 TTGGCCCTGCTTCTGTGCCATCAGCTTTAGGATATACAGGGAGTTATCCAGGCATC 356
Qy      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db      357 CAAAGTCCGATGAAGGCCATCCATTAGGGCTTACTTGGAGTCTGTAGTGTGTCT 416
Qy      82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db      417 GAAGAGCTGATTGAGAAATACAGACAGTGTGTGCTTGTGTGTCATCAACGGCACAGTCAAG 476
Qy      102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121

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Db      477 GAGCTGAGACGCCCTCTCTCGTTGATGACTTGGTTGATTCTCTGAAGTTTGACGTGTTG 536
Qy      122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
Db      537 ATGTGGGTGTTTCACTACGTAGCTTGGTGGCTTGTATATGTTGTTGACATTACTGATCGGT 596
Qy      142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db      597 TTGATTTCCGCTGTTTCAGTGTCTCTGTTATTTATGAGACATCAGCCCGACATCGACCAT 656
Qy      162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      657 TATTTGGGAGCTAGTGAACAAGACGTCAAAGATGCGTGGCAAGATCCAAAGCAAGATC 716
Qy      182 ProGlyLeuLysArgLysAlaGlu 189
Db      717 CCTGGCTGAAGCGCAAAACTGAG 740
RESULT 89
CR353502
LOCUS   CR353502      1578 bp      mRNA      linear      VRT 11-MAR-2004
DEFINITION Gallus gallus finished cDNA, clone CHEST12704.
ACCESSION CR353502
VERSION   CR353502.1 GI:45424789
KEYWORDS . Gallus gallus (chicken)
SOURCE    Gallus gallus
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
          Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 1578)
AUTHORS Boardman,P.E., Bonfield,J.K., Brown,W.R.A., Carder,C., Chalk,S.E.,
          Croning,M.D.R., Davies,R.M., Francis,M.D., Graham,D.V.,
          Hubbard,S.J., Humphray,S.J., Hunt,P.J., Maddison,M., McLaren,S.R.,
          Niblett,D., Overton,I.M., Rogers,J., Scott,C.E., Taylor,R.G.,
          Tickle,C. and Wilson,S.A.
DIRECT SUBMISSION
Submitted (09-MAR-2004) Sanger Institute, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: chickest@bms.unist.ac.uk
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
sequencing project.
This sequence is from the
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection,
from a library constructed by Elizabeth Bosch. cDNA was prepared
from RNA extracted from cerebrum, and poly A-trimmed. EcoRI-NotI
cut cDNA was then ligated into the vector. Vector: pBluescript II
KS(+); Site 1: EcoRI; Site 2: NotI Host: Escherichia coli DH10B.
FEATURES             Location/Qualifiers
     source            1..1578
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                        /dev_stage="adult"
ORIGIN
Alignment Scores:
Pred. No.:      2.1e-82      Length:      1578
Score:          885.00      Matches:    177
Percent Similarity: 97.34%      Conservative: 6
Best Local Similarity: 94.15%      Mismatches: 5
Query Match:    95.06%      Indels:     0
DB:              5          Gaps:       0

US-09-830-972-29_COPY_990_1178 (1-189) x CR353502 (1-1578)

Qy      2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db      174 GTTGTGTACCTCCTTACTGCGAGACATTAAAGACAGAGGTGGTCTTGGTGCCAGC 233

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QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
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Db 234 TTGTTCTCTGCTCTCTATTAAACAGTGTTCAGCATCGTGAGCGTGACAGCTTACATTCGC 293
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|
|
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
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|
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Db 294 TTGGCCCTGCTTCTCTGTGACCATCAGCTTTAGGATATACAGGAGGTTATCCAGGCAATC 353
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QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
|
|
|
Db 354 CAAAGTCCGATGAAGGCCATCCATTTAGGGCTTACTTGGAGTCTGATGTAGTGTCT 413
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QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
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QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
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RESULT 90
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LOCUS Gallus gallus RTN4-C (RTN4) mRNA, complete cds.
DEFINITION
ACCESSION AY164737
VERSION AY164737.1 GI:32331274
KEYWORDS
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
REFERENCE
AUTHORS Certie,T., Klinger,M., Stuermer,C.A. and Schwab,M.E.
TITLE A reticular rhapsody: phylogenetic evolution and nomenclature of the RTN/Nogo gene family
JOURNAL PASEB J. 17 (10), 1238-1247 (2003)
PUBMED 12832288
REFERENCE
AUTHORS Certie,T. and Schwab,M.E.
TITLE Direct Submission
JOURNAL Submitted (16-OCT-2002) Brain Research Institute and Department Biology, University of Zurich and ETH Zurich, Winterthurerstr.190, Zurich 8057, Switzerland
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Query Match: 94.74% Indels: 0
DB: 5 Gaps: 0

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Db 339 CAAAGTCCGATGAAGGCCATCCATTTAGGGCTTACTTGGAGTCTGATGTGTGTCT 398
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RESULT 91
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LOCUS Xenopus laevis RTN4.1-A3 (RTN4) mRNA, complete cds; alternatively
spliced.
DEFINITION
ACCESSION AY316195
VERSION AY316195.1 GI:34809221
KEYWORDS
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Xenopodinae; Xenopus; Xenopus.

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REFERENCE
AUTHORS      1 (bases 1 to 3967)
Klinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hannbeck von
Hanwehr,S., Petrausch,B., Oertle,T., Schwab,M.E. and Stuermer,C.A.
TITLE        Identification of two NOGO/RTN4 genes and analysis of Nogo-A
JOURNAL      Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
PUBMED       15019938
REFERENCE    2 (bases 1 to 3967)
AUTHORS      Klinger,M., Diekmann,H., Heinz,D., Hirsch,C., Hannbeck von
              Hanwehr,S., Petrausch,B., Oertle,T., Schwab,M.E. and
              Stuermer,C.A.O.
TITLE        Direct Submission
JOURNAL      Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,
              Universitaetstrasse 10, Konstanz 78457, Germany
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Query Match:  83.89%      Indels:    0
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QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
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QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 604 ATCCAGAAAGTCAGAGGAAGGACCCATTCAGATCCATCTTGGAGTCCCAACCTGGCGGTG 663
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
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RESULT 96
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DEFINITION
ACCESSION BC059960.1 GI:37747766
VERSION MGC.
KEYWORDS Xenopus laevis (African clawed frog)
SOURCE Xenopus laevis
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
REFERENCE 1 (bases 1 to 1512)
AUTHORS Klein, S.L., Strausberg, R.L., Wagner, L., Pontius, J., Clifton, S.W.
and Richardson, P.
TITLE Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative
JOURNAL Dev. Dyn. 225 (4), 384-391 (2002)
PUBMED 12454917
REFERENCE 2 (bases 1 to 1512)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
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Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
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Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
TITLE Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 3 (bases 1 to 1512)
AUTHORS Klein, S. and Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (10-OCT-2003) National Institutes of Health, Xenopus Gene
Collection (XGC), National Institute of Child Health and Human
Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD
20892-7510, USA
REMARK NIH-MGC Project
COMMENT Contact: XGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Igor Dawid
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Ahter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
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Young, A., Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found
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Series: IRAC Plate: 128 Row: c Column: 9

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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

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US-09-830-972-29 COPY 990 1178 (1-189) X BC059960 (1-1512)

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 AV316192 1543 bp mRNA linear VRT 25-MAY-2004  
 LOCUS Xenopus laevis RTN4.1-C (RTN4) mRNA, complete cds; alternatively  
 DEFINITION spliced.  
 ACCESSION AV316192  
 VERSION AV316192.1 GI:34809215  
 KEYWORDS  
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 Xenopus laevis (African clawed frog)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 Xenopodinae; Xenopus; Xenopus.  
 REFERENCE 1 (bases 1 to 1543)  
 AUTHORS Klinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hannbeck von  
 Hanwehr, S., Petrusch, B., Oertle, T., Schwab, M.E. and Stuermer, C.A.  
 TITLE Identification of two NOGO/RTN4 genes and analysis of Nogo-A  
 expression in Xenopus laevis  
 JOURNAL Mol. Cell. Neurosci. 25 (2), 205-216 (2004)  
 PUBMED 15019338  
 PUBLISHED 2 (bases 1 to 1543)  
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 AUTHORS Klinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hannbeck von  
 Hanwehr, S., Petrusch, B., Oertle, T., Schwab, M.E. and  
 Stuermer, C.A.O.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz,  
 Universitaetsstrasse 10, Konstanz 78457, Germany  
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QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 288 TTGTTCTCTGCTCTCTGAGTGTTGTTGAGTATGTGAGGTGCTCGCTTATATGTC 347
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 348 CTGGCCCTGCTCTCCGTCACCATCAGTTTAAAGATATACAAAGGAGTTCCTGCAGCCATC 407
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 408 CAGAAAGTCAGAGGAAGGACACCATTCAGATCCATCTTGGAGTCCAAACCTGGCGGTGCCA 467
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db 468 GAGGATCTGCTCAGAAATCTGCAATGTGGCCCTGAACCATGTCAACTGCACAGTCAAG 527
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 528 GAGCTGGGACCTCTCTCTGTAGAGACCTGGTGGATTCCTGAAGTTTGCAGTATG 587
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 588 ATGTGGGTCTTACCTATATGTCCTTGTTCATATGAGTGTCTCACCTGCTCATTTGGCA 647
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 648 CTGATTTCTCTGTCATTTCTGTCATTTAAGAGCATCAGACTCAAGTGGATCAC 707
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 708 TACCTGGCACTCGTAAACAGAAATCTCAAGAGCACATCAGACCTGATCTCTCTAAAGTT 767
QY 182 ProGlyLeuLysArgLysAlaGlu 189
Db 768 CCCGGGCTGAAACGCAAGCTGAA 791
RESULT 98
AY316194
LOCUS
DEFINITION
Xenopus laevis RTN4.1-B1 (RTN4) mRNA, complete cds; alternatively spliced.
ACCESSION
AY316194
VERSION
AY316194.1 GI:34809219
KEYWORDS
Xenopus laevis (African clawed frog)
ORGANISM
Xenopus laevis
REFERENCE
1 Klinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hambeck von Hanwehr, S., Petrusch, B., Oertle, T., Schwab, M.E. and Stuermer, C.A. Identification of two NOGO/RTN4 genes and analysis of Nogo-A expression in Xenopus laevis
Mol. Cell. Neurosci. 25 (2), 205-216 (2004)
15019938
2 (bases 1 to 1701)
AUTHORS
Klinger, M., Diekmann, H., Heinz, D., Hirsch, C., Hambeck von Hanwehr, S., Petrusch, B., Oertle, T., Schwab, M.E. and Stuermer, C.A.O.
TITLE
Direct Submission
JOURNAL
Submitted (05-JUN-2003) Dept. of Biology, University of Konstanz, Universitaetsstrasse 10, Konstanz 78457, Germany
PUBMED
Location/Qualifiers
1. .1701
FEATURES
source
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Best Local Similarity: 78.31% Mismatches: 19  
Query Match: 80.77% Indels: 0  
DB: 5 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AV316190 (1-3943)

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Db 2648 TCAGTTGCGATCTGATTACTGCGCGGACATTAGAGATCTGGAGTGGTGTGGGGCG 2707  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 2708 AGCTTGTTCTCTCTACTGTTCTGAGTGTGTTGAGTATTGTCAGTGTACTCGCTTATATT 2767  
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QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleuGluSerGluValAlaIle 80  
Db 2828 ATCCAGAAGTCTGAGGAAGACACCCCAATTCAGGTCCATCTTGGAGTCCAACCTGGCGCTG 2887  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 2888 CCGGAGGACGTGGTCCAGAAACCTGCACCGTGGCCCTGAATCAGGTCAATCGCACAGTC 2947  
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 2948 GCTGAGCTCGGGCGCTCTTCCTCGTAGAAGACTTGGTGATTCCCTCAAGTTTGCAGTA 3007  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 3008 TTGATGTGGGTCTTCATCTATATATCGGTGCTGTTTAAATGGCCCTGACCTCCTCATTTG 3067  
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160

Db 3068 GCTCTCATTTCCCTGTTTCAGTATTCTGTATTATGAAGGCATCAGACTCAAGTGGAT 3127  
QY 161 HistyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3128 CACTATCTGGCGCTGATAACAAGAACCCTGAAAAATACTTTCAGACCTGATTTTGGCTAAA 3187  
QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
Db 3188 GTCCCGGGGCTGAAGCGCAAAATCAGAA 3214

Search completed: June 19, 2005, 08:52:40  
Job time : 2797 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 19, 2005, 04:27:16 ; Search time 354 Seconds  
(without alignments)  
3160.540 Million cell updates/sec

Title: US-09-830-972-29\_COPY\_990\_1178  
Perfect score: 931  
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Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- N Geneseq\_16Dec04:\*
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- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
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- 13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	931	100.0	3579	3	Aaz56886 Human MAG
2	931	100.0	3579	4	Aaf90324 Human NOG
3	931	100.0	3579	6	Abk90134 DNA encod
4	931	100.0	3579	6	Abn86601 Human neu
5	931	100.0	3579	12	Ado07886 Human pol

6	931	100.0	3579	12	Adri13965	Adri13965 Human NOG
7	931	100.0	3833	3	AA001174	AA001174 Bovine ne
8	931	100.0	3919	12	ADP45550	ADP45550 Human Nog
9	931	100.0	4053	4	AA509453	AA509453 Human cDN
10	931	100.0	4053	9	ACC81048	ACC81048 Human NOG
11	931	100.0	4053	12	ADP13574	ADP13574 Renal cel
12	931	100.0	4093	3	AAA23454	AAA23454 cDNA enco
13	931	100.0	4632	6	ABV94680	ABV94680 Human pan
14	931	100.0	4632	10	ADG32772	ADG32772 Human DNA
15	931	100.0	4698	8	ABX34563	ABX34563 Human medd
16	931	100.0	4789	13	ADR83534	ADR83534 Human ret
17	931	100.0	4822	6	ABS70449	ABS70449 Human bon
18	928	99.7	1758	4	AAF32725	AAF32725 Human sec
19	927	99.6	600	4	AAF90323	AAF90323 Human NOG
20	927	99.6	770	3	AA72983	AA72983 Human NSP
21	927	99.6	799	2	AAV23695	AAV23695 Human NSP
22	927	99.6	1122	3	AAZ56888	AAZ56888 Human MAG
23	927	99.6	1122	4	AAF90325	AAF90325 Human NOG
24	927	99.6	1213	2	AAO4379	AAO4379 Human sec
25	927	99.6	1216	6	ABA05903	ABA05903 Human RTN
26	927	99.6	1599	10	ADI62860	ADI62860 Human apo
27	927	99.6	1610	3	AAZ36230	AAZ36230 cDNA enco
28	927	99.6	1785	12	ADK14166	ADK14166 Human aut
29	927	99.6	2052	6	ABK90133	ABK90133 DNA encod
30	927	99.6	2235	6	ABV94681	ABV94681 Human pan
31	927	99.6	2240	3	AA64406	AA64406 Human NOG
32	927	99.1	1694	4	AAK94408	AAK94408 Human ful
33	923	99.1	1694	12	ADL31137	ADL31137 Full leng
34	921	98.9	1980	4	AAI98079	AAI98079 Human neu
35	918	98.6	991	2	AAI97587	AAI97587 Extended
36	918	98.6	994	12	ADP18854	ADP18854 Human sec
37	914	98.2	2610	11	ADI13056	ADI13056 Human cDN
38	911	97.9	734	12	ADP42781	ADP42781 Mouse CYP
39	908	97.5	3492	12	ADP45571	ADP45571 Rat NogoA
40	908	97.5	4684	3	AA001173	AA001173 Rat neuroi
41	908	97.5	4684	6	ABN86600	ABN86600 Rat neuro
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43	904.5	97.2	3492	12	ADO07888	ADO07888 Mouse pol
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ALIGNMENTS

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DT	25-APR-2000 (first entry)
DE	Human MAGI polypeptide encoding DNA.
KW	MAGI protein; neuroendocrine-specific protein; neuropathy; human;
KW	spinal injury; neuronal degeneration; neuromuscular disorder; cancer;
KW	psychiatric disorder; developmental disorder; inflammatory disorder;
KW	stroke; cytostatic; cerebroprotective; neuroprotective; ds.
OS	Homo sapiens.
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EH	Key
FT	CDS
FT	Location/Qualifiers
FT	1..3579
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FT	/product= "MAGI polypeptide"
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PN	WO200005364-A1.
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PD	03-FEB-2000.
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PF	21-JUL-1999; 99WO-GB002360.
XX	
PR	22-JUL-1998; 98GB-00016024.

PR 19-JUL-1999; 99GB-00016898.  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 PA Michalovich D, Prinjha RK;  
 XX WPI; 2000-182693/16.  
 DR P-PSDB; AAY56967.  
 XX Novel polypeptides related to neuroendocrine-specific proteins and  
 PT polynucleotides useful for diagnosis of various diseases and for  
 PT treatment of cancer and neurological disorders.  
 XX Claim 5; Page 19-20; 35pp; English.  
 XX The invention relates to human MAGI protein, which is similar to  
 CC neuroendocrine-specific protein. The MAGI protein can be expressed by  
 CC standard recombinant methodology. The MAGI polypeptides, polynucleotides  
 CC and antibodies are useful for treating diseases, including neuropathies,  
 CC spinal injury, neuronal degeneration, neuromuscular disorders,  
 CC psychiatric disorders and developmental disorders, cancer, stroke and  
 CC inflammatory disorders. The polynucleotide is also useful for chromosome  
 CC localization and for tissue expression studies. The present sequence  
 CC represents a DNA encoding the human MAGI protein  
 XX  
 SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;

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 Pred. No.: 1.01e-102 Length: 3579  
 Score: 931.00 Matches: 189  
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US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAZ56886 (1-3579)

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 QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 3070 AGCCTATTCTGCTGCTTTTCATTGACAGTATTGAGCATTTGTGAGCGTAAAGCCTACATT 3129  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 3130 GCCTTGGCCCTGCTCTCTGACCATCAGCTTTAGCATATACAAGGCTGTGATCCAAGCT 3189  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 3190 ATCCAGAAATCAGATGAAGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGTCTATA 3249  
 QY 81 SerGluLeuLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
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 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 3310 AAGGAATCAGGCGCCTCTCTTAGTTGATGATTAGTTAGTTCTCTGAAGTTTGAGTG 3369  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 DB 3370 TTGATGTGGGTATTACCTATGTTGGTGGCTTCTTTAATGGTCTGACACTACTGATTTTGG 3429  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 DB 3430 GCTCTCATTTTCATCTTCAGTGTCCTGTTATTATTATGAACGGCATCAGGCGCAGATAGAT 3489  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 3490 CATTATCTAGGACTTGCATAATAAGATGTTTAAAGATGCTATGCTTAAATCCCAAGCAAA 3549

QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
 DB 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

RESULT 2  
 AAF90324  
 ID AAF90324 standard; cDNA; 3579 BP.  
 XX AAF90324;  
 AC AAF90324;  
 XX 23-JUL-2001 (first entry)  
 DT Human NOGO-A cDNA.  
 DE  
 XX NOGO-A; human; chromosome 2p21; neuropathy; spinal injury; brain injury;  
 KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;  
 KW neuromuscular disorder; psychiatric disorder; developmental disorder;  
 KW neuroprotective; nootropic; neuroleptic; antiparkinsonian;  
 KW cerebroprotective; neuroleptic; diagnosis; therapy; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200136631-A1.  
 PN  
 XX 25-MAY-2001.  
 PD  
 XX 14-NOV-2000; 2000WO-GB004345.  
 XX  
 PR 15-NOV-1999; 99GB-00026995.  
 PR 24-JAN-2000; 2000GB-00001550.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX Michalovich D, Prinjha R;  
 PI WPI; 2001-343822/36.  
 DR P-PSDB; AAB82349.  
 DR  
 XX New polypeptide designated NOGO-C is a splice variant of the human NOGO  
 PT gene and may be useful in the treatment of neural disorders including  
 PT Alzheimer's and Parkinson's diseases.  
 PS Disclosure; Page 25-26; 25pp; English.  
 XX  
 CC The present sequence is that of cDNA encoding human NOGO-A (see  
 CC AAB82349). NOGO-A is a previously known splice variant of the human NOGO  
 CC gene on chromosome 2p21. NOGO-A cDNA was obtained by PCR amplification of  
 CC human spinal cord cDNA. The invention relates to a novel splice variant,  
 CC NOGO-C (see AAF90323). It provides NOGO-C polypeptides and  
 CC polynucleotides, and methods for producing such polypeptides by  
 CC recombinant techniques. Also disclosed are methods for utilising NOGO-C  
 CC polypeptides and polynucleotides in the treatment of diseases including  
 CC neuropathies, spinal injury, brain injury, stroke, neuronal degeneration,  
 CC for example Alzheimer's disease and Parkinson's disease, neuromuscular  
 CC disorders, psychiatric disorders and developmental disorders. Also  
 CC provided are methods for identifying agonists and antagonists for use in  
 CC treating conditions associated with NOGO-C imbalance, and diagnostic  
 CC assays for detecting diseases associated with inappropriate NOGO-C  
 CC activity or levels  
 CC  
 XX Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1.01e-102 Length: 3579  
 Score: 931.00 Matches: 189  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAF90324 (1-3579)

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Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrlle 40  
Db 3070 AGCCTATTCTCTGCTCTCTTCATTCAGACATTAATCAGCATTTGAGCGTAACAGCCTACATTT 3129  
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrlsGlyValIleGlnAla 60  
Db 3130 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCT 3189  
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Qy 81 SerGluGluLeuValGlnLysTyrlsSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 3250 TCTGAGGAGTGGTTCAGAGTACAGTAATCTCTCTCTGTCATGTGAAGTTCAGCAGATA 3309  
Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3310 AAGGAATCAGCGGCTCTCTTCTAGTATGATTTAGTTGATTTCTCTGAAGTTGCACTG 3369  
Qy 121 LeuMetTrpValPheThrTyrlsValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 3370 TTGATGTGGTATTACCTATGTTGGTCTGCTGTTGTTAAATGGTCTGACACTACTGATTTTG 3429  
Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrlsGluArgHisGlnAlaGlnIleAsp 160  
Db 3430 GCTCTCATTTCACTCTTCACTGTTCTGATGTTCTGATGATTTAGTTGATTTCTCTGAAGTTGCACTG 3489  
Qy 161 HisTyrlsGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3490 CATATCTAGGACTTGCATTAAGATGTTTAAAGATGCTATGGCTAAATCCAGCAAAA 3549  
Qy 181 IleProGlyLeuLysArgLysAlaGlu 189  
Db 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

RESULT 3  
ABK90134  
ID ABK90134 standard; DNA; 3579 BP.

XX AC ABK90134;  
XX DT 21-OCT-2002 (first entry)  
XX DE DNA encoding human NogoA protein.  
XX KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;  
KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;  
KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;  
KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;  
KW tissue hyper trophy; central nervous system; axon regeneration; NogoA;  
KW Nogo-associated disease; metastasis; gene; ds.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX CDS 1..3579  
XX FT /\*tag= a  
XX FT /product= "Human NogoA protein"  
XX  
XX WO200257483-A2.  
XX  
XX 25-JUL-2002.  
XX  
XX 18-JAN-2002; 2002WO-GB000228.  
XX  
XX 18-JAN-2001; 2001GB-00001312.  
XX (GLAX ) GLAXO GROUP LTD.  
XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Blackstock WP, Hale RS, Prinjha R, Rowley A;  
XX WPI, 2002-599722/64.  
XX P-PSDB; ABG30938.  
XX  
XX Identifying modulators of Nogo or BACE activity for treating acute  
XX neuronal injuries, neoplastic or dysproliferative disorders, comprises  
XX providing and monitoring interaction between Nogo and BACE polypeptides.  
XX  
XX Disclosure; Page 53-58; 69pp; English.  
XX  
XX The present invention relates to a new method of identifying modulators  
XX of Nogo function or BACE activity. The method involves providing Nogo and  
XX BACE polypeptides capable of binding with each other, monitoring the  
XX interaction between these polypeptides, and determining if the test agent  
XX is a modulator of Nogo or BACE activity. The method is useful in treating  
XX acute neuronal injuries, such as spinal or head injury, stroke,  
XX peripheral nerve damage, and in neoplastic (e.g. glioblastomas,  
XX neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.  
XX cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue  
XX hypertrophy) of the central nervous system. The BACE polypeptide is  
XX useful in screening methods to identify agents that may act as modulators  
XX of BACE activity and in particular agents that may be useful in treating  
XX Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,  
XX and the polynucleotide encoding the BACE polypeptide are useful in  
XX manufacturing a medicament for the treatment or prevention of disorders  
XX responsive to the modulation of Nogo activity, in alleviating the  
XX symptoms or improving the condition of a patient suffering from this  
XX disorder, in axon regeneration, or in preventing metastasis or spreading  
XX of a cancer. The polynucleotide may also be an essential component in  
XX assays, a probe, in recombinant protein synthesis, and in gene therapy  
XX techniques. The present nucleic acid sequence encodes the human NogoA  
XX protein of the invention  
XX  
XX SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 1.01e-102 Length: 3579  
Score: 931.00 Matches: 189  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x ABK90134 (1-3579)  
  
Qy 1 SerValValAspLeuLeuTyrlsTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 3010 TCAGTTGTTGACCTCTGCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGGTCC 3069  
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrlle 40  
Db 3070 AGCCTATTCTCTGCTCTCTTCATTCAGACATTAATCAGCATTTGAGCGTAACAGCCTACATTT 3129  
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrlsGlyValIleGlnAla 60  
Db 3130 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCT 3189  
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrlsLeuGluSerGluValAlaIle 80  
Db 3190 ATCCAGAAATCAGATCAAGGCCACCCATTCAGGCGATATCTGGAATCTCAAGTTGCTATA 3249  
Qy 81 SerGluGluLeuValGlnLysTyrlsSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 3250 TCTGAGGAGTGGTTCAGAGTACAGTAATCTCTCTCTGTCATGTGAAGTTCAGCAGATA 3309  
Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3310 AAGGAATCAGCGGCTCTCTTCTAGTATGATTTAGTTGATTTCTCTGAAGTTGCACTG 3369  
Qy 121 LeuMetTrpValPheThrTyrlsValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140

Db 3370 TTGATGGGTATTTACCTATGTTGGTGGCTGCTTTAAATGCTGTGACACTACTGATTTTG 3429  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 Db 3430 GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGGCGCAGATAGAT 3489  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 3490 CATTATCTAGGACTTGCAATAGAAATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAA 3549  
 QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
 Db 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576  
 RESULT 4  
 ID ABN86601 standard; DNA; 3579 BP.  
 AC ABN86601;  
 XX 05-NOV-2002 (first entry)  
 XX Human neurotransmitter receptor protein Nogo encoding DNA.  
 XX Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;  
 KW central nervous system; peripheral nervous system; tranquilizer; Nogo;  
 KW vulnerability; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;  
 KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;  
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;  
 KW neurotransmitter receptor; human; gene; db.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FH 1. 3579  
 CDS /tag= a  
 FT /product= "Nogo"  
 FT /note= "Nogo-A, Nogo-B and Nogo-C"  
 FT  
 XX US2002072493-A1.  
 XX 13-JUN-2002.  
 XX 28-JUN-2001; 2001US-00893348.  
 XX 19-MAY-1998; 98IL-00124500.  
 PR 21-JUL-1998; 98WO-US014715.  
 PR 22-DEC-1998; 98US-00218277.  
 PR 19-MAY-1999; 99US-00314161.  
 XX (YEDA ) YEDA RES & DEV CO LTD.  
 XX Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;  
 PI Moalem G;  
 XX WPI; 2002-607255/65.  
 DR P-PSDB; ABB81078, ABB81079, ABB81080.  
 XX Promoting nerve regeneration and preventing neuronal degeneration in the  
 PT central/peripheral nervous system from injury/disease, comprises  
 PT administering nervous system-specific activated T cells/antigen, or  
 PT analogs/peptides.  
 XX Disclosure; Page 49-53; 93pp; English.  
 XX The invention relates to promoting nerve regeneration or conferring  
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the  
 CC central/peripheral nervous system (NS). The method involves administering  
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its  
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or  
 CC combinations. The method is useful for promoting nerve regeneration and  
 CC preventing neuronal degeneration in central/peripheral nervous system  
 CC from injury/disease, where the injury is spinal cord injury, blunt

CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or  
 CC damages caused by surgery such as tumour excision. The disease is not an  
 CC autoimmune disease or neoplasm. The disease results in a degenerative  
 CC process occurring in either gray or white matter or both. The disease is  
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,  
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and  
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such  
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral  
 CC neuropathies associated with various diseases, including but not limited  
 CC to uremia, porphyria, hypoglycemia, Sjogren Larsson syndrome, acute  
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary  
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption  
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-  
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins  
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia  
 CC telangiectasia, Friedreich's ataxia, amyloid polyneuropathies,  
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's  
 CC disease, or lipoproteinemia. The present sequence represents a DNA  
 CC encoding the human neurotransmitter receptor protein Nogo (Nogo-A, Nogo-B  
 CC and Nogo-C), an example of NS-specific antigen  
 XX  
 SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.01e-102 Length: 3579  
 Score: 931.00 Matches: 189  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x ABN86601 (1-3579)  
 QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
 Db 3010 TCAGTTGTTGACCTCTCTGTACTGGAGAGACATTAGAGACTGGAGTGGTGGTGGCC 3069  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 3070 AGCCTATTCTCTGCTTCTTTCATTGACAGTATTTCAGCATTGTGAGCGTAACAGCTACATT 3129  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 3130 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAAGCT 3189  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 3190 ATCCAGAAATCAGATGAGGCCACCCATTCAGGGCATATCTGGATCTGAAGTTGCTATA 3249  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 Db 3250 TCTGAGGAGTGTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTTCATGTGAACTCGACGATA 3309  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 3310 AAGGAACTCAGCGGCTCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTGCGATG 3369  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 Db 3370 TTGATGTGGGTATTTACCTATGTTGGTGGCTTTGTTTAATGGTCTGCACACTACTGATTTTG 3429  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 Db 3430 GCTCTCATTTCACTCTTCTCAGTGTCTCTGTTATTTATGAACGGCATCAGGGCGCAGATAGAT 3489  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 3490 CATTATCTAGGACTTGCAATAGAAATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAA 3549  
 QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
 Db 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

RESULT 5  
 ADO07886  
 ID ADO07886 standard; cDNA; 3579 BP.  
 XX  
 AC ADO07886;  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Human polynucleotide #65.  
 XX  
 KW Human; gene; ss; fat cell number; fat cell size; obesity; diabetes;  
 KW anorectic; antidiabetic.  
 XX  
 OS Homo sapiens.  
 XX  
 FN US2004071700-A1.  
 XX  
 PD 15-APR-2004.  
 XX  
 PF 09-OCT-2002; 2002US-00267502.  
 XX  
 PR 09-OCT-2002; 2002US-00267502.  
 XX  
 PA (LIFE-) LIFE SCI DEV CORP.  
 XX  
 PI Kim J, Galant R;  
 XX  
 DR WPI; 2004-328526/30.  
 DR P-PSDB; ADO08103.  
 XX  
 PT Identifying compounds that influence fat cell number or size for treating  
 PT or preventing obesity or diabetes by exposing the cell to the agent and  
 PT identifying fat cell number or size relative to cells not exposed to the  
 PT agent.  
 XX  
 PS Claim 1; SEQ ID NO 212; 275pp; English.  
 CC  
 CC The invention relates to a method of identifying compounds that influence  
 CC fat cell number or size comprising providing a cell that expresses a gene  
 CC and an agent, exposing the cell to the agent and identifying fat cell  
 CC number or size relative to cells not exposed to the agent. The method  
 CC also comprises providing an expression vector and an agent, exposing the  
 CC vector to the agent, detecting a change in expression of the gene  
 CC relative to expression of the gene in an expression vector not exposed to  
 CC the agent, treating a subject with the agent and identifying fat cell  
 CC number or size in the subject. The agent comprises an antisense  
 CC oligonucleotide. The subject comprises a mammal, preferably a human. The  
 CC method also comprises providing a polypeptide and an agent, exposing the  
 CC polypeptide to the agent, detecting binding of the agent to the  
 CC subject with the agent and identifying fat cell number or size in the  
 CC subject. The agent comprises an antibody. A method of regulating fat cell  
 CC number or size comprises providing a subject containing fat cells and an  
 CC agent that changes the expression of a gene, and treating the subject  
 CC with the agent under conditions so that fat cell size or number in the  
 CC subject is altered. The method is useful for identifying compounds that  
 CC influence fat cell number or size, for preparing a composition for  
 CC treating or preventing obesity or diabetes. This sequence represents  
 CC human cDNA used in the scope of the invention.  
 XX  
 SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.01e-102 Length: 3579  
 Score: 931.00 Matches: 189  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 12 Gaps: 0  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADO07886 (1-3579)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 DB TCAGTTGTTGACCTCCTCTACTGGAGACACATTAAAGAGACTGGAGTGGTGTGGTGC 3069  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB AGCCTATTCTCTGCTCTTTCATTGACAGTATTTCAGCATTTGTGAGCGTAAACAGCTACATT 3129  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCAAGCT 3189  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB TCTGAGGAGTTGGTTTCAGAGTACAGTAATTTCTGCTCTTGGTTCATGTGAACCTGCACGATA 3309  
 DB ATCCAGAAATCAGATGAAGGCCACCCATTACGGGCATATCTGGATCTGAAGTTGCTATA 3249  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 DB TCTGAGGAGTTGGTTTCAGAGTACAGTAATTTCTGCTCTTGGTTCATGTGAACCTGCACGATA 3309  
 QY 101 LysGluLeuLeuArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
 DB AAGGAACCTCAGCGCCCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGACGAG 3369  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 DB TTGATGGGTATTTACCTATGTTGGTCCCTGTTTAAATGTTCTGACACTACTGATTTTG 3429  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleLeu 160  
 DB GCTCTCATTTCTCCTCTTCTGAGTCTTCTGTTTATTTATGAACGCGCATCAGCGCGCAGATAGAT 3489  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysValLysPheAlaMetAlaLysIleGlnAlaLys 180  
 DB CATTATCTAGGACTTGCATAATGAAGATGTTAAAGATGCTATGGCTAAATAATCCAGCAAAA 3549  
 QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
 DB ATCCCTGGATTGAAGCGCAAGCTGAA 3576  
 RESULT 6  
 ADR13965  
 ID ADR13965 standard; cDNA; 3579 BP.  
 XX  
 AC ADR13965;  
 DT 23-SEP-2004 (first entry)  
 XX  
 DE Human NOGO-A cDNA.  
 KW ss; gene; human; myelin-associated glycoprotein; MAG; neural growth;  
 KW neural regeneration; apoptosis; amyotrophic lateral sclerosis;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease;  
 KW multiple sclerosis; Creutzfeldt-Jacob disease; kuru;  
 KW multiple system atrophy; Lou Gehrig's disease;  
 KW progressive supranuclear palsy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..3579  
 FT /\*tag= a  
 FT /product= "NOGO-A"  
 FT  
 XX US2004121341-A1.  
 XX  
 PD 24-JUN-2004.  
 XX  
 PF 20-DEC-2002; 2002US-00327213.  
 XX  
 PR 20-DEC-2002; 2002US-00327213.  
 XX  
 PA (FILB/) FILBIN M T.





QY 121 LeuMetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuLeu 140  
 DB 3370 TTGATGGGTATTTACCTATGTTGGTGGCTTGTGTTAAAGGCTGACACTACTGATTTG 3429  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 DB 3430 GCTCTCATTTCACTCTTCAGTGTCTGTTATTTATGACGGCATCAGGCACAGATAGAT 3489  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 3490 CATTATCTAGGACTTGCAATAAGATGTTAAAGATGCTATGGCTAAATAATCAAGCAAAA 3549  
 QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
 DB 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

## RESULT 9

AAS09453

ID AAS09453 standard; cDNA; 4053 BP.

AC AAS09453;

XX

DT 26-SEP-2001 (first entry)

XX

DE Human cDNA encoding the Nogo protein.

XX

KW Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein;  
 KW cranial trauma; cerebral trauma; spinal cord injury; stroke;  
 KW demyelinating disease; multiple sclerosis; monophasis demyelination;  
 KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis;  
 KW Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy;  
 KW Pelizaeus-Werzbacher disease; pontine myelinolysis; adrenoleukodystrophy;  
 KW Canavan's disease; metachromatic leukodystrophy; viral infection;  
 KW Krabbe's disease; AB020693; ss.

OS Homo sapiens.  
 XX

FH Key Location/Qualifiers

FT CDS 135..3713

FT /tag= a

FT /product= "Nogo protein"

XX

WO200151520-A2.

XX

PD 19-JUL-2001.

XX

PF 12-JAN-2001; 2001WO-US001041.

XX

PR 12-JAN-2000; 2000US-0175707P.

PR

PR 26-MAY-2000; 2000US-0207366P.

PR

PR 29-SEP-2000; 2000US-0236378P.

XX

XX (UYUA ) UNIV YALE.

XX

XX Strittmatter SM;

XX

XX WPI; 2001-442138/47.

DR

DR P-PSDB; AAU09453.

XX

PT Novel Nogo receptor protein useful for identifying modulator of Nogo  
 PT protein or Nogo receptor protein, which is useful for treating central  
 PT nervous system disorders.  
 PT  
 XX

PS Example 1; Page 95-100; 109pp; English.  
 XX

XX The sequence (Genbank accession number AB020693) encodes the human Nogo  
 CC protein, a 250kDa myelin-associated axon growth inhibitor. The invention  
 CC relates to the use of the nogo receptor, nogo protein, their nucleic  
 CC acids, vectors expressing them and antibodies against them, to isolate  
 CC agents which block nogo receptor mediated axonal growth. The agent is  
 CC useful for treating a central nervous system disorder which is a result  
 CC of cranial or cerebral trauma, spinal cord injury, stroke or a  
 CC demyelinating disease selected from multiple sclerosis, monophasis

CC demyelination, encephalomyelitis, multifocal leukoencephalopathy,  
 CC panencephalitis, Marchiafava-Bignami disease, pontine myelinolysis,  
 CC adrenoleukodystrophy, Pelizaeus-Werzbacher disease, Spongy degeneration,  
 CC Alexander's disease, Canavan's disease, metachromatic leukodystrophy,  
 XX viral infection and Krabbe's disease  
 SQ Sequence 4053 BP; 1189 A; 922 C; 922 G; 1020 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.21e-102 Length: 4053  
 Score: 931.00 Matches: 189  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 4

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAS09453 (1-4053)

QY 1 SerValValAspLeuLeuTyrTyrArgAspIleLysLysThrGlyValValPheGlyAla 20  
 DB 3144 TCAGTTGTTGACCTCTCTGTACTGGAGAGACATTAGAGACTGGAGTGGTGGTGGCC 3203  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 3204 AGCCTATTCTCTGCTCTTTCAITTCAGTATTTCAGCATTTGTCAGCGTAACAGCTACATT 3263  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 3264 GCCTTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGTATCCAAGCT 3323  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 3324 ATCCAGAAATCAGATGAAGCCACCACCTTCAGGCATATCTGGATCTGAAGTTGCTATA 3383  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 DB 3384 TCTGAGGAGTTGGTTTCAGAAGTACAGTAATTCCTGCTCTTGGTCATGTGAACCTGCACGATA 3443  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspLeuLysPheAlaVal 120  
 DB 3444 AAGGAACTCAGCGCCCTCTTCTTAGTATGATGATTTAGTTGATTTCTCTGAAGTTTGAGTG 3503  
 QY 121 LeuMetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuLeu 140  
 DB 3504 TTGATGTGGTATTTACCTATGTTGGTGGCTTGTGTTAAAGTCTGACACTACTGATTTG 3563  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 DB 3564 GCTCTCATTTCACTCTTCAGTGTCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 3623  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 3624 CATTATCTAGGACTTGCAATAAGATGTTAAAGATGCTATGGCTAAATAATCAAGCAAAA 3683  
 QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
 DB 3684 ATCCCTGGATTGAAGCGCAAGCTGAA 3710

## RESULT 10

ACC81048

ID ACC81048 standard; cDNA; 4053 BP.

XX

AC ACC81048;

XX

DT 22-JUL-2003 (first entry)

XX

XX Human NogoA gene.

XX

KW Human; Nogo receptor; NGR; CTS domain; neuroprotective; gene therapy;  
 KW axonal growth; central nervous system; CNS; Nogo; spinal cord injury;  
 KW cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;  
 KW demyelinating disease; multiple sclerosis; monophasic demyelination;  
 KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; gene;



KW ss.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 XX CDS 135..3713  
 FT /\*tag= a  
 FT /product= "Human NogoA"  
 XX  
 XX WO2003031462-A2.  
 XX  
 XX 17-APR-2003.  
 XX  
 XX 04-OCT-2002; 2002WO-US032007.  
 XX  
 XX 06-OCT-2001; 2001US-00972599.  
 XX  
 XX (UYVA ) UNIV YALE.  
 XX Strittmatter SM;  
 XX  
 XX WPI; 2003-393433/37.  
 XX P-PSDB; ABR59667.  
 XX  
 XX New human Nogo receptor polypeptides and nucleic acids, useful for  
 PT decreasing inhibition of axonal growth by a central nervous system  
 PT neuron, or in treating central nervous system disease, disorder or  
 PT injury, e.g. spinal cord injury.  
 XX  
 XX Disclosure; Page 126-131; 148pp; English.  
 XX  
 XX The invention relates to a novel nucleic acid encoding a polypeptide  
 CC comprising amino acid residues 27-309 of a 473 amino acid sequence (P1,  
 CC human Nogo receptor (NGR) NTLR2CT domain), or residues 27-309 of P1 with  
 CC 1-20 conservative amino acid substitutions, and less than a complete CTS  
 CC domain, provided that a partial CTS domain, if present, consists of no  
 CC more than the first 39 consecutive residues. The nucleic acid of the  
 CC invention has neuroprotective activity. The polynucleotide may have a use  
 CC in gene therapy. The nucleic acid is useful for decreasing inhibition of  
 CC axonal growth by a central nervous system (CNS) neuron. The NGR  
 CC polypeptide or an agent inhibits the binding of Nogo to NGR or NGR-  
 CC dependent signal transduction in the central nervous system neuron may be  
 CC used in treating central nervous system disease, disorder or injury, e.g.  
 CC spinal cord injury. Expression of an NGR protein may be associated with  
 CC inhibition of axonal regeneration following cranial, cerebral or spinal  
 CC trauma, stroke or a demyelinating disease, such as multiple sclerosis,  
 CC monophasic demyelination, encephalomyelitis, multifocal  
 CC leukoencephalopathy, panencephalitis, or Krabbe's disease. The present  
 CC sequence is used in the exemplification of the invention  
 XX  
 XX Sequence 4053 BP; 1189 A; 922 C; 922 G; 1020 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 1.21e-102 Length: 4053  
 Score: 931.00 Matches: 189  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0  
 US-09-830-972-29\_copy\_990\_1178 (1-189) x ACC81048 (1-4053)  
 QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
 DB 3144 TCAGTTGTGACCTCTCTGTCTGAGACATTAAGAGACTGGAGTGGTGTGGTGCC 3203  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 3204 AGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTTGAGCGTTACAGCTACATT 3263  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 3264 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCT 3323

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 3324 ATCCAGAAATCAGATGAAGGCCACCCTATTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3383  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 DB 3384 TCTGAGGAGTTGGTTTCAGAGGTACAGTAATCTCTGCTCTTGGTCACTGTGAACCTGCAGATA 3443  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspPheLeuValAspSerLeuLysPheAlaVal 120  
 DB 3444 AAGGAACCTCAGCGCCCTCTTCTTAGTTAGTATTGATTCTCTCTGAAAGTTTCAGTG 3503  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 DB 3504 TTGATGTGGGTATTTACCTATGTTGGTGCCCTGTTTAATGGTCTGACACTACTGATTTTG 3563  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 DB 3564 GCTCTCAITTCACITCTTCAGTGTCTCTGTTATTATGAACGGCATCAGGCACAGATAGAT 3623  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 3624 CATTATCTAGGACTTGCATAATAAGAAATCTTAAAGATGCTATGGCTATAAATCCAGCAAAA 3683  
 QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
 DB 3684 ATCCCTGGATTGAAGCGCAAAAGCTGAA 3710  
 RESULT 11  
 ADP13574  
 ID ADP13574 standard; DNA; 4053 BP.  
 XX  
 AC ADP13574;  
 XX  
 DT 26-AUG-2004 (first entry)  
 XX  
 DE Renal cell carcinoma differentially expressed gene #310.  
 XX  
 KW ds; diagnosis; non-blood disease; solid tumor; gene expression;  
 KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;  
 KW head/neck cancer; differential expression.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2004048933-A2.  
 XX  
 PD 10-JUN-2004.  
 XX  
 PF 21-NOV-2003; 2003WO-US037481.  
 XX  
 PR 21-NOV-2002; 2002US-0427982P.  
 PR 03-APR-2003; 2003US-0459782P.  
 XX  
 PA (AMHP ) WYETH.  
 PA (TWIN/) TWINE N C.  
 PA (BURC/) BURCZYNSKI M E.  
 PA (TREP/) TREPICCHIO W L.  
 PA (DORN/) DORNER A.  
 PA (STOV/) STOVER J A.  
 PA (SLON/) SLONI D K.  
 XX  
 PI Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;  
 PI Sloni DK;  
 XX  
 DR WPI; 2004-460799/43.  
 XX  
 PT Diagnosing non-blood disease such as solid tumor, involves comparing  
 PT differential expression profile of specific genes in peripheral blood  
 PT sample of subject with reference expression profile of specific genes.  
 PS Disclosure; SEQ ID NO 310; 350pp; English.  
 XX

CC The invention relate to a method of diagnosing (M1) non-blood disease  
CC such as solid tumor by providing peripheral blood sample of human having  
CC non-blood disease, and comparing an expression profile of specific genes  
CC in the peripheral blood sample to reference expression profile of the  
CC genes, where each of the genes is differentially expressed in peripheral  
CC blood mononuclear cells (PBMCs) of patients having the disease as  
CC compared to PBMCs of normal humans. The method is useful for diagnosing  
CC non-blood disease such as solid tumor. The solid tumor is chosen from  
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The  
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood  
CC sample is a whole blood sample (claimed). (M1) is useful for identifying  
CC genes that are differentially expressed in peripheral blood samples  
CC isolated at different stages of progression, development or treatment of  
CC RCC and/or other solid tumors. This sequence corresponds to a gene that  
CC is differentially expressed and detected by the method of the invention.  
CC (Note: this sequence is not given as part of the printed specification  
CC but was obtained from WIPO in electronic format at  
CC ftp.wipo./pub/published\_pct\_sequences).

XX SQ Sequence 4053 BP; 1189 A; 922 C; 922 G; 1020 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1-21e-102 Length: 4053  
Score: 931.00 Matches: 189  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADP13574 (1-4053)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 3144 TCAGTGTGTTGACCTCTCTACTGAGAGACATTAAAGAGAGTGGTGTGTGGTCC 3203  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 3204 AGCCTATTCTGCTGCTTTTCATGACAGTATTGAGCATTTGAGCGTAAACGCTACATT 3263  
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60  
Db 3264 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGCTGTGATCCAGCT 3323  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleuGluSerGluValAlaIle 80  
Db 3324 ATCCAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGAAGTTGCTATA 3383  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 3384 TCTGAGGAGTTGGTTTCTGAGAGTACAGTAATCTGCTCTTGGTCAATGTAAGTACGACATA 3443  
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3444 AAGGAATCAGGCGCTCTTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTCAGTG 3503  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 3504 TTGATGTGGGTATTTACCTATGTTGGTGGCTCTTTAATGTTGCTGACACTACTGATTTTG 3563  
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db 3564 GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 3623  
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3624 CATTAATCAGACTTGCATAATAGATGTTAAAGATGCTATGCTAAATCCCAAGCAAAA 3683  
QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
Db 3684 ATCCCTGGATTGAAGCGCAAAAGCTGAA 3710

RESULT 12  
AAA23454

ID AAA23454 standard; cDNA; 4093 BP.  
XX AAA23454;  
AC 19-JUN-2000 (first entry)  
DT cDNA encoding human secreted protein vb22\_1, SEQ ID NO:63.  
XX  
DE Human; secreted protein; cancer; tumour; cardiovascular disorder;  
XX blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;  
KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;  
KW neurodegenerative disease; asthma; contraceptive; ss.  
XX Homo sapiens.  
OS  
FH Key Location/Qualifiers  
FT 152..1006  
FT CDS /tag= b  
FT /product= "Clone vb22\_1 ORF2"  
FT 1048..3729  
FT CDS /tag= a  
FT /product= "Human secreted protein vb22\_1"  
FT  
XX WO200011015-A1.  
XX  
XX 02-MAR-2000.  
PD  
XX 24-AUG-1999; 99WO-US019351.  
PF  
XX 24-AUG-1999; 98US-0097638P.  
PR 24-AUG-1999; 98US-0097659P.  
PR 09-SEP-1999; 98US-0099618P.  
PR 28-SEP-1999; 98US-0102092P.  
PR 25-NOV-1999; 98US-0109978P.  
PR 23-DEC-1999; 98US-0113645P.  
PR 23-DEC-1999; 98US-0113646P.  
PR 23-AUG-1999; 99US-00379246.  
XX  
XX (ALPH-) ALPHAGENE INC.  
XX Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;  
XX WPI: 2000-224657/19.  
XX P-PSDB; AA195012, AA195030.  
XX New secreted or transmembrane proteins and polynucleotides encoding them,  
XX useful for treating neurodegenerative disorders, autoimmune diseases and  
XX cancer.  
XX Claim 72; Page 321-322; 357pp; English.  
XX The invention relates to 40 human secreted proteins (AA194981-Y95020),  
XX and cDNA sequences encoding them (AAA23423-A23462). The secreted proteins  
XX of the invention include those that are thought to be only partially  
XX secreted, i.e., transmembrane proteins. The proteins of the invention may  
XX exhibit one or more activities selected from the following: cytokine  
XX activity; cell proliferation; differentiation; immune modulation;  
XX haematopoiesis regulation; tissue growth activity; activin/inhibin  
XX activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic  
XX activity; anti-inflammatory activity; and tumour inhibition activity. The  
XX proteins may be administered to patients as vaccines, and the nucleotides  
XX may be used as part of a gene therapy regime. Diseases or conditions that  
XX may be treated using the proteins or nucleotides of the invention include  
XX autoimmune diseases; genetic disorders; haemophilia; cardiovascular  
XX diseases; cancer; bacterial, fungal and viral infections, especially HIV;  
XX multiple sclerosis; rheumatoid arthritis; pulmonary inflammation;  
XX Guillain-Barre syndrome; insulin dependent diabetes mellitus; and  
XX allergic reactions such as asthma and anaemia. They may also be used for  
XX treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal  
XX diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease  
XX and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin  
XX activity may additionally be useful as contraceptives. Nucleic acid  
XX sequences of the invention may be used in chromosome mapping, and as a

CC source of diagnostic primers and probes. The present sequence represents  
CC cDNA encoding one of the 40 proteins of the invention  
XX  
SQ Sequence 4093 BP; 1213 A; 926 C; 928 G; 1026 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.22e-102 Length: 4093  
Score: 931.00 Matches: 189  
Percent Similarity: 100.00% Conservativity: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAA23454 (1-4093)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLeuValValPheGlyAla 20  
Db 3160 TCAGTTGTGGACCTCTCTGCTGAGGACATTAAGAAGCTGGAGTGGTGGTGGTGC 3219  
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 3220 AGCCTATTCTCTGCTCTTTCATTGACAGTATTCACAGTTGTGAGGTAAACAGCTACATT 3279  
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 3280 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCT 3339  
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 3340 ATCCAGAAATCAGATGAAGGCCACCATTCAGGGCATATCTGGAATCTGGAAGTTGCTATA 3399  
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 3400 TCTGAGGAGTGGTTCAGAGTACAGTAACTCTCTCTGTCATGTGATGCACTGACGATA 3459  
Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3460 AAGGAACCTCAGCGGCTCTCTCTAGTATGATTTAGTTGATCTCTCAAGTTGTCAGTG 3519  
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 3520 TTGATGTGGGTATTTACCTATGTTGGTGCCTTGTGTTAATGGTCTGACACTACTGATTTG 3579  
Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db 3580 GCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAAACGGCATCAGCGCAAGATAGAT 3639  
Qy 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3640 CATTATCTAGGACTTGGCAATAAAGAAATGTTAAAGATGCTATGGCTTAAATAATCCAGCAAA 3699  
Qy 181 IleProGlyLeuLysArgLysAlaGlu 189  
Db 3700 ATCCCTGGATTGAAGCGCAAGCTGAA 3726

RESULT 13

ABV94680

ID ABV94680 standard; cDNA; 4632 BP.

XX

AC ABV94680;

XX 14-JAN-2003 (first entry)

DT Human pancreatic cancer expressed cDNA SEQ ID NO 53.

XX Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;

XX cytostatic; tumour; gene; ss.

XX Homo sapiens.

OS WO200260317-A2.

XX 08-AUG-2002.

XX

XX

XX

XX

XX

XX

XX 30-JAN-2002; 2002WO-US002781.  
XX  
XX 30-JAN-2001; 2001US-0255305P.  
PR 31-JAN-2001; 2001US-0265682P.  
PR 09-FEB-2001; 2001US-0267568P.  
PR 21-MAR-2001; 2001US-0278651P.  
PR 28-APR-2001; 2001US-0287112P.  
PR 16-MAY-2001; 2001US-0291631P.  
PR 12-JUL-2001; 2001US-0305484P.  
PR 20-AUG-2001; 2001US-0313999P.  
PR 27-NOV-2001; 2001US-0333626P.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;  
XX WPI; 2002-627435/67.  
XX P-PSDB; ABP68600.  
XX  
XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for  
PT diagnosing, preventing and/or treating cancer, particularly pancreatic  
PT cancer.  
XX  
XX Claim 1; SEQ ID NO 53; 300pp + Sequence Listing; English.  
XX  
XX The invention relates to an isolated polynucleotide (I) comprising: (a)  
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)  
CC complements of (a); (c) sequences consisting of at least 20 contiguous  
CC residues of (a); (d) sequences that hybridize to (a), under moderately  
CC stringent conditions; (e) sequences having at least 75% or 90% identity  
CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-  
CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer  
CC in a patient and compositions comprising polypeptides, polynucleotides,  
CC antibodies, fusion proteins, T cell populations and antigen presenting  
CC cells expressing the polypeptide are useful in treating pancreatic cancer  
CC and stimulating an immune response. The polynucleotides can be used as  
CC probes or primers for nucleic acid hybridisation, in the design and  
CC preparation of ribozyme molecules for inhibiting expression of the tumour  
CC polypeptides and proteins in the tumour cells, in vaccines and for gene  
CC therapy. Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 4632 BP; 1398 A; 1013 C; 1011 G; 1210 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.46e-102 Length: 4632  
Score: 931.00 Matches: 189  
Percent Similarity: 100.00% Conservativity: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ABV94680 (1-4632)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLeuValValPheGlyAla 20  
Db 3151 TCAGTTGTGGACCTCTCTGCTGAGGACATTAAGAAGCTGGAGTGGTGGTGGTGC 3210  
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 3211 AGCCTATTCTCTGCTCTTTCATTGACAGTATTCAGCATTTGAGGGTAAACAGCTACATT 3270  
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 3271 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCT 3330  
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 3331 ATCCAGAAATCAGATGAAGGCCACCATTCAGGCAATATCTGGAATCTGGAAGTTGCTATA 3390  
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100

Db 3391 TCTAGGAGTGTCTCAGAAAGTACAGTAATTCCTCTTGGTCATGTGAACGACGATA 3450  
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3451 AAGGAACTCAGGCGCTCTCTTAGTTGATTTAGTTGATCTCTGAAGTTGACGTG 3510  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
Db 3511 TTGATGTGGGTATTTACCTATGTGTGGCTTGTGTTAAATGGTCTGACACTACTGATTTG 3570  
QY 141 AlaLeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnLeuAsp 160  
Db 3571 GCTCTCATTTCACTCTTCAGTGTTCCTGTATTATGAACGGCATCAGGCACAGATAGAT 3630  
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3631 CATTATCTAGGACTTGCANAATAAGATGTTAAGATGCTATGGCTAAATCCAGCAAAA 3690  
QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
Db 3691 ATCCCTGGATTGAAGCGCAAGCTGAA 3717

## RESULT 14

ID ADG32772 standard; DNA; 4632 BP.

AC ADG32772;

XX 26-FEB-2004 (first entry)

DT Human DNA differentially expressed in patients with SLE SeqID96.

XX human; ds; autoimmune; chronic inflammatory disease; SLE;

KW systemic lupus erythematosus; rheumatoid arthritis; cholecystitis;

KW Sjogren's disease; CREST syndrome; scleroderma; ankylosing spondylitis;

KW ulcerative colitis; primary sclerosing cholangitis; appendicitis;

XX diverticulitis; primary biliary sclerosis.

XX Homo sapiens.

XX WO2003090694-A2.

XX 06-NOV-2003.

XX 24-APR-2003; 2003WO-US013015.

XX 24-APR-2002; 2002US-00131827.

XX (EXPR-) EXPRESSION DIAGNOSTICS INC.

XX Wohlgemuth J, Fry K, Woodward R, Ly N;

XX WPI; 2003-877243/81.

XX Diagnosing or monitoring autoimmune and chronic inflammatory diseases, such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative colitis, psoriasis and asthma by detecting the expression level of one or more genes.

PS Claim 18; SEQ ID NO 96; 877pp; English.

XX This invention relates to novel methods for diagnosing and monitoring autoimmune and chronic inflammatory diseases. Specifically, it refers to the identification of genes that have a clinical utility as diagnostic tools for the management of, in particular, patients with systemic lupus erythematosus (SLE) or rheumatoid arthritis (RA). Accordingly, the present invention describes a method for determining the levels of multiple differentially expressed genes of a patient, in a concerted manner, in order to achieve an improved diagnostic assay with sensitivity and specificity for the disease in question. As such, these genes are useful for the diagnosis of various other inflammatory disorders including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma,

CC ankylosing spondylitis, ulcerative colitis, primary sclerosing  
CC cholangitis, appendicitis, diverticulitis, and primary biliary sclerosis.  
CC This polynucleotide is a DNA sequence representing human mRNA that is  
CC differentially expressed in patients with SLE, used in an exemplification  
CC of the invention.

XX Sequence 4632 BP; 1398 A; 1013 C; 1011 G; 1210 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.46e-102 Length: 4632  
Score: 931.00 Matches: 189  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADG32772 (1-4632)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 3151 TCAGTTGTTGACCTCTCTGCTACTGGAGAGACATTAAAGAGACTGGAGTGGTGTGGTCC 3210  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 3211 AGCCTATTCTCTGCTGCTTTTCATTGACAGTATTGACGATTTGAGCGTAACAGCTACATT 3270  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 3271 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCT 3330  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 3331 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGGAATGCTATA 3390  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 3391 TCTGAGGAGTTGGTTTCAGAGGTACAGTAATCTCTCTTGGTCATGTGAACGACGATA 3450  
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3451 AAGGAACTCAGCGCGCTCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTG 3510  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
Db 3511 TTGATGTGGGTATTTACCTATGTGTGGCTTGTGTTAAATGGTCTGACACTACTGATTTG 3570  
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnLeuAsp 160  
Db 3571 GCTCTCATTTCACTCTCTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 3630  
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3631 CATTATCTAGGACTTGCANAATAAGATGTTAAGATGCTATGGCTAAATCCAGCAAAA 3690  
QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
Db 3691 ATCCCTGGATTGAAGCGCAAGCTGAA 3717

## RESULT 15

ID ABX34563

XX ABX34563 standard; cDNA; 4698 BP.

XX AC ABX34563;

XX 13-FEB-2003 (first entry)

XX Human mddt cDNA SEQ ID 124.

XX MDDT; human; disease detection and treatment molecule polypeptide;

XX anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;

XX haemostatic; nephrotropic; antianemic; antiproliferative; hepatotropic;

XX gene therapy; protein replacement therapy; cell proliferative disorder;

XX cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; sarcoma;

anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;  
 Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;  
 psoriasis; hepatitis; gene; ss.  
 Homo sapiens.  
 WO200279449-A2.  
 10-OCT-2002.  
 27-MAR-2002; 2002WO-US0009944.  
 28-MAR-2001; 2001US-0279619P.  
 29-MAR-2001; 2001US-0280067P.  
 29-MAR-2001; 2001US-0280068P.  
 16-MAY-2001; 2001US-0291280P.  
 17-MAY-2001; 2001US-0291829P.  
 17-MAY-2001; 2001US-0291849P.  
 19-JUN-2001; 2001US-0299428P.  
 20-JUN-2001; 2001US-0299776P.  
 20-JUN-2001; 2001US-0300001P.  
 (INCY-) INCYTE GENOMICS INC.  
 Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;  
 Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;  
 Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;  
 Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;  
 Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;  
 WPI; 2003-058431/05.  
 P-PSDB; ABU11573.  
 New purified disease detection and treatment molecule proteins and  
 polynucleotides, useful for diagnosing, treating or preventing cancers  
 (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis  
 or hepatitis.  
 Claim 1; SEQ ID NO 124; 339pp + Sequence Listing; English.  
 This invention describes a novel disease detection and treatment molecule  
 polypeptide (MDPR) which has anti-inflammatory, immunosuppressive,  
 osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,  
 antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides  
 and the polypeptides of the invention can be used for gene therapy,  
 protein replacement therapy and are useful for treating a variety of  
 diseases or conditions. These polypeptides or polynucleotides are  
 particularly useful for diagnosing, treating or preventing cell  
 proliferative disorders (e.g. cancers including adenocarcinoma,  
 leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's  
 disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's  
 syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or  
 hepatitis. ABX34440-ABX34835 encode the MDPR polypeptides represented in  
 ABU11450-ABU11845, described in the disclosure of the invention. NOTE:  
 The sequence data for this patent did not form part of the printed  
 specification, but was obtained in electronic format from WIPO at  
 ftp.wipo.int/pub/published\_pct\_sequences  
 SQ Sequence 4698 BP; 1410 A; 1028 C; 1022 G; 1238 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.49e-102 Length: 4698  
 Score: 931.00 Matches: 189  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 8 Gaps: 0  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x ABX34563 (1-4698)  
 Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
 Db TCAGTTGTTGACCTCCTCTACTGAGAGACATTAGAGACATGGAGTGGTGTGTTGGTCC 3214

Qy 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db AGCCTATTCCTGCTGCTTTTCATTGACAGTATTACAGCATTTGAGCGTACAGCCATCAT 3274  
 Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATATCAAGGGTGTGATCCAAGCT 3334  
 Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db ATCCAGAAATCAGATGAAGGCCACCCATTACAGGCATATCTGGAATCTGAAAGTTGCTATA 3394  
 Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 Db TCTGAGGAGTTGGTTTTCAGAGTACAGTAATTTCTGCTCTTGTTCATGTGAATCTGCAGATA 3454  
 Qy 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
 Db AAGAACTCAGCGCCCTCTCTTAGTTGATGATTAGTTGATTCTCTGAAGTTTGCAGTG 3514  
 Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 Db TTGATGTGGTATTTTACCTATGTTGGTGCCTTGTATATGCTGACACTACTGATTTTG 3574  
 Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 Db GCTCTCATTTTCATCTTCAGTGTTCCTGTTTATTTATGAACGGCATCAGGCACAGATAGAT 3634  
 Qy 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db CATTATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCAACGCAAAA 3694  
 Qy 181 IleProGlyLeuLysArgLysAlaGlu 189  
 Db ATCCCTGGATTGAAGCGCAAGCTGAA 3721  
 RESULT 16  
 ADR83534  
 ID ADR83534 standard; DNA; 4789 BP.  
 AC ADR83534;  
 XX ADR83534;  
 DT 02-DEC-2004 (first entry)  
 XX Human reticulon 4 DNA, target gene of miRNA.  
 DE Human reticulon 4 DNA, target gene of miRNA.  
 XX human; ds; miRNA; microRNA; ontogenesis; cell therapy; cancer;  
 KW immune disease; nerve disorder; amyotrophic lateral sclerosis;  
 KW Parkinson's disease; Alzheimer's disease; inflammatory disease;  
 KW siRNA silencing precursor; cytostatic; immunosuppressive; nootropic;  
 KW neuroprotective; antiinflammatory; immunotherapy; reticulon 4.  
 XX Homo sapiens.  
 OS WO2004076622-A2.  
 XX  
 PN 10-SEP-2004.  
 XX  
 PD 10-FEB-2004; 2004WO-JP001433.  
 XX  
 PF 10-FEB-2003; 2003US-0445829P.  
 PR (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
 PA Taira K, Kawasaki H;  
 XX WPI; 2004-653393/63.  
 DR  
 XX Modulating expression of a target gene in a cell, for treating cancer, an  
 PT immune disease, or a nerve disorder, comprises introducing into the cell  
 PT a polynucleotide that forms a duplex region with an mRNA transcribed from  
 PT the target gene.

XX Claim 9; SEQ ID NO 436; 865pp; English.

XX This invention relates to a novel method for modulating the expression of

CC a target gene in a cell. Specifically, it refers to the introduction into

CC a cell of a polynucleotide that forms a duplex region with an mRNA

CC transcribed from the target gene, where the duplex region comprises a

CC mammalian mRNA target region i.e. a non-coding microRNA (miRNA) that

CC regulates mRNA at a post-transcriptional level. The present invention

CC describes a method for controlling ontogenesis of a mammal, function of a

CC mammalian cell, differentiation of a mammalian cell or viability of a

CC mammalian cell in the post-transcriptional phase, which comprises

CC introducing a plasmid vector comprising a promoter and nucleic acid

CC molecule expressing an mRNA or siRNA silencing precursor to the mRNA.

CC Accordingly, it provides a cell therapy method for treating cancer,

CC immune disease, nerve disorder (e.g. amyotrophic lateral sclerosis,

CC Parkinson's disease, or Alzheimer's disease) or an inflammatory disease

CC by introducing into the cell the mRNA, siRNA silencing precursor to the

CC mRNA or the plasmid vector. As such, they can be developed into

CC pharmaceutical compositions that exhibit cytostatic, immunosuppressive,

CC neurotropic, neuroprotective and antiinflammatory activities and hence can

CC be used for immunotherapy. This polynucleotide sequence is a human target

CC gene whose expression is modulated by miRNAs of the invention.

XX

SQ Sequence 4789 BP; 1422 A; 1052 C; 1075 G; 1240 T; 0 U; 0 Other;

## Alignment Scores:

Align Pred. No.: 1.53e-102 Length: 4789

Score: 931.00 Matches: 189

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 13 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADR83534 (1-4789)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20

DB 3254 TCAGTTGTTGACCTCTCTGACTGGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGC 3313

QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40

DB 3314 AGCCTATTCTGCTGCTTTCATTCAGACATTCAGCATTTGTGAGCGTAAACAGCTACATT 3373

QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIlysglyValIleGlnAla 60

DB 3374 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCT 3433

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleuGluSerGluValAlaIle 80

DB 3434 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3493

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100

DB 3494 TCTGAGAGATTGGTTTCAGAACTACAGATTAATTCCTCTGCTCATGTGACTGCACGATA 3553

QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120

DB 3554 AAGGAATCAGGGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTGAACTGTCAGTGTG 3613

QY 121 LeuMetTrpValPheThrTrpValGlyAlaLeuPheAsnGlyLeuThrIleuLeuIleLeu 140

DB 3614 TTGATGGGTATTTACCTATGTTGGTGGCTTCTTAAATGGTCTGACACTGATGATTTTG 3673

QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160

DB 3674 GCTCTCATTTCACTCTCTTCAGTGTCTCTGTTATTATGAACGGCATCAGGCACAGATAGAT 3733

QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180

DB 3734 CATATCTAGCACTTGCMAATAAGAATGTTAAAGATGCTATGCTAAATATCCAAAGCAAAA 3793

QY 181 IleProGlyLeuLysArgLysAlaGlu 189

DB 3794 ATCCCTGGATTGAAGCGCAAGCTGAA 3820

RESULT 17

ABS70449

ID ABS70449 standard; cDNA; 4822 BP.

XX

AC ABS70449;

XX

DT 27-NOV-2002 (first entry)

XX

DE Human bone remodelling gene #106.

XX

KW Bone remodelling; osteoporosis; human; gene; ss.

XX

OS Homo sapiens.

XX

PN US6426186-B1.

XX

PD 30-JUL-2002.

XX

PF 18-JAN-2000; 2000US-00484970.

XX

PR 18-JAN-2000; 2000US-00484970.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Jones KA, Volkmut W, Walker MG;

XX

DR WPI; 2002-673014/72.

XX

PT A combination of polynucleotides which are co-expressed with genes known

PT to be involved in bone remodeling and osteoporosis are useful in an array

PT for the diagnosis of bone remodeling and osteoporosis associated

PT disorders.

XX

PS Claim 1; Col 283-288; 206pp; English.

XX

CC The invention relates to a combination comprising a number of

CC substantially purified and isolated polynucleotides which are co-

CC expressed with genes known to be involved in bone remodeling and

CC osteoporosis. The invention is used to diagnose disorders associated with

CC bone remodeling or osteoporosis. ABS70344-ABS70512 represent human bone

CC remodelling genes of the invention

XX

SQ Sequence 4822 BP; 1441 A; 1046 C; 1073 G; 1247 T; 0 U; 15 Other;

Alignment Scores:

Align Pred. No.: 1.54e-102 Length: 4822

Score: 931.00 Matches: 189

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ABS70449 (1-4822)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20

DB 3265 TCAGTTGTTGACCTCTCTGACTGGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGC 3324

QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40

DB 3325 AGCCTATTCTCTGCTGCTTTCATTTGACGATTTTCAGCATTTGTGAGCGTAAACAGCTACATT 3384

QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60

DB 3385 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGATATACAGGGTGTGATCCAGCT 3444

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80

DB 3445 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3504







## Alignment Scores:

Pred. No.: 3,62e-103 Length: 770  
 Score: 927.00 Matches: 188  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.57% Indels: 0  
 DB: 3 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAU72983 (1-770)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 DB 114 GTTGTGTACCTCTCTACTCGGAGACATTAAGAAGACTGGAGTGGTGTGGTCCAGC 173  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValAlaTyrIleAla 41  
 DB 174 CTATTCCTGCTGCTTTCATTTGACATGATTCAGCATTTGAGCGTAACAGCTTACATGCC 233  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 DB 234 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 293  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 294 CAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGAATCTGAAAGTTGCTATATCT 353  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 DB 354 GAGGAGTGGTTCAGAAATGACAGTAAATCTGCTCTTGGTCAATGTAAGCTGACGATAAAG 413  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 DB 414 GAATCAGCGCGCTCTCTTAGTGTATGATTTAGTTGATCTCTGAAAGTTGCAAGTTGCTGTTG 473  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
 DB 474 ATGTGGGTATTTACCTATGTTGGTGCCTGTTTAAATGGTCTGCACACTACTGATTTGGCT 533  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 DB 534 CTCAATTCACCTCTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCGACAGATAGATCAT 593  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 DB 594 TATCTAGGACTTGCAATTAAGATGTTAAAGATGCTATGGCTATGCTAAATCCAGCAAAATC 653  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 DB 654 CTGGATTGAAGCGCAAGCTGAA 677

## RESULT 21

AAV23695  
 ID AAV23695 standard; cDNA; 799 BP.

AC AAV23695;

XX 24-JUL-1998 (first entry)

DE Human NSPLP protein A coding sequence.

XX NSPLP; neuroendocrine-specific protein-like protein; human; gene therapy;  
 KW neurodegenerative disease; amyotrophic lateral sclerosis; cancer; ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FT 75..674  
 CDS /tag= a  
 FT /product= "NSPLPA"

XX WO9806841-A2.

XX

PD 19-FEB-1998.

XX 24-JUL-1997; 97WO-US013469.

PR 12-AUG-1996; 96US-00700607.

XX (INCY-) INCYTE PHARM INC.

XX Bandman O, Au-Young J, Goli SK, Hillman J;

XX WPI, 1998-159533/14.

DR P-PsDB; AAWS3947.

PT Human neuro-endocrine-specific protein-like proteins - useful for  
 diagnosis, monitoring and treatment of cancer and neuro-degenerative  
 disease.

PS Claim 3; Page 38-39; 73pp; English.

CC This sequence encodes a human neuroendocrine-specific protein-like  
 protein (NSPLP) of the invention. Recombinant cells transformed with the  
 DNA are used to express the NSPLP proteins, which are used to treat  
 cancer and neurodegenerative diseases such as amyotrophic lateral  
 sclerosis. Also antisense nucleic acids and antagonists of NSPLP can be  
 used to inhibit activity of the NSPLP proteins. Antibodies specific for  
 NSPLP are used for diagnosis and monitoring treatment of diseases  
 associated with NSPLP expression, in usual immunoassays, and to isolate  
 NSPLP from natural sources. The NSPLP proteins, or their fragments can  
 also be used in drug screening to identify NSPLP antagonists. The nucleic  
 acid can be used diagnostically and for monitoring treatment (in  
 hybridisation or amplification assays); to isolate closely related  
 sequences; in gene therapy for both sense and antisense applications  
 (including use of ribozymes) and for mapping the natural genomic sequence

SQ Sequence 799 BP; 218 A; 141 C; 196 G; 242 T; 0 U; 2 Other;

## Alignment Scores:

Pred. No.: 3.81e-103 Length: 799  
 Score: 927.00 Matches: 188  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.57% Indels: 0  
 DB: 2 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAV23695 (1-799)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 DB 108 GTTGTGTACCTCTCTACTCGGAGACATTAAGAAGACTGGAGTGGTGTGGTCCAGC 167  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 DB 168 CTATTCCTGCTGCTTTCATTTGACATGATTCAGCATTTGAGCGTAACAGCTTACATGCC 227  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 DB 228 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 287  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 288 CAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGAATCTGAAAGTTGCTATATCT 347  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 DB 348 GAGGAGTGGTTCAGAAATGACAGTAAATCTCTCTTGGTCAATGTAAGCTGACGATAAAG 407  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 DB 408 GAATCAGCGCGCTCTCTTAGTGTATGATTTAGTTGATCTCTGAAAGTTGCAAGTTGCTG 467  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
 DB 468 ATGTGGGTATTTACCTATGTTGGTGCCTGTTTAAATGGTCTGCACACTACTGATTTGGCT 527

QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 DB 528 CTCATTTCACCTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 587  
 QY 162 TyrLeuGlyLeuAlaGlnIleValLeuValLeuValLeuValLeuValLeuValLeu 181  
 DB 588 TATCTAGGACTTGCACAAATAGAAATGTTAAAGATGCTATGCTAAATCCAAAGCAAAATC 647  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 DB 648 CCTGGATTGAGCGCAAGCTGAA 671

## RESULT 22

AAZ56888  
 ID AAZ56888 standard; DNA; 1122 BP.

AC AAZ56888;

XX 25-APR-2000 (first entry)

DT Human MAGI polypeptide variant encoding DNA.

DE MAGI protein; neuroendocrine-specific protein; neuropathy; human;  
 KW spinal injury; neuronal degeneration; neuromuscular disorder; cancer;  
 KW psychiatric disorder; developmental disorder; inflammatory disorder;  
 KW stroke; cytostatic; cerebroprotective; neuroprotective; variant; ds.  
 XX Homo sapiens.

PH Key Location/Qualifiers

FT CDS 1..1122

FT /\*tag= a

FT /product= "MAGI polypeptide"

PN WO200005364-A1.

PD 03-FEB-2000.

PF 21-JUL-1999; 99WO-GB002360.

PR 22-JUL-1998; 98GB-00016024.

PR 19-JUL-1999; 99GB-00016898.

XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Michalovich D, Prinjha RK;

XX WPI; 2000-182693/16.

DR P-PSDB; AAY56969.

XX Novel polypeptides related to neuroendocrine-specific proteins and  
 PT polynucleotides useful for diagnosis of various diseases and for  
 PT treatment of cancer and neurological disorders.

XX Claim 5; Page 21-22; 35pp; English.

XX The invention relates to human MAGI protein, which is similar to  
 CC neuroendocrine-specific protein. The MAGI protein can be expressed by  
 CC standard recombinant methodology. The MAGI polypeptides, polynucleotides  
 CC and antibodies are useful for treating diseases, including neuropathies,  
 CC spinal injury, neuronal degeneration, neuromuscular disorders,  
 CC psychiatric disorders and developmental disorders, cancer, stroke and  
 CC inflammatory disorders. The polynucleotide is also useful for chromosome  
 CC localization and for tissue expression studies. The present sequence  
 CC represents a DNA encoding the human MAGI protein variant

XX Sequence 1122 BP; 224 A; 339 C; 316 G; 243 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 6.13e-103 Length: 1122  
 Score: 927.00 Matches: 188  
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.57% Indels: 0  
 DB: 3 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAZ56888 (1-1122)

QY 2 ValValAspLeuLeuTyrTyrPargAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 DB 556 GTTGTGACCTCCTCTACTGAGAGACATTAAAGAGATGGAGTGGTGTGTTGGTCCAGC 615  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValIleAla 41  
 DB 616 CTATTCTGCTGCTTTTCATTGACAGTATTACAGTATTGAGCGTAAACAGCTACATTGCC 675  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 DB 676 TTGGCCCTGCTCTCTGTGACCATCAGCTTTTAGGATATACAAGGGTGTGATCCAAGCTATC 735  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 736 CAGAAATCAGATGAAGGCCACCCATTTCAGGCATATCTGGAATCTGAAGTTGCTATATCT 795  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 DB 796 GAGGAGTTGGTTCAGAGGTACAGTAATCTCTGCTTGGTTCATGTGAACGACGATAAAG 855  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 DB 856 GAACTCAGCGGCTCTCTCTTAGTGTAGTATTTAGTTGATTCTCTGAAGTTTCAGTGTG 915  
 QY 122 MetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
 DB 916 ATGTGGGTATTTACCTATGTTGGTCTGTTTAAATGGTCTGACACTACTGATTTGGCT 975  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 DB 976 CTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGCGCATCAGGCACAGATAGATCAT 1035  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 DB 1036 TATCTAGGACTTGCACAAATAGAAATGTTAAAGATGCTATGCTTAAATCCAAAGCAAAATC 1095  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 DB 1096 CCTGGATTGAGCGCAAGCTGAA 1119

## RESULT 23

AAF90325

ID AAF90325 standard; cDNA; 1122 BP.

XX AAF90325;

XX 23-JUL-2001 (first entry)

XX Human NOGO-B cDNA.

XX NOGO-B; human; chromosome 2p21; neuropathy; spinal injury; brain injury;  
 KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;  
 KW neuromuscular disorder; psychiatric disorder; developmental disorder;  
 KW neuroprotective; neurotropic; neuroleptic; antiparkinsonian;  
 KW cerebroprotective; neuroleptic; diagnosis; therapy; ss.

XX Homo sapiens.

XX WO200136631-A1.

XX 25-MAY-2001.

XX 14-NOV-2000; 2000WO-GB004345.

XX 15-NOV-1999; 99GB-00026995.

XX 24-JAN-2000; 2000GB-00001550.

XX

PA (SMIK ) SMITHKLINE BEECHAM PLC.

XX Michalovich D, Prinjha R;

XX WPI; 2001-343822/36.

DR P-PSDB; AAB82350.

XX

PT New polypeptide designated NOGO-C is a splice variant of the human NOGO  
PT gene and may be useful in the treatment of neural disorders including  
PT Alzheimer's and Parkinson's diseases.

XX Disclosure; Page 27; 25pp; English.

XX The present sequence is that of cDNA encoding human NOGO-B (see  
CC AAB82350). NOGO-B is a previously known splice variant of the human NOGO  
CC gene on chromosome 2p21. The invention relates to a novel NOGO gene  
CC splice variant, NOGO-C (see AAF90323). It provides NOGO-C polypeptides  
CC and polynucleotides, and methods for producing such polypeptides by  
CC recombinant techniques. Also disclosed are methods for utilizing NOGO-C  
CC polypeptides and polynucleotides in the treatment of diseases including  
CC neuropathies, spinal injury, brain injury, stroke, neuronal degeneration,  
CC for example Alzheimer's disease and Parkinson's disease, neuromuscular  
CC disorders, psychiatric disorders and developmental disorders. Also  
CC provided are methods for identifying agonists and agonists for use in  
CC treating conditions associated with NOGO-C imbalance, and diagnostic  
CC assays for detecting diseases associated with inappropriate NOGO-C  
CC activity or levels

XX SQ Sequence 1122 BP; 224 A; 339 C; 316 G; 243 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6.13e-103 Length: 1122  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAF90325 (1-1122)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 556 GTTGTGACCTCTGTACGAGACATTAAGAAGACTGGAGTGGTGTGGTGCCAGC 615  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 616 CTATTCTGCTGCTTTCATTGACAGTATTCAGCATTTGGAGCGTAACAGCTACATTGCC 675  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 676 TTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 735  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 736 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGGAAGTTGCTATATCT 795  
QY 82 GluGluLeuValGlnIleTyrSerAsnSerAlaLeuGlyHisValAsnCyethrIleLys 101  
DB 796 GAGGAGTGGTTCAGAAATACAGTAAATCTGCTTTGTCATGTGAACCTGCACGATAAAG 855  
QY 102 GluLeuAtgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 856 GNACTCAGCGGCTCTTCTTAGTTGATGATTTAGTTGATTTCTGGAAGTTTGCAGTGTG 915  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeuAla 141  
DB 916 ATGCGGTATTTACCTATGTTGGTCCCTGTTTATGCTGTGACACTACTGATTTGGCT 975  
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
DB 976 CTCATTTTCACCTTCAGTGTTCCTGTTTATGTAACGGCATCAGGCACAGATAGATCAT 1035  
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

Db 1036 TATCTAGGACTTGCAATAAGATGTTAAAGATGCTATGCTATAAATCCAGCAAAATC 1095  
QY 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 1096 CCTGGATTGAAGCGCAAAAGCTGAA 1119  
RESULT 24  
AAX04379  
ID AAX04379 standard; DNA; 1213 BP.  
XX AC AAX04379;  
XX DT 13-APR-1999 (first entry)  
XX DE Human secreted protein gene 69 clone HAGFT48.  
XX KW Human; secreted protein; fusion protein; gene therapy; protein therapy;  
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;  
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
XX OS Homo sapiens.  
XX FN WO9856804-A1.  
XX PD 17-DEC-1998.  
XX PF 11-JUN-1998; 98WO-US012125.  
XX PR 13-JUN-1997; 97US-0049547P.  
PR 13-JUN-1997; 97US-0049548P.  
PR 13-JUN-1997; 97US-0049549P.  
PR 13-JUN-1997; 97US-0049550P.  
PR 13-JUN-1997; 97US-0049556P.  
PR 13-JUN-1997; 97US-0049606P.  
PR 13-JUN-1997; 97US-0049607P.  
PR 13-JUN-1997; 97US-0049608P.  
PR 13-JUN-1997; 97US-0049610P.  
PR 13-JUN-1997; 97US-0049611P.  
PR 13-JUN-1997; 97US-0050901P.  
PR 13-JUN-1997; 97US-0052989P.  
PR 08-JUL-1997; 97US-0051919P.  
PR 18-AUG-1997; 97US-0055984P.  
PR 12-SEP-1997; 97US-0058665P.  
PR 12-SEP-1997; 97US-0058668P.  
PR 12-SEP-1997; 97US-0058669P.  
PR 12-SEP-1997; 97US-0058715P.  
PR 12-SEP-1997; 97US-0058971P.  
PR 12-SEP-1997; 97US-0058972P.  
PR 12-SEP-1997; 97US-0058975P.  
PR 02-OCT-1997; 97US-0060834P.  
PR 02-OCT-1997; 97US-0060841P.  
PR 02-OCT-1997; 97US-0060844P.  
PR 02-OCT-1997; 97US-0060865P.  
PR 02-OCT-1997; 97US-0061059P.  
PR 02-OCT-1997; 97US-0061060P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Moore PA, Shi Y, Rosen CA, Ruben SM, Lafleur DW, Olsen HS;  
PI Ebner R, Brewer LA, Young P, Greene JM, Ferrie AM, Yu G, Ni J;  
PI Feng P;  
XX WPI; 1999-080881/07.  
DR P-PSDB; AAW78194.  
XX New isolated human genes and the secreted polypeptides they encode -

PT useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.

XX  
PS Claim 1; Page 235-236; 380pp; English.

This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AA04302) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 86 novel genes and their fragments (nucleic acid sequences: AA04311-X04410; amino acid sequences AA078126-W8225) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of, new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed in (see AA04311 for described uses)

Sequence 1213 BP; 335 A; 222 C; 297 G; 355 T; 0 U; 4 Other;

```

Alignment Scores:
Pred. No.:      6,848-103      Length:      1213
Score:          927.00        Matches:      188
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    99.57%         Indels:       0
DB:             2             Gaps:        0

```

US-09-830-972-29 COPY 990 1178 (1-189) x AAX04379 (1-1213)

Qy	2	ValValAspLeuLeuTyrTrrpArgAspIleLysLysThrGlyValValPheGlyAlaSer	21
Db	248	GTGTGTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTGGTGCCACG	307
Qy	22	LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla	41
Db	308	CTATTCTCGCTGCTTTCATTGACAGTATTTCAGCATTGTGAGCGTAAACGCTACATTGCC	367
Qy	42	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle	61
Db	368	TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC	427
Qy	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer	81
Db	428	CAGAAATCAGATGAAGGCCACCCCATTTCAAGGCATATCTGGAAATCTCAAGTTCCTATATCT	487
Qy	82	GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys	101
Db	488	GAGGAGTTGGTTCAGAGTACAGTAATTTCTGCTCTTGGTCATGTGACTGCACGATAAAG	547
Qy	102	GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu	121
Db	548	GAACCTCAGCGCCCTCTCTTAGTTCATGATTAGTTGATTCCTCAAGTTTGCAGTGTG	607
Qy	122	MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla	141
Db	608	ATGTGGGTATTTACCTATGTGTGGTGCTGTGTTAATGTGCTCAGACTACTGATTTTGGCT	667
Qy	142	LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis	161
Db	668	CTCATTTTCACCTCTCAGTGTTCCTGTATTATTGAACCGGCATCAGGCACAGATAGATCAT	727
Qy	162	TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle	181
Db	728	TATCTAGAGCTTGCAATAAGAAATGTTAAAGATGCTATGGCTAAAATCCAGCAAAAATC	787
Qy	182	ProGlyLeuLysArgLysAlaGlu	189
Db	788	CCTGGATTGAAGCGCAAGCTGAA	811

RESULT 25

ABA05903	US-09-830-972-29_COPY_990_1178 (1-189) x ABA05903
ID	ABA05903 standard; cDNA; 1216 BP.
XX	
XX	ABA05903;
XX	
DT	04-MAR-2002 (first entry)
XX	
DE	Human RTN4B encoding cDNA SEQ ID NO 3.
XX	
KW	Human; RTN4B; gene; ss.
XX	
OS	Homo sapiens.
XX	
PH	Key Location/Qualifiers
FT	CDS 5..1126
FT	/tag= a
FT	/product= "RTN4B"
XX	
PN	CN1311439-A.
XX	
PD	05-SEP-2001.
XX	
PF	02-MAR-2000; 2000CN-00111791.
XX	
PR	02-MAR-2000; 2000CN-00111791.
XX	
PA	(UYFU-) UNIV FUDAN.
XX	
PI	Yu L, Fu Q, Zhao Y;
XX	
DR	WPI; 2002-049934/07.
DR	P-PSDB; AAM47954.
XX	
PT	Human RTN 4B protein and coding sequence
XX	
PS	Claim 9; Page 20 (Disclosure); 27pp; C
XX	
CC	The invention relates to human RTN4B p
CC	for providing a cDNA sequence of human
CC	RTN4 with RTN family members. The prese
CC	polypeptide encoded by a nucleotide seq
CC	application of the polypeptide and pol
XX	
SQ	Sequence 1216 BP; 256 A; 354 C; 341 G;
Alignment Scores:	
Pred. No.:	6.86e-103
Score:	927.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	99.57%
DB:	6
US-09-830-972-29_COPY_990_1178 (1-189) x ABA05903	
Qy	2 valvalaspLeuLeuTyTtpargaspill
Db	560 GTTGTTGACCTCTGTACTGGAGACAT
Qy	22 LeuPheLeuLeuSerLeuThrValPlp
Db	620 CTATTCCTGCTGCTTTCATGACAGTAT
Qy	42 LeuAlaLeuSerValThrIleSerPh
Db	680 TTGGCCCTGCTCTCTGTGACCATCAGCTT
Qy	62 GlnLysSerAspGluGlyHisProPheA
Db	740 CAGAAATCAGATGAGGCCCAACCCATTCAG
Qy	82 GluGluLeuValGlnLysTySerAsnSe

Alignment Scores:	
Pred. No.:	6.86e-103
Score:	927.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	99.57%
DB:	6
	Gaps: 0
	Indels: 0
	Mismatches: 0
	Conservative: 0
	Matches: 188
	Length: 1216

US-09-830-972-29 COPY 990 1178 (1-189) X ABA05903 (1-1216)

Qy	2	ValValAspLeuLeuTyrTrrpArgAspIleLysIysThrGlyValValPheGlyAlaSer	21
Db	560	GTTGTTGACCTTCCTGTACTGAGAGACATTAAAGAACTGGAGTGGTGTTCGTGGCCAGC	619
Qy	22	LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla	41
Db	620	CTATTCTCGTGCCTTTTCATTGACACGATATTCAGCATTTGTGAGCGTAACAGCCTACACTGGC	679
Qy	42	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle	61
Db	680	TTGGCCCTCGTCTCTGTGACCACTCAGCTTTAGGATATACAGGCGTGTGATCCAAAGCTATC	739
Qy	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer	81
Db	740	CAGAAATCAGATGAAGGCCACCCATTTCAGGCGCATATCTGGAAATCTGAAGTGTCTATATCT	799
Qy	82	GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys	101

Db 800 GAGGAGTGGTTTCAGAGTACAGTAATTCCTGCTTGGTTCATGTGAACCTGCACGATAAAG 859  
Qy 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLeuPheAlaValLeu 121  
Db 860 GAATCAGCGGCTCTTCTTAGTTGATGATTTAGTTGATTTCTGAAGTTTCAGTGTG 919  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
Db 920 ATGTGGTATTTACCTATGTTGGTCCCTGTTGTTTAATGGTCTGCACACTACTGATTTGGCT 979  
Qy 142 LeuLeuSerLeuPheSerValProValLeuTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 980 CTCATTTTCATCTTCAGTGTCTCTCTTATTTATGAACGCGCATFCAGGCACAGATAGATCAT 1039  
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 1040 TATCTAGAGCTTGCATTAAGAAATGTTAAAGATGCTATGGCTAAATTCAGCAAAATC 1099  
Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 1100 CTGGATTGAGCGCAAGCTCAA 1123

RESULT 26  
ADI62860  
ID ADI62860 standard; cDNA; 1599 BP.  
XX AC ADI62860;  
XX DT 22-APR-2004 (first entry)  
XX DE Human apoptosis-associated cDNA SEQ ID 303.  
KW apoptosis; cell death; cytostatic; neuroprotective; immunosuppressive;  
KW antirheumatic; antiarthritic; dermatological; antiinflammatory;  
KW hepatotropic; virucide; nontropic; anticonvulsant; antiparkinsonian;  
KW vasotropic; cerebroprotective; antialcoholic; gene therapy; tumour;  
KW autoimmune disease; degenerative disease; viral infection; leukaemia;  
KW carcinoma; sarcoma; multiple sclerosis; rheumatoid arthritis; diabetes;  
KW lupus; hepatitis; influenza viruses; Alzheimer's disease;  
KW Huntington's disease; Parkinson's disease; reperfusion injury; stroke;  
KW alcoholic liver disease; human; gene; ss.  
XX HO Homo sapiens.  
XX OS  
XX PN WO2003058021-A2.  
XX PD 17-JUL-2003.  
XX PF 13-JAN-2003; 2003WO-EP000270.  
XX PR 11-JAN-2002; 2002DE-01000856.  
XX PA (XANT-) XANTOS BIOMEDICINE AG.  
XX PI Koenig-Hoffman K, Kazinski M, Schaefer R, Kesper B;  
XX WPI; 2003-542134/51.  
XX New nucleic acids involved in apoptosis, useful for diagnosis and  
PT treatment of e.g. tumors and degenerative disease, also related proteins,  
PT antibodies and modulators.  
XX PS Claim 1b; SEQ ID NO 303; 517pp; German.  
XX This invention describes novel nucleic acid molecules that are associated  
CC with apoptosis and encode a polypeptide and are derived from a normalised  
CC gene library (embryonic or liver) or clone collections, and the extent of  
CC apoptosis measured by cell death detection assay or the CPRG assay  
CC (measuring loss of membrane integrity). The products of the invention  
CC have cytostatic, neuroprotective, immunosuppressive, antirheumatic,  
CC antiarthritic, dermatological, antiinflammatory, hepatotropic, virucide,  
CC nontropic, anticonvulsant, antiparkinsonian, vasotropic,  
CC cerebroprotective and antialcoholic activity and can be used for gene

CC therapy. The polynucleotides also related vectors, hosts (or their  
CC extracts), encoded polypeptide (or their receptors) and/or agents that  
CC inhibit their activity (including antisense sequences) are used for  
CC treatment or prevention of tumours, autoimmune or degenerative diseases  
CC and viral infections, specifically leukaemia, carcinoma, sarcoma,  
CC multiple sclerosis, rheumatoid arthritis, diabetes, lupus, or infection  
CC with hepatitis or influenza viruses, Alzheimer's, Huntington's or  
CC Parkinson's diseases, reperfusion injury, stroke and alcoholic liver  
CC disease. Detection of the polynucleotides and derived polypeptides can  
CC also be used for diagnosis of these diseases. This sequence encodes an  
CC apoptosis-associated protein described in the disclosure of the  
CC invention.  
XX SQ Sequence 1599 BP; 354 A; 452 C; 422 G; 371 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 1.01e-102 Length: 1599  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 10 Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADI62860 (1-1599)  
Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 671 GTTGTGACCTCTGTTACTGGAGACATTAAAGACTGGAGTGGTGGTGGCCAGC 730  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 731 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCTTACATTC 790  
Qy 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 791 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCAAGCTATC 850  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 851 CAGAAATCAGATGAAGCCACCCATTCAGGCGCATCTCGAATCTGGAAGTTGCTATATCT 910  
Qy 82 GluLysLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 911 GAGGAGTTGGTTCAGAGTACAGTAATTCCTGCTCTTGGTTCATGTGAACCTGCACGATAAAG 970  
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 971 GAATCAGCGGCTCTCTTCTTAGTTGATTTAGTTGATTTCTCTGAAGTTTCAGTGTG 1030  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
Db 1031 ATGTGGTATTTACTATGTTGGTCCCTTGTAAATGGTCTGCACACTACTGATTTGGCT 1090  
Qy 142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 1091 CTCATTTTCATCTTCAGTGTCTCTGTTATTTATGAACGCGCATFCAGGCACAGATAGATCAT 1150  
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 1151 TATCTAGAGCTTGCATTAAGAAATGTTAAAGATGCTATGGCTAAATTCAGCAAAATC 1210  
Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 1211 CTGGATTGAGCGCAAGCTCAA 1234  
RESULT 27  
AAZ36230  
ID AAZ36230 standard; cDNA; 1610 BP.  
XX AC AAZ36230;  
XX DT 22-FEB-2000 (first entry)  
XX

DE CDNA encoding a bone marrow secreted protein designated BMS112.

XX Bone marrow secreted protein; bone marrow stromal cell; cytokine;

KW cell proliferation; cell differentiation; hematopoiesis; anaemia;

KW myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;

KW erythroid progenitor cell; colony stimulating factor; granulocyte;

KW monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;

KW platelet disorder; thrombocytopenia; hematopoietic stem cell;

KW stem cell disorder; aplastic anaemia; bone differentiation;

KW paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon;

KW ligament; nerve; wound healing; tissue repair; burn; incision; ulcer;

KW bone fracture; cartilage damage; artificial joint; ss.

XX Homo sapiens.

OS

XX

FH Key Location/Qualifiers

FT CDS 132..1253

FT FT /\*tag= a

FT FT /product= "bone marrow secreted protein"

FT polyA\_signal 1516..1521

FT FT /\*tag= b

XX

XX WO9933979-A2.

XX

XX

XX 08-JUL-1999.

XX

XX 18-DEC-1998; 98WO-US027008.

XX

XX 30-DEC-1997; 97US-0068958P.

XX 24-SEP-1998; 98US-0101603P.

XX 30-SEP-1998; 98US-0102540P.

XX

XX (CHIR ) CHIRON CORP.

XX

XX Lin H, Cao L;

XX WPI; 2000-038344/03.

XX P-FSDB; AAY53624.

XX

XX New isolated human polynucleotide and secreted proteins can induce

XX production of other cytokines in certain cell populations.

XX

XX Claim 11; Page 72-74; 120pp; English.

XX

XX AAZ36228-49 encode bone marrow secreted proteins of human bone marrow

XX stromal cells. The proteins can exhibit cytokine, cell proliferation, or

XX cell differentiation activity (either inducing or inhibiting). They can

XX be used to support colony forming cells or factor-dependent cell lines,

XX to regulate hematopoiesis, and to treat myeloid or lymphoid cell

XX deficiencies. In addition, they may be used to support the growth and

XX proliferation of erythroid progenitor cells, and to treat various

XX anaemias. They can have colony stimulating factor (CSF) activity and can

XX be used to support the growth and proliferation of myeloid cells such as

XX granulocytes, monocytes or macrophages, to prevent or treat myelo-

XX suppression, to support the growth and proliferation of megakaryocytes

XX and platelets, thereby allowing prevention or treatment of platelet

XX disorders such as thrombocytopenia, to support the growth and

XX proliferation of hematopoietic stem cells, either in place of or in

XX conjunction with platelet transfusions, to treat stem cell disorders,

XX such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to

XX repopulate the stem cell compartment after irradiation or chemotherapy.

XX They can be used for growth or differentiation of bone, cartilage,

XX tendon, ligament, or nerve tissue, as well as for wound healing and

XX tissue repair and replacement, and in the treatment of burns, incisions

XX and ulcers, to induce cartilage and/or bone growth in circumstances where

XX bone is not normally formed and thus have an application in healing bone

XX fractures and cartilage damage or defects, prophylactic use in fracture

XX reduction and also in the improved fixation of artificial joints

XX

XX Sequence 1610 BP; 354 A; 458 C; 426 G; 372 T; 0 U; 0 Other;

SQ

Alignment Scores:

Pred. No.:

1.02e-102 Length: 1610

Score: 927.00 Matches: 188

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 99.57% Indels: 0

DB: 3 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAZ36230 (1-1610)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleYsThsRgYValValPheGlyAlaSer 21

DB 687 GTTGTGGACCTCCTCTACTGGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGGCCAGC 746

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

DB 747 CTATTTCCTGCTGCTTTTCATTGACAGTATTGACGATTTGAGCGTAAACAGCCCTACATTTGCC 806

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

DB 807 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAGCTATC 866

QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81

DB 867 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTCAAGTTGCTATATCT 926

QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101

DB 927 GAGGAGTTGGTTTCAGAAGTACAGTAATTTCTGCTCTTTGGTCATGTCAACTGCACGATAAG 986

QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121

DB 987 GNACTCAGGGCCCTCTTCTTAGTTGATTTAGTTGATTTCTCTCAAGTTGTCAGTGTG 1046

QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141

DB 1047 ATGTGGGTATTTACCTATGTTGGTGCCTTTGTTTAATGGTCTGACACTACTGATTTGGCT 1106

QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161

DB 1107 CTCATTTCACCTCTTCAGTGTTCCTGTTATTATGAACGCGATCAGGCACAGATGATCAT 1166

QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

DB 1167 TATCTAGGACTTGCATAATAAGAATGTAAAGATGCTATGGCTAAATCCACGCAAAATC 1226

QY 182 ProGlyLeuLysArgLysAlaGlu 189

DB 1227 CCTGGATTGAAGCGCAAGCTGAA 1250

RESULT 28

ADK14166

ID ADK14166 standard; cDNA; 1785 BP.

XX

XX ADK14166;

AC

XX

DT 06-MAY-2004 (first entry)

XX

DE Human autoimmune disorder gene #62.

XX

KW gene; ss; autoimmune disorder; peripheral blood mononuclear cell;

KW rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;

KW type 1 (insulin-dependent) diabetes; human.

XX

OS Homo sapiens.

XX

XX US2003228617-A1.

XX

XX 11-DEC-2003.

PD

XX

XX 16-MAY-2003; 2003US-00439388.

PF

XX

XX 16-MAY-2002; 2002US-0381055P.

PR

XX

XX (UYVA-) UNIV VANDERBILT.

PA

XX PI Anne TM, Olsen NJ;  
XX DR WPI; 2004-061002/06.  
XX PT Detecting an autoimmune disorder in a subject comprising comparing the  
XX PT expression level of each gene determined with a standard, where the  
XX PT comparing detects the presence of an autoimmune disorder in the subject.  
XX PS Claim 10; SEQ ID NO 62; 86pp; English.  
XX CC The invention relates to a method of detecting an autoimmune disorder in  
XX CC a subject comprising obtaining a biological sample, preferably a  
XX CC peripheral blood mononuclear cell, from a subject, determining expression  
XX CC levels of at least two genes in the biological sample, and comparing the  
XX CC expression level of each gene determined with a standard, where the  
XX CC comparison detects the presence of an autoimmune disorder in the subject.  
XX CC The method is useful for detecting or diagnosing an autoimmune disorder,  
XX CC e.g. rheumatoid arthritis, systemic lupus erythematosus, multiple  
XX CC sclerosis, or type 1 (insulin-dependent) diabetes. The present sequence  
XX CC represents one of seventy genes used to detect autoimmune disorders with  
XX CC the described method.  
XX SQ Sequence 1785 BP; 520 A; 316 C; 402 G; 547 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 1.18e-102 Length: 1785  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 12 Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADK14166 (1-1785)  
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 247 GTTGTGACCTCCTGCTGAGAGACATTAAAGACTGGAGTGGTGTGGTCCAGC 306  
QY 22 LeupheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 307 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTTGGAGCGTAAACGCTACATTC 366  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 367 TTGGCCCTGCTCTCTGACCATCATGCTTTAGGATATACAGGGTGTGATCCAGCTATC 426  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 427 CAGAAATCAGATGAAGGCCACCCATTTCAGGCGATATCTGGAATCTGGAAGTTGCTATATCT 486  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
DB 487 GAGGAGTTGGTTTCAGAAATACAGTAATTTCTGCTTGTGTCATGTGAACGACCATTAAG 546  
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 547 GAATCAGGCGCCTCTTCTTGTGATGATTTAGTTGATTTCTGAAAGTTTGCAGTGTG 606  
QY 122 MetTrpValPheThrTyrValGlyValAlaLeuPheAsnGlyLeuThrLeuIleLeuAla 141  
DB 607 ATGTGGGTATTACCTATGTTGGTCTTGTATTAATGCTGCTGACACTACTGATTTGGCT 666  
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
DB 667 CTCATTTTCACCTTCAGTGTTCCTGTTATTTATGAACGGCATTCAGGCGACATGATCAT 726  
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaIle 181  
DB 727 TATCTAGACCTTGCATTAAGATGTTAAAGATGCTATGGCTAAATCAAGCAAAATC 786  
QY 182 ProGlyLeuLysArgLysAlaGlu 189  
|||||

Db 787 CCTGGATTGAAGCGCAAGCTGAA 810  
RESULT 29  
ABK90133  
ID ABK90133 standard; DNA; 2052 BP.  
XX AC ABK90133;  
XX DT 21-OCT-2002 (first entry)  
XX DE DNA encoding human NogoB protein.  
XX KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;  
XX KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;  
XX KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;  
XX KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;  
XX KW tissue hypertrophy; central nervous system; axon regeneration; NogoB;  
XX KW Nogo-associated disease; metastasis; gene; ds.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX FT CDS 67..1188  
XX FT /\*tag= a  
XX FT /product= "Human NogoB protein"  
XX FN WO200257483-A2.  
XX PD 25-JUL-2002.  
XX PF 18-JAN-2002; 2002WO-GB000228.  
XX PR 18-JAN-2001; 2001GB-00001312.  
XX PA (GLAXO) GLAXO GROUP LTD.  
XX PP (SMIK) SMITHKLINE BEECHAM PLC.  
XX PI Blackstock WP, Hale RS, Prinjha R, Rowley A;  
XX DR WPI; 2002-599722/64.  
XX DR P-PSDB; ABG30937.  
XX PT Identifying modulators of Nogo or BACE activity for treating acute  
XX PT neuronal injuries, neoplastic or dysproliferative disorders, comprises  
XX PT providing and monitoring interaction between Nogo and BACE polypeptides.  
XX PS Disclosure; Page 50-52; 68pp; English.  
XX CC The present invention relates to a new method of identifying modulators  
XX CC of Nogo function or BACE activity. The method involves providing Nogo and  
XX CC BACE polypeptides capable of binding with each other, monitoring the  
XX CC interaction between these polypeptides, and determining if the test agent  
XX CC is a modulator of Nogo or BACE activity. The method is useful in treating  
XX CC acute neuronal injuries, such as spinal or head injury, stroke,  
XX CC peripheral nerve damage, and in neoplastic (e.g. glioblastomas,  
XX CC neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.  
XX CC cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue  
XX CC hypertrophy) of the central nervous system. The BACE polypeptide is  
XX CC useful in screening methods to identify agents that may act as modulators  
XX CC of BACE activity and in particular agents that may be useful in treating  
XX CC Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,  
XX CC and the polynucleotide encoding the BACE polypeptide are useful in  
XX CC manufacturing a medicament for the treatment or prevention of disorders  
XX CC responsive to the modulation of Nogo activity, in alleviating the  
XX CC symptoms or improving the condition of a patient suffering from this  
XX CC disorder, in axon regeneration, or in preventing metastasis or spreading  
XX CC of a cancer. The polynucleotide may also be an essential component in  
XX CC assays, a probe, in recombinant protein synthesis, and in gene therapy  
XX CC techniques. The present nucleic acid sequence encodes the human NogoB  
XX CC protein of the invention  
XX SQ Sequence 2052 BP; 511 A; 512 C; 506 G; 523 T; 0 U; 0 Other;

```
Alignment Scores:
Pred. No.: 1.43e-102 Length: 2052
Score: 927.00 Matches: 188
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.57% Indels: 0
DB: 6 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x ABK90133 (1-2052)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
DB 622 GTTGTGACCTCTCTGTGACCATTTAAGAGACTGGAGTGTGTGGTCCAGC 681
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 682 CTATTCTGCTCTTTCAATTCAGCATTTGAGCGTAAACAGCCTACATTGCC 741
QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAlaIle 61
DB 742 TTGGCCCTGCTCTCTGTGACCATTTGAGGATATACAGGGTGTGATCCAAAGCTATC 801
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 802 CAGAAATCAGATGAAGCCACCCATTCAGGCGCATATCTGGATCTGGAATCTGCTATCT 861
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
DB 862 GAGGAGTTGGTTCAGAAAGTACAGTAATTCCTGCTCTTGGTCAATGTAAGTGCAGATAAG 921
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 922 GAATCAGGCGCTCTCTTAGTGTGATGATTTAGTTGATTTCTGGAATCTGAGTGTG 981
QY 122 MetTrpValPheThrTrpValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
DB 982 ATGTGGGTATTTACCTATGTTGTGCTTGTATTAATGGTCTGACATCTGATTTGGCT 1041
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
DB 1042 CTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATTCAGGCACAGATGATCAT 1101
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
DB 1102 TATCTAGGACTTCGAATTAAGATGTTAAAGATGCTATGCTAAATCCAAAGCAAAATC 1161
QY 182 ProGlyLeuLysArgLysAlaGlu 189
DB 1162 CCTGGATTGAGCGCAAGCTGAA 1185

RESULT 30
ABV94681
ID ABV94681 standard; cDNA; 2235 BP.
XX
AC ABV94681;
XX
DT 14-JAN-2003 (first entry)
XX
DE Human pancreatic cancer expressed cDNA SEQ ID NO 54.
XX
KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW cytosolic; tumour; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200260317-A2.
XX
PD 08-AUG-2002.
XX
PF 30-JAN-2002; 2002WO-US0002781.
XX
PR 30-JAN-2001; 2001US-0265305P.
PR 31-JAN-2001; 2001US-0265682P.
PR
```

09-FEB-2001; 2001US-0267568P.  
21-MAR-2001; 2001US-0278651P.  
28-APR-2001; 2001US-0287112P.  
16-MAY-2001; 2001US-0291631P.  
12-JUL-2001; 2001US-0305484P.  
20-AUG-2001; 2001US-0313999P.  
27-NOV-2001; 2001US-0333626P.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;  
XX  
XX  
XX WPI; 2002-627435/67.  
DR P-PSDB; ABP68601.  
XX  
XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for  
PT diagnosing, preventing and/or treating cancer, particularly pancreatic  
PT cancer.  
XX  
XX Claim 1; SEQ ID NO 54; 300pp + Sequence Listing; English.  
XX  
XX The invention relates to an isolated polynucleotide (I) comprising: (a)  
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)  
CC complements of (a); (c) sequences consisting of at least 20 contiguous  
CC residues of (a); (d) sequences that hybridize to (a); under moderately  
CC stringent conditions; (e) sequences having at least 75% or 90% identity  
CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-  
CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer  
CC in a patient and compositions comprising polypeptides, polynucleotides,  
CC antibodies, fusion proteins, T cell populations and antigen presenting  
CC cells expressing the polypeptide are useful in treating pancreatic cancer  
CC and stimulating an immune response. The polynucleotides can be used as  
CC probes or primers for nucleic acid hybridisation, in the design and  
CC preparation of ribozyme molecules for inhibiting expression of the tumour  
CC polypeptides and proteins in the tumour cells, in vaccines and for gene  
CC therapy. Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 2235 BP; 562 A; 560 C; 537 G; 576 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.61e-102 Length: 2235  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 6 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ABV94681 (1-2235)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 697 GTTGTGACCTCTCTGTGACCATTTAAGAGACTGGAGTGTGTGGTCCAGC 756  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 757 CTATTCTGCTCTCTTTCAATTCAGCATTTGAGCGTAAACAGCCTACATTGCC 816  
QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 817 TTGGCCCTGCTCTCTGTGACCATTCAGTCTTAGATATACAGGGTGTGATCCAAAGCTATC 876  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 877 CAGAAATCAGATGAAGCCACCCATTCAGGCGCATATCTGGAATCTGGAATCTGCTATCT 936  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
DB 937 GAGGAGTTGGTTCAGAAAGTACAGTAATTCCTGCTCTTGGTCAATGTAAGTGCAGATAAG 996  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121



Db 997 GAACCTCAGGCGCCTCTCTTCTAGTGTGATGATTTAGTTGATCTCTGAAGTTTGCAGTGTG 1056  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
Db 1057 ATGCGGTATTTACCTATGTTGGTCCCTGTTTAAATGCTGACACTACTGATTTGGCT 1116  
Qy 142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 1117 CTCATTTTCACTCTTTCAGTGTCTCTGTTTATGAAAGGATCAGGCACAGATAGATCAT 1176  
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 1177 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAATC 1236  
Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 1237 CTGTGATTGAAGCGCAAGCTGAA 1260  
RESULT 31  
AAC64406  
ID AAC64406 standard; cDNA; 2240 BP.  
XX  
AC AAC64406;  
XX  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE Human Nogo B nucleotide sequence SEQ ID NO:1.  
XX  
KW Human; Nogo B; cell stress response; hyperphosphorylated; brain tumour;  
KW stress-phosphorylated endoplasmic reticulum protein; cytoskeletal;  
KW gene therapy; cell growth; cellular stress response; neuron growth;  
KW regulator of oxidative stress; inhibitor of neurite outgrowth;  
KW axon regeneration; diagnosis; cancer; identification; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO200606083-A1.  
XX  
PD 12-OCT-2000.  
XX  
PF 07-APR-2000; 2000WO-US0009383.  
XX  
PR 08-APR-1999; 99US-0128372P.  
PR 21-JUN-1999; 99US-0140331P.  
XX  
PA (CHIR ) CHIRON CORP.  
XX  
XX Wei D, Halenbeck R, Williams LT;  
XX  
XX WPI; 2000-665007/64.  
DR P-PSDB; AAB24242.  
XX  
XX Novel protein associated with cell stress response useful for modulating  
PT stress levels, cell growth, diagnosis and treatment of cancer and  
PT malignant growth and for identifying agonists and antagonists.  
XX  
XX Claim 2; Page 63-64; 68pp; English.  
PS  
CC The present sequence encodes a human stress-phosphorylated endoplasmic  
CC reticulum protein, designated Nogo B. Nogo B has cytoskeletal activity and  
CC is a modulator of the storage and exchange of calcium, cell growth and  
CC cellular stress response. It can regulate oxidative stress; inhibit  
CC neurite outgrowth, neuron growth and axon regeneration. Nogo B  
CC polypeptides and polynucleotides are useful for modulating stress levels  
CC and cellular stress-response, cell growth and viability, diagnosis and  
CC treatment of cancer, malignant growth and other Nogo B related diseases.  
CC Nogo B polypeptides are also useful to screen combinatorial libraries to  
CC identify agonist or antagonist. Antibodies against Nogo B polypeptides  
CC are useful for affinity chromatography and distinguishing Nogo B  
CC polypeptides  
XX  
SQ Sequence 2240 BP; 570 A; 558 C; 536 G; 576 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.62e-102 Length: 2240  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 3 Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAC64406 (1-2240)  
Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 693 GTTGTGACCTCTCTGACTGAGAGACATTAGAAGACTGGAGTGTGTTTGGTCCAGC 752  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 753 CTATTCTCTGCTGCTTTTCAATGACAGTATTGAGCATTTGAGCGTAAACAGCTTACATTGCC 812  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 813 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCTATC 872  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 873 CAGAAATCAGATGAAGGCCACCCATTTCAGGCATATCTGGAATCTGAAAGTTGCTATATCT 932  
Qy 82 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 933 GAGGAGTGGTTCAGAAAGTACAGTAATTTCTGCTCTTGGTTCATGTAAGCTGCACGATAAG 992  
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 993 GAACCTCAGCGCCCTCTCTTAGTTGATGATTTAGTTCCTCTGAAAGTTGCAAGTGTG 1052  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
Db 1053 ATGTGGGTATTTACCTATGTTGGTGCCTGTTTAAATGGTCTGACACTACTGATTTGGCT 1112  
Qy 142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 1113 CTCATTTTCACTCTTTCAGTGTCTCTGTTTATGAAAGCGCATCAGGCACAGATAGATCAT 1172  
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 1173 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAATC 1232  
Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 1233 CCTGGATTGAAGCGCAAGCTGAA 1256  
RESULT 32  
AAC94408  
ID AAC94408 standard; cDNA; 1694 BP.  
XX  
XX  
AC AAC94408;  
XX  
DT 06-NOV-2001 (first entry)  
XX  
DE Human full-length cDNA, SEQ ID NO: 3170.  
XX  
KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.  
XX  
OS Homo sapiens.  
XX  
FN EP1130094-A2.  
XX  
PD 05-SEP-2001.  
XX  
PF 07-JUL-2000; 2000EP-00114089.  
XX  
PR 08-JUL-1999; 99JP-00194486.  
PR 11-JAN-2000; 2000JP-00118774.  
PR 02-MAY-2000; 2000JP-00183765.

XX (HELI-) HELIX RES INST.  
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
XX  
XX  
DR WPI; 2001-524255/58.  
XX P-PSDB; AAM93484.  
XX  
XX 830 Primers useful for synthesizing full length cDNA clones and their use  
PT in genetic manipulation.  
XX  
XX  
PS Claim 8; SEQ ID NO 3170; 1380pp + Sequence Listing; English.  
XX  
CC The invention relates to primers for synthesizing full length cDNA  
CC clones. 830 cDNA molecules encoding a human protein have been isolated  
CC and nucleotide sequences of 5' - and 3' - ends of the cDNA molecules have  
CC been determined. Primers for synthesizing the full length cDNA are useful  
CC for clarifying the function of the protein encoded by the cDNA. The full  
CC length clones were obtained by construction of full length enriched cDNA  
CC libraries that were synthesised by the oligo-capping method. The primers  
CC enable the production of the full length cDNA easily without any special  
CC methods. The present sequence is a full length human cDNA of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in CD-ROM format directly  
CC from EPO  
XX  
SQ Sequence 1694 BP; 353 A; 484 C; 469 G; 388 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 3,36e-102 Length: 1694  
Score: 923.00 Matches: 187  
Percent Similarity: 99.47% Conservative: 0  
Best Local Similarity: 99.47% Mismatches: 1  
Query Match: 99.14% Indels: 0  
DB: 4 Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAK94408 (1-1694)  
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
DB 788 GTTGTGACCTCTGTTACTGGAGACATTAAAGACACTGGAGTGGTGTGGTGTGCAC 847  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 848 CTATTCCTGCTGCTTTTCATGACAGTATTACAGCAATGTGAGCGTAACAGCCTACATGTC 907  
QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 908 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 967  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 968 CAGAAATCAGATCAGAGCGCCACCCATTTCAGGCGCATATCTGGAATCTCAGTGTCTATCT 1027  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
DB 1028 GAGGAGTTGGTTTCAGAAATACAGTAATCTCTGCTCTTGGTCATGTGAACGACGATAAAG 1087  
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 1088 GAACCTCAGGCGCCCTCTCTTAGTTAGTATGATTAGTTGATCTCTGAAGTTGACGATGTTG 1147  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
DB 1148 ATGTGGGTATTTACCTATGTTGTGCTGCTGTTTAAATGGTCTGACACTACTGATTTGGCT 1207  
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
DB 1208 CTCAATTCATCTCTCAGTGTCTCTGTTATTTATGAACGGCATCAGCAGATAGATCAT 1267  
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

DB 1268 TATCTAGGACTTGCAATAAGAAATCTTAAAGATGCTATGCTAAATCCAGCAAAATC 1327  
QY 182 ProGlyLeuLysArgLysAlaGlu 189  
DB 1328 CCTGGATTGAGCGCAAGACTGAA 1351  
RESULT 33  
ADL31137  
ID ADL31137 standard; cDNA; 1694 BP.  
XX AC  
XX ADL31137;  
XX DT 20-MAY-2004 (first entry)  
XX  
XX Full length human cDNA clone SeqID 3170.  
XX human; medicine; signal transduction; glycoprotein; transcription;  
KW oligo-capping method; ss; gene.  
XX  
XX Homo sapiens.  
XX EP1396543-A2.  
XX 10-MAR-2004.  
XX  
XX 07-JUL-2000; 2003EP-00025638.  
XX  
XX 08-JUL-1999; 99JP-00194486.  
PR 11-JAN-2000; 2000JP-00118774.  
PR 02-MAY-2000; 2000JP-00183865.  
PR 07-JUL-2000; 2000EP-00114089.  
XX (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
XX  
XX WPI; 2004-204755/20.  
DR P-PSDB; ADL31138.  
XX  
XX New oligonucleotide primers (830 cDNAs) useful for synthesizing full  
PT length human cDNAs.  
XX  
XX Example 1; SEQ ID NO 3170; 1340pp; English.  
XX  
XX This invention relates to a novel primers useful for synthesising full  
CC length cDNA molecules that encode human proteins. Specifically, it refers  
CC to secretory or membrane proteins that are potential therapeutic agents/  
CC target molecules in the field of medicine, and in particular genes  
CC encoding proteins that are associated with signal transduction,  
CC glycoproteins and transcription. The present invention describes a method  
CC for efficiently cloning a full length human cDNA from both the 5' and 3'  
CC ends using the oligo-capping method. This polynucleotide sequence is a  
CC full length human cDNA clone of the invention.  
XX  
SQ Sequence 1694 BP; 353 A; 484 C; 469 G; 388 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 3,36e-102 Length: 1694  
Score: 923.00 Matches: 187  
Percent Similarity: 99.47% Conservative: 0  
Best Local Similarity: 99.47% Mismatches: 1  
Query Match: 99.14% Indels: 0  
DB: 4 Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADL31137 (1-1694)  
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
DB 788 GTTGTGACCTCTGTTACTGGAGACATTAAAGACACTGGAGTGGTGTGGTGTGCAC 847  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

Db 848 CTATTCTCTGCTCTTTCATTGACAGTATTGACAGTATTGAGCGTAAACAGCCTACATTTGCC 907  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 908 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGATATACAAAGGTTGATCCAGCTATC 967  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 968 CAGAAATCAGATGAAGCCACCATTCAGGGCATATCTGGAATCTGGAAGTTGCTATATCT 1027  
Qy 82 GluGluLeuValGlnLysTyrSerIleSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 1028 GAGGAGTTGGTTTCAGAGTACAGTAAATCTGCTCTTGGTCAATGTAAGTAAAG 1087  
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 1088 GNACTCAGCGGCTCTTCTAGTTGATGATTTAGTTGATTTCTGAAAGTTTGCAGTTG 1147  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
Db 1148 ATGTGGGTATTTACCTATGTTGGTGCCTGTTTAAATGGTCTGACACTACTGATTTGGCT 1207  
Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 1208 CTCAATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGCGCATCAGGCGACAGATCAT 1267  
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 1268 TATCTAGAGCTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAATC 1327  
Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 1328 CCTGGATTGAAGCGCAAGCTGAA 1351  
RESULT 34  
ID AAI98079 standard; cDNA; 1980 BP.  
XX  
AC AAI98079;  
XX  
DT 04-DEC-2001 (first entry)  
XX  
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 22.  
XX  
KW Human; neuroblastoma; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200166733-A1.  
XX  
PD 13-SEP-2001.  
XX  
PF 02-MAR-2001; 2001WO-JP001631.  
XX  
PR 07-MAR-2000; 2000JP-00159195.  
XX  
PR 12-MAY-2000; 2000JP-00140387.  
XX  
PA (CHIB-) CHIBA PREFECTURE.  
XX  
PA (HISM) HISAMITSU PHARM CO LTD.  
XX  
PI Nakagawara A;  
XX  
DR WPI; 2001-602630/68.  
XX  
PT Nucleic acids for prognosis of human neuroblastoma comprise nucleic acids  
PT expressed by human neuroblastomas.  
XX  
PS Claim 1; Page 69-70; 159pp; Japanese.  
XX  
CC The invention relates to nucleic acids (AAI98058-AAI98161) or their  
CC homologues expressed by human neuroblastomas useful for detecting genes  
CC expressed by neuroblastoma and for analysing their structure and  
CC function. The nucleic acids are useful for the diagnosis and prognosis of

CC neuroblastoma  
XX  
SQ Sequence 1980 BP; 601 A; 373 C; 423 G; 583 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 7.34e-102 Length: 1980  
Score: 921.00 Matches: 187  
Percent Similarity: 99.47% Conservative: 1  
Best Local Similarity: 98.94% Mismatches: 1  
Query Match: 98.93% Indels: 0  
DB: 4 Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAI98079 (1-1980)  
Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 1006 TCAGTTTGTGACCTCTCTGCTGAGAGACATTAAGAAGCTGGAGTGGTGTGGTGGC 1065  
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 1066 AGCCTATTCCAGCTGCTTTTCATTGACAGTATTGACAGCTTGTGAGCGTAACAGCCTACATT 1125  
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 1126 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCT 1185  
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 1186 ATCCAGAANTCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA 1245  
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 1246 TCTGAGGAGTTGGTTTCAGAGTACAGTAAATCTGCTCTTGTGTCATGTGAACCTGCAGATA 1305  
Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 1306 AAGAACTCAGCGCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAGTTTGCAGTG 1365  
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 1366 TTGATGGGTATTTACCTATGTTGGTGCCTTGTTTAAAGTCTGACACTACTGATTTTG 1425  
Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db 1426 GCTCTCAATTCACCTTCAGTGTTCCTGTTATTTATGAACGCGCATCAGGCGACAGATAGAT 1485  
Qy 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 1486 CATTATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAA 1545  
Qy 181 IleProGlyLeuLysArgLysAlaGlu 189  
Db 1546 ATCCCTGGATTGAAGCGCAAGCTGAA 1572  
RESULT 35  
ID AAX97587 standard; DNA; 991 BP.  
XX  
AC AAX97587;  
XX  
DT 13-SEP-1999 (first entry)  
XX  
DE Extended human secreted protein coding sequence, SEQ ID NO. 51.  
XX  
KW Secreted protein; human; cytokine; cellular proliferation; cell movement;  
KW cellular differentiation; immune system regulator; anti-inflammatory;  
KW haematopoiesis regulator; tissue growth regulator; tumour inhibitor;  
KW reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;  
KW genetic disease; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9931236-A2.

```
XX 24-JUN-1999.
XX
XX 17-DEC-1998; 98WO-IB002122.
XX
XX 17-DEC-1997; 97US-0069957P.
XX
XX 09-FEB-1998; 98US-0074121P.
XX
XX 13-APR-1998; 98US-0081563P.
XX
XX 10-AUG-1998; 98US-0096116P.
XX
XX (GEST ) GENSET.
XX
XX Bougueleret L, Duclert A, Dumas Milne Edwards J;
XX
XX WPI; 1999-385906/32.
XX
XX P-PSDB; AA35903.
XX
XX New isolated human secreted proteins.
XX
XX Claim 1; Page 185-186; 516pp; English.
XX
XX This sequence represents an extended human secreted protein coding
XX sequence of the invention. The secreted proteins can be used in treating
XX or controlling a variety of human conditions. The secreted proteins may
XX act as cytokines or may affect cellular proliferation or differentiation
XX or may act as immune system regulators, haematopoiesis regulators, tissue
XX growth regulators, regulators of reproductive hormones or cell movement
XX or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or
XX tumour inhibition activity. The DNAs can be used in forensic procedures
XX to identify individuals or in diagnostic procedures to identify
XX individuals having genetic diseases resulting from abnormal expression of
XX the genes corresponding to the extended cDNAs. They are also useful for
XX constructing a high resolution map of the human chromosomes. They can
XX also be used for gene therapy to control or treat genetic diseases
XX
XX SQ Sequence 991 BP; 280 A; 175 C; 232 G; 304 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6,46e-102 Length: 991
Score: 918.00 Matches: 187
Percent Similarity: 99.47% Conservative: 0
Best Local Similarity: 99.47% Mismatches: 1
Query Match: 98.60% Indels: 0
DB: 2 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x AA397587 (1-991)

QY 2 ValValAspLeuLeuThrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
DB 68 GTTGTTGACCTCTGCTACTGGAGAGACATTAGAAGACTGGAGTGTGTGGTCCAGC 127
QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaThrIleAla 41
DB 128 CTATTCCTGCTGCTTTCATTGACAGTATTTCAGCATTTGTCAGCGTACAGCCTACATGCC 187
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIlyGlyValIleGlnAlaIle 61
DB 188 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGGTGTGATCCAAGCTATC 247
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 248 CAGAAATCAGATGAAGCCACCCATTTCAGGGCCATATCTGGAATCTGGAATGTGATATCT 307
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
DB 308 GAGGAGTTGGTTCAGAGTACAGTAATCTGCTCTTGGTCACTGAGTGAAGTGCAGATAAG 367
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 368 GAACCTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAATCTGAGTGTG 427
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
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DB 428 ATGTGGGTATTTTACCTACTGTTGGTGCCTTGTTTTAATGGTCTGACACTACTGATTTTGGCT 487
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
DB 488 CTCATTTTCACTCTTCAGTGTCTCTGTTATTATGAACGGCATCAGGCACAGATGATCAT 547
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
DB 548 TATCTAGTACTTGCACAAATAAGAAATGTTAAAGATGCTATGGCTAAATCCAGCAAAATC 607
QY 182 ProGlyLeuLysArgLysAlaGlu 189
DB 608 CCTGGATTGAGCGCAAGCTGAA 631

RESULT 36
ADP18854
ID ADP18854 standard; cDNA; 994 BP.
XX
XX ADP18854;
AC
XX
XX 26-AUG-2004 (first entry)
DT
XX
XX Human secreted polynucleotide #110.
DE
XX
XX Human; secreted protein; gene; ss; genetic disease.
KW
XX
XX Homo sapiens.
OS
XX
XX US2004110939-A1.
PN
XX
XX 10-JUN-2004.
PD
XX
XX 15-OCT-2001; 2001US-00978360.
PF
XX
XX 17-DEC-1998; 98WO-IB002122.
PR
XX
XX 09-FEB-1999; 98WO-IB000282.
PR
XX
XX 21-JUN-2000; 2000WO-IB000951.
PR
XX
XX 15-SEP-2000; 2000US-00663600.
PR
XX
XX (GEST ) GENSET SA.
PI
XX
XX Dumas Milne Edwards J, Bougueleret L, Jobert S, Clusel C;
PI
XX
XX Duclert A;
XX
XX WPI; 2004-440404/41.
DR
XX
XX P-PSDB; ADP19259.
XX
XX New isolated polynucleotide encoding secreted polypeptide, useful for
XX gene therapy, or in diagnostic procedures to identify individuals having
XX genetic diseases resulting from abnormal expression of the genes.
XX
XX Claim 1; SEQ ID NO 110; 113pp; English.
XX
XX The invention relates to human cDNA sequences that encode human secreted
XX proteins. The invention also relates to an antibody that specifically
XX binds to a polypeptide of the invention and a method of binding the
XX polypeptide to an antibody. The polynucleotides are useful for expressing
XX the entire secreted proteins which they encode and for distinguishing
XX human tissues and cells from non-human tissues and cells, and for
XX distinguishing between human tissues and cells that do or do not express
XX the polynucleotides comprising the cDNAs. The polynucleotides and
XX polypeptides are useful in forensic procedures or diagnostic procedures
XX to identify individuals with genetic diseases resulting from abnormal
XX expression of the genes corresponding to the cDNAs. The sequences are
XX also useful in gene therapy to control or treat genetic diseases. This
XX sequence represents a human secreted polynucleotide of the invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification.gov was obtained in electronic format from USPTO at
XX seqdata.uspto.gov/sequence.html.
XX
XX Sequence 994 BP; 283 A; 175 C; 232 G; 304 T; 0 U; 0 Other;
SQ
XX
XX Alignment Scores:
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Pred. No.: 6.48e-102 Length: 994
Score: 918.00 Matches: 187
Percent Similarity: 99.47% Conservative: 0
Best Local Similarity: 99.47% Mismatches: 1
Query Match: 98.60% Indels: 0
DB: 12 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x ADP18854 (1-994)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleValSerThrGlyValValPheGlyAlaSer 21
Db 68 GTTGTGACCTCTCTGAGAGACATTAAGAGACTGGAGTGGTGTGGTGGCCAGC 127

Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 128 CTATTCTGCTGCTTTCATTCAGCATTTTCAGCATTTGAGCGTAACAGCCTACATTGCC 187

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 188 TTGGCCCTGCTCTCTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 247

Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 248 CAGAAATCAGATGAAGGCCACCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 307

Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCyThrIleLys 101
Db 308 GAGAGTTGGTTTCAGAGTACAGTAATTTCTGCTCTTGTCTCATGTGAATGACGATTAAG 367

Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 368 GAACCTCAGCGCCCTCTCTTAGTTGATGATTAGTTGATTTCTCTGAAGTTTGCAGTGTG 427

Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 428 ATGTGGGTATTTACCTATGTTGGTGGCTTGTATTAATGCTGTGACACTACTGATTTGGCT 487

Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 488 CTCAATTCACCTCTTCAGTGTCTCTGTTATTTATGACGGCATTCAGGCACAGTATGATCAT 547

Qy 162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 548 TATCTAGTACTTGCATAAAGATGTTAAAGATGCTATGCTGCTAAATCCAAAGCAAAATC 607

Qy 182 ProGlyLeuLysArgLysAlaGlu 189
Db 608 CCTGGATTGAAGCGCAAGCTGAA 631

RESULT 37
AD131056
ID AD131056 standard; cDNA; 2610 BP.
XX AC AD131056;
XX DT 17-JUN-2004 (first entry)
XX DE Human cDNA #382.
XX
KW Human; gene; ss; immunological response; immunopathological condition;
KW Crohn's disease; asthma; ulcerative colitis; hypersensitization;
KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
KW acute monocytic leukaemia; anti-inflammatory; antitumor; antiulcer;
KW osteopathic; antiarthritic; antirheumatic; cytostatic.
XX OS Homo sapiens.
XX FN US6607879-B1.
XX PD 19-AUG-2003.
XX
XX 09-FEB-1998; 98US-00023655.
XX
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PR 09-FEB-1998; 98US-00023655.
XX (INCY-) INCYTE CORP.
XX Cocks BG, Stuart SG, Seilhamer JJ;
XX WPI; 2003-895307/82.
XX
PT A composition comprising a plurality of cDNAs, useful for detecting
PT altered expression of genes in an immunological response or for
PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
PT or osteoarthritis.
XX
PS Claim 1; SEQ ID NO 382; 50pp; English.
XX
CC The invention relates to a composition comprising a plurality of cDNAs
CC for detecting the altered expression of genes in an immunological
CC response. The invention also relates to a method of diagnosing or
CC monitoring the treatment of an immunopathological condition in a sample,
CC comprising obtaining nucleic acids from a sample, contacting the nucleic
CC acids of the sample with an array comprising the plurality of cDNAs under
CC conditions to form one or more hybridisation complexes, detecting the
CC hybridisation complexes and comparing the levels of the detected
CC hybridisation complexes with the level of hybridisation complexes
CC detected in a non-diseased sample, where an altered level of the detected
CC hybridisation complexes correlates with the presence of an
CC immunopathological condition. Also disclosed are an expression profile
CC comprising a microarray and a plurality of detectable complexes and a
CC method for identifying a plurality of polynucleotide probes. The cDNAs
CC are useful as hybridisable array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray can be used in
CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,
CC ulcerative colitis, hypersensitization, irritable bowel syndrome,
CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
CC identifying agents for the treatment of the diseases. The microarray may
CC also be used in drug discovery and development, toxicological and
CC carcinogenicity studies, forensics or pharmacogenomics. The composition
CC may also be used in purification of a subpopulation of mRNAs, cDNAs or
CC genomic fragments. This sequence represents a human cDNA of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 2610 BP; 773 A; 434 C; 557 G; 820 T; 0 U; 26 Other;
```

```
Alignment Scores:
Pred. NO.: 7.73e-101 Length: 2610
Score: 914.00 Matches: 188
Percent Similarity: 99.47% Conservative: 0
Best Local Similarity: 99.47% Mismatches: 0
Query Match: 98.17% Indels: 1
DB: 11 Gaps: 0
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US-09-830-972-29\_COPY\_990\_1178 (1-189) x AD131056 (1-2610)

```
Qy 2 ValValAspLeuLeuTyrTrpArgAspIleValSerThrGlyValValPheGlyAlaSer 21
Db 1311 GTTGTGACCTCTCTGAGAGACATTAAGAGACTGGAGTGGTGTGGTGGCCAGC 1370

Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr-IleAl 41
Db 1371 CTATTCTGCTGCTTTCATTCAGCATTTTCAGCATTTGAGCGTAACAGCCTACAAATGC 1430

Qy 41 aLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 1431 CTTGGCCCTGCTCTCTGTCACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTAT 1490

Qy 61 eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 81
Db 1491 CCAGAAATCAGATGAAGGCCACCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATC 1550

Qy 81 rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCyThrIleLys 101
```

Db 1551 TGAGGAGTTGGTTTCAGAGTACAGTAATTCCTGCTTGTGTCATGTCAACTGCACGATATAA 1610  
QY 101 sGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValle 121  
|||  
Db 1611 GGAACCTCAGCGCCTCTCTTAGTTCATGATTAGTTGATCTCTGAAAGTTGCAGTGT 1670  
QY 121 uMetTrpValPheThrTyrrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAl 141  
|||  
Db 1671 GATGTGGTATTACCTATGTTGGTCCCTTGTATTAATGCTCTGACACTACTGATTTTGGC 1730  
QY 141 aleuileSerLeuPheSerValProValIleTyrrGluArgHisGlnAlaGlnIleAspHi 161  
1731 TCTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACCGCATCAGCGACAGATATCA 1790  
QY 161 sTyrrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysI 181  
1791 TTATCTAGGACCTTGCAATTAAGAATGTTAAAGATGCTATGGCTAAATCCAGCAAAAT 1850  
QY 181 eProGlyLeuLysArgLysAlaGlu 189  
Db 1851 CCTGGGTTGAAGCGCAAAAGCTGAA 1875

## RESULT 38

ADP42781  
ID ADP42781 standard; cDNA; 734 BP.

XX AC ADP42781;

XX DT 26-FEB-2004 (first entry)

XX DE Mouse CYP27 nucleotide sequence SEQ ID NO:87.

XX KW diabetic; pre-diabetic; Type 2 diabetes; antidiabetic; gene therapy;  
KW diabetes; insulin resistance; metabolic disease; mouse; gene; ss.

XX OS Mus sp.

XX PN WO2003102163-A2.

XX PD 11-DEC-2003.

XX PF 04-JUN-2003; 2003WO-US017825.

XX PR 04-JUN-2002; 2002US-0385957P.

XX PR 04-JUN-2002; 2002US-0386013P.

XX PR 04-JUN-2002; 2002US-0386074P.

XX PR 05-JUN-2002; 2002US-0386107P.

XX PR 05-JUN-2002; 2002US-0386314P.

XX PR 05-JUN-2002; 2002US-0386326P.

XX PR 05-JUN-2002; 2002US-0386332P.

XX PR 05-JUN-2002; 2002US-0386481P.

XX PR 05-JUN-2002; 2002US-0386512P.

XX PR 05-JUN-2002; 2002US-0386513P.

XX PR 05-JUN-2002; 2002US-0386558P.

XX PR 05-JUN-2002; 2002US-0386600P.

XX PR 05-JUN-2002; 2002US-0386615P.

XX PR 05-JUN-2002; 2002US-0386654P.

XX PR 06-JUN-2002; 2002US-0386838P.

XX PR 06-JUN-2002; 2002US-0386861P.

XX PR 06-JUN-2002; 2002US-0386944P.

XX PR 06-JUN-2002; 2002US-0386955P.

PT Identifying an agent for treating diabetic or pre-diabetic individuals  
PT comprises contacting an agent with a polypeptide, e.g., human ceramidase,  
PT and selecting an agent that modulates the expression or activity of the  
PT polypeptide.

PS Disclosure; SEQ ID NO 87; 209pp; English.

XX The present invention describes a method for identifying an agent for  
CC treating a diabetic or pre-diabetic individual. The method comprises  
CC contacting an agent to a mixture comprising a polypeptide encoded by a  
CC nucleic acid that hybridizes under stringent conditions to a nucleic acid  
CC encoding any of the 23 fully defined amino acid sequences given in the  
CC specification, and selecting an agent that modulates the expression or  
CC activity of the polypeptide. Also described: (1) a method of treating a  
CC diabetic or pre-diabetic animal, comprising administering to the animal a  
CC therapeutic amount of an agent identified by the method described above;  
CC (2) a method of introducing an expression cassette into a cell,  
CC comprising introducing into the cell an expression cassette comprising a  
CC promoter operably linked to a polynucleotide encoding a polypeptide,  
CC where the polynucleotide hybridizes under stringent conditions to a  
CC nucleic acid encoding the above amino acid sequences; and (3) a method of  
CC diagnosing an individual who has Type 2 diabetes or is pre-diabetic,  
CC comprising detecting in a sample from the individual the level of a  
CC polypeptide or the level of the above-mentioned polynucleotide encoding  
CC the polypeptide, where a modulated level of the polypeptide or  
CC polynucleotide in the sample compared to a level of the polypeptide or  
CC polynucleotide in either a lean individual or a previous sample from the  
CC individual indicates that the individual is diabetic or pre-diabetic. The  
CC method is useful in diagnosing and treating diabetes, insulin resistance  
CC or related metabolic diseases in human subjects. The method may also be  
CC used in identifying agents for treating diabetic or pre-diabetic  
CC individuals. The present sequence is used in the exemplification of the  
CC present invention.

XX SQ Sequence 734 BP; 202 A; 138 C; 179 G; 215 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 3.03e-101 Length: 734  
Score: 911.00 Matches: 185  
Percent Similarity: 99.47% Conservative: 2  
Best Local Similarity: 98.40% Mismatches: 1  
Query Match: 97.85% Indels: 0  
DB: 12 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADF42781 (1-734)

QY 2 ValValAspLeuLeuTyrrTipArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 100 GTTGTGGACCTCTCTACTGAGACACATTAAAGAGACTGGAGTGGTGTGGTGCACG 159  
QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrrIleAla 41  
Db 160 TTATTCCTGCTGCTCTCTGACAGTTTCAGCAATTTGTCAGTGTAAACGGCTTACATTC 219  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrrLysGlyValIleGlnAlaIle 61  
Db 220 TTGGCCCTGCTCTCTGTGACTATCAGCTTAGGATATATAAGGGTGTGATCAAGCTATC 279  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrrLeuGluSerGluValAlaIleSer 81  
Db 280 CAGAAATCAGATGAAGGCCACCCATTAGGGCATATTTGGAATCTGAGTTCGCATATCA 339  
QY 82 GluGluLeuValGlnLysTyrrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 340 GAGGAATTTGGTTCAGAAATATAGTAATCTCTGCTCTTGGTCTGTGTGAACACGCAATAAAA 399  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 400 GAAATTGAGCGGCTCTCTTCTTAGTGAATTTAGTTGATTTCCCTGAAAGTTTCAGTGTG 459  
QY 122 MetTrpValPheThrTyrrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
Db 460 ATGTGGGTATTTACTTACGTTGGTGGCTTGTTCATGTTTGCACACTACTGATTTTAGCC 519

QY 142 LeuileSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 DB 520 CTGATCTACCTCTTCTGATTTCTCTTATATATGATGACGGCATCAGCGCAGATAGATCAT 579  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 DB 580 TATCTAGGACTTGCAAAACAAGAGTGTAAAGGATGCGCATGGCCAAATCCAAAGCAAAATC 639  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 DB 640 CCTGGATTGAAGCGCAAGACAGAA 663  
 RESULT 39  
 ID ADP45571 standard; cDNA; 3492 BP.  
 XX  
 AC ADP45571;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Rat NogoA encoding cDNA SEQ ID NO:25.  
 XX  
 KW binding molecule; human; NogoA; NiG; NiG-D20; NogoA\_623-640;  
 KW nerve repair; neuroprotective; gene therapy;  
 KW central nervous system injury; CNS injury; neurodegenerative disorder;  
 KW rat; gene; ss.  
 XX  
 OS Rattus norvegicus.  
 XX  
 FH Location/Qualifiers  
 FT 1..3492  
 FT /\*tag= a  
 FT /product= "NogoA"  
 XX  
 WO2004052932-A2.  
 XX  
 PD 24-JUN-2004.  
 XX  
 PF 09-DEC-2003; 2003WO-EP013960.  
 XX  
 PR 10-DEC-2002; 2002GB-00028832.  
 XX  
 PA (NOVS ) NOVARTIS AG.  
 PA (NOVS ) NOVARTIS PHARMA GMBH.  
 PA (UYZU-) UNIV ZUERICH.  
 XX  
 PI Barske C, Mir AK, Oertle T, Schnell L, Schwab ME, Vitaliti A;  
 PI Zurini M;  
 XX  
 DR WPI; 2004-468818/44.  
 DR P-PSDB; ADP45572.  
 XX  
 PT New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-  
 PT D20 or NogoA623-640, useful in preparing a composition for treating CNS  
 PT injury or neurodegenerative disorders.  
 XX  
 PS Disclosure; SEQ ID NO 25; 121pp; English.  
 XX  
 CC The present invention describes a binding molecule which binds to human  
 CC NogoA polypeptide, human NiG, human NiG-D20 or human NogoA\_623-640 with a  
 CC dissociation constant of less than 100nM. Also described: (1) a  
 CC polynucleotide encoding the binding molecule; (2) an expression vector or  
 CC system comprising the polynucleotide; (3) a host cell comprising the  
 CC expression system; (4) a pharmaceutical composition comprising the  
 CC binding molecule and a carrier or diluent; and (5) treating diseases  
 CC associated with nerve repair. The binding molecule has neuroprotective  
 CC activity, and can be used in gene therapy. The binding molecule is useful  
 CC in preparing a composition for treating central nervous system (CNS)  
 CC injury or neurodegenerative disorders. The present sequence encodes rat  
 CC NogoA, which is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 3492 BP; 1031 A; 804 C; 822 G; 835 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 6, 27e-100 Length: 3492  
 Score: 908.00 Matches: 184  
 Percent Similarity: 98.94% Conservatives: 3  
 Best Local Similarity: 97.35% Mismatches: 2  
 Query Match: 97.53% Indels: 0  
 DB: 12 Gaps: 0  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADP45571 (1-3492)  
 QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 DB 2923 TCAGTTGTTGACCTCCTCTACTGAGAGACATTAAGAAGACTGGAGTGGTGTTCGGTCC 2982  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 2983 AGCTTATTCCTGCTGCTGCTCTGACAGTGTTCAGCATTTGTCAGTGTAAAGCCCTACAT 3042  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 3043 GCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAGGGCGTGTATCCAGGCT 3102  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 3103 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAAATCTGAAGTTGCTATA 3162  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 DB 3163 TCAGAGGAATTTGGTTTCAGAAATACAGTAAATTCCTCTTGTGTCATGTGAACAGACAATA 3222  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 3223 AAAGACTGAGCGCGCTTTCTTAGTTGATGATTTAGTTGATTCCTGAAGTTTGCAGTG 3282  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 DB 3283 TTGATGTGGTGTCTTACTTATGTTGGTGCCTTGTTCATGTGCTGACACTACTGATTTTA 3342  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleLeu 160  
 DB 3343 GCTCTGATCTCACCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGAT 3402  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 3403 CATTTATCTAGACTTGCACAACAGAGTGTTAAGGATGCGCATGGCCAAATCCAAAGCAAA 3462  
 QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
 DB 3463 ATCCCTGGATTGAAGCGCAAGACAGAT 3489  
 RESULT 40  
 ID AAD01173 standard; cDNA; 4684 BP.  
 XX  
 AC AAD01173;  
 XX  
 DT 02-NOV-2000 (first entry)  
 XX  
 DE Rat neurite growth inhibitor Nogo A cDNA.  
 XX  
 KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
 KW central nervous system; neoplastic disease; antiproliferative; glioma;  
 KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
 KW hyperproliferative disorder; benign dysplastic disorder; diagnosis;  
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
 KW structural plasticity; screening; ss.  
 XX  
 OS Rattus sp.  
 XX  
 FH Location/Qualifiers  
 FT 253..3744

```

FT      /*tag= a
FT      /product= "Nogo A"
FT      /transl_except= (pos:1462..1464, aa:Ile)
XX      WO200031235-A2.
XX      02-JUN-2000.
XX      05-NOV-1999; 99WO-US026160.
XX      06-NOV-1998; 98US-0107446P.
XX      (SCHW/) SCHWAB M E.
XX      (CHEN/) CHEN M S.
XX      Schwab ME, Chen MS;
XX      WPI; 2000-400052/34.
XX      P-PSDB; AAY71310.
XX      Nogo proteins and nucleic acids useful for treating neoplastic disorders
XX      of the central nervous system and inducing regeneration of neurons.
XX      Claim 26; Fig 2A; 122pp; English.
XX      The present sequence is a cDNA encoding rat Nogo A protein which is a
XX      potent neural cell growth inhibitor and is free of all central nervous
XX      system (CNS) myelin material with which it is natively associated. The
XX      present sequence was generated by fusing RO18U37-3, R1-3U21 cDNA
XX      sequences isolated from hexanucleotide-primed rat brain stem/spinal cord
XX      library, and Oli18 cDNA from an oligo d(T)-primed rat oligodendrocyte
XX      library. Nogo proteins and fragments displaying neurite growth inhibitory
XX      activity are used in the treatment of neoplastic disease of the CNS e.g.
XX      glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma,
XX      pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma,
XX      meningioma, neuroblastoma or retinoblastoma and degenerative nerve
XX      diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which
XX      promote Nogo activity can be used to treat or prevent hyperproliferative
XX      or benign dysproliferative disorders e.g. psoriasis and tissue
XX      hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to
XX      inhibit production of Nogo protein to induce regeneration of neurons or
XX      to promote structural plasticity of the CNS in disorders where neurite
XX      growth, regeneration or maintenance are deficient or desired. The animal
XX      models can be used in diagnostic and screening methods for predisposition
XX      to disorders and to screen for or test molecules which can treat or
XX      prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are
XX      referred in claim 32 and SEQ ID NO: 29 in disclosure of the
XX      specification. However the specification does not include sequences for
XX      these SEQ ID numbers
XX      SQ      Sequence 4684 BP; 1358 A; 1048 C; 1112 G; 1166 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      9,47e-100      Length:      4684
Score:          908.00      Matches:      184
Percent Similarity: 98.94%      Conservative: 3
Best Local Similarity: 97.35%      Mismatches: 2
Query Match:    97.53%      Indels:      0
DB:            3      Gaps:        0

US-09-830-972-29_COPY_990_1178 (1-189) x AAD01173 (1-4684)
QY      1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
DB      3175 TCAGTTGTGTGACCTCCTACTCTGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGC 3234
QY      21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB      3235 AGCTTATTCTGCTGCTGCTCTGAGAGTTCAGCATGTTCAGTAAAGCGGCTACAT 3294
QY      41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAla 60
DB      3295 GCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGCGGTGATCCAGGCT 3354

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QY      61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB      3355 ATCCAGAAATCAGATGAAGGCCACCACCATTTAGAGATCTGAAGTTGCTATA 3414
QY      81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
DB      3415 TCAGAGGAATTGGTTCAGAAATACAGTAATCTCTCTTGGTCATGTGACACGACAAATA 3474
QY      101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
DB      3475 AAGAAGCTGAGCGCGCTTTCTTCTAGTGTATTTAGTTCTCCCTGAAGTTGCAGTG 3534
QY      121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
DB      3535 TTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCATTTGTTCAATGGTCTGACACTACTGATTTTA 3594
QY      141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
DB      3715 ATCCCTGGATTGAAGCGCAAAACAGAT 3741
XX      ID ABN86600 standard; DNA; 4684 BP.
XX      AC ABN86600;
XX      DT 05-NOV-2002 (first entry)
XX      DE Rat neurotransmitter receptor protein Nogo encoding DNA.
XX      KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
XX      KW central nervous system; peripheral nervous system; tranquilizer; Nogo;
XX      KW vulnery; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
XX      KW neotropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
XX      KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
XX      KW neurotransmitter receptor; rat; gene; ds.
XX      OS Rattus norvegicus.
XX      FH Key Location/Qualifiers
XX      CDS 253..3744
XX      FT /*tag= a
XX      FT /product= "Nogo-A"
XX      PN US2002072493-A1.
XX      PD 13-JUN-2002.
XX      PF 28-JUN-2001; 2001US-00893348.
XX      PR 19-MAY-1998; 98IL-00124500.
XX      PR 21-JUL-1998; 98WO-US014715.
XX      PR 22-DEC-1998; 98US-00218277.
XX      PR 19-MAY-1999; 99US-00314161.
XX      PA (YEDA ) YEDA RES & DEV CO LTD.
XX      PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;
XX      PI Moalem G;
XX      DR WPI; 2002-607255/65.
XX      DR P-PSDB; ABB81074, ABB81076, ABB81077.
XX      PT Promoting nerve regeneration and preventing neuronal degeneration in the

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PT central/peripheral nervous system from injury/disease, comprises  
 PT administering nervous system-specific activated T cells/antigen, or  
 PT analogs/peptides.

PS Disclosure; Page 40-44; 93pp; English.

XX The invention relates to promoting nerve regeneration or conferring  
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the  
 CC central/peripheral nervous system (NS). The method involves administering  
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its  
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or  
 CC combinations. The method is useful for promoting nerve regeneration and  
 CC preventing neuronal degeneration in central/peripheral nervous system  
 CC from injury/disease, where the injury is spinal cord injury, blunt  
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or  
 CC damages caused by surgery such as tumour excision. The disease is not an  
 CC autoimmune disease or neoplasm. The disease results in a degenerative  
 CC process occurring in either gray or white matter or both. The disease is  
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,  
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and  
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such  
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral  
 CC neuropathies associated with various diseases, including but not limited  
 CC to uremia, porphyria, hypoglycemia, Sjogren Larsson syndrome, acute  
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary  
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption  
 CC syndromes, polycythemia vera, immunoglobulin (IgA- and IgG gamma-  
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins  
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia  
 CC telangiectasia, Friedreich's ataxia, amyloid polyneuropathies,  
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's  
 CC disease, or lipoproteinemia. The present sequence represents a DNA  
 CC encoding the rat neurotrophin receptor protein Nogo (Nogo-A, Nogo-B  
 CC and Nogo-C), an example of NS-specific antigen

XX Sequence 4684 BP; 1358 A; 1047 C; 1112 G; 1167 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 9,478-100 Length: 4684  
 Score: 908.00 Matches: 184  
 Percent Similarity: 98.94% Conservative: 3  
 Best Local Similarity: 97.35% Mismatches: 2  
 Query Match: 97.53% Indels: 0  
 DB: 6 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ABN86600 (1-4684)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 DB 3175 TCAGTTGTGACCTCTCTACTGGAGAGACATTAGAGACTGGAGTGGTGTGGTGGC 3234  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 3235 AGCTTATTCTGCTGCTGCTCTGACAGTGTTCAGCATTTGTCAGTGAACGGCTACATT 3294  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60  
 DB 3295 GCGTTGGCCCTCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGGTGATCCAGGCT 3354  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 3355 ATCCAGAAATCAGATGAGGCCACCCATTCAGGGCATATTTAGATCTGAAATCTGCTATA 3414  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 DB 3415 TCAGAGGAATTGTTTCAGAAATACAGTAATTCCTCTGCTTGGTGTGATGTAACAGCAATA 3474  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 3475 AAAGAACTGAGGGGGCTTTCTTAGTTGATGATTTAGTTGATTCCTCGAAGTTTCAGTG 3534  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140

DB 3535 TTGATGTGGTGTTTACTTATGTTGGCTTGTTCAATGGTCTGACACTACTGATTTTA 3594  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 DB 3595 GCTCTGATCTCACTCTTCTAGTATTCTGTTATTTATGAACGGCATCAGGTGCAGATAGAT 3654  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 3655 CATTATCTAGGACTTGCACCAAGAGTGTTAAGGATGCCATGCGCCAAATATCCAGCAAAA 3714  
 QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
 DB 3715 ATCCCTGGATTGAAGCGCAAGCAGAT 3741

#### RESULT 42

ADB85284  
 ID ADB85284 standard; DNA; 2782 BP.

XX ADB85284;  
 XX AC  
 XX 04-DEC-2003 (first entry)  
 DT Rat foocen-m2 reticulon gene SEQ ID NO:165.  
 XX  
 DE rat; streptozocin; kinase; phosphatase; ion channel protein; receptor;  
 XX transporter; G-protein coupled receptor; GPCR; DNA-binding proteins;  
 KW protease; enzyme; analgesic; gene therapy; pain; diabetes; ds; gene.  
 KW  
 OS Rattus norvegicus.  
 XX  
 PN EP1284297-A2.  
 XX  
 XX 19-FEB-2003.  
 XX  
 XX 26-JUL-2002; 2002EP-00255228.  
 PF  
 XX 27-JUL-2001; 2001GB-00018354.  
 PR  
 XX 07-FEB-2002; 2002GB-00002880.  
 XX  
 XX (WARN ) WARNER LAMBERT CO.  
 XX  
 XX Brooksbank RA, Dixon AK, Lee K, Pinnock RD;  
 PI  
 XX WPI: 2003-364994/35.  
 DR  
 XX P-PSDB; ADB85283.

PT Use of gene sequence that is down-regulated in response to streptozocin-  
 PT induced diabetes, vector, host cell, animal, polypeptide and antibody, in  
 PT screening of compounds for treating or diagnosing pain.  
 PT  
 XX Claim 1; Page 240-241; 256pp; English.

XX The invention relates to a novel isolated gene sequence that is down-  
 CC regulated in the spinal cord in response to streptozocin-induced  
 CC diabetes, or comprising, hybridising or having at least 80% sequence  
 CC identity to a sequence whose expression products are kinases,  
 CC phosphatases, ion channel proteins, receptors, transporters, G-protein  
 CC coupled receptor proteins, DNA-binding proteins, proteases or enzymes,  
 CC given in the specification. A gene of the invention has analgesic  
 CC activity, and may have a use in gene therapy. The gene sequences, vector,  
 CC host cell, animal, polypeptide and antibody are useful for screening of  
 CC compounds for diagnosing or treating pain. The kits are useful for  
 CC simultaneous, separate or sequential detecting and/or quantifying down-  
 CC regulation of a gene sequence in the spinal cord of a mammal in response  
 CC to streptozocin-induced diabetes. The compound or pharmaceutical  
 CC composition is useful as a medicament for treating or diagnosing pain.  
 CC The present sequence represents a gene of the invention.

SQ Sequence 2782 BP; 635 A; 728 C; 765 G; 654 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.06e-99 Length: 2782



Db 3280 GTGTTGATGGGTATTTACTTACGTGGTGGCTTGTTCATAGGTTTGACACTACTGATT 3339

Qy 140 LeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIle 159

Db 3340 TTAGCTCTGATCTCACTCTTCAGTATTCCTGTATATATGAACGGCATCAGCGCAGATA 3399

Qy 160 AspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAla 179

Db 3400 GATCATTATCTAGGACTTGCAACAGAGCGTTAAGGATGCCATGGCCAAATCCAGCA 3459

Qy 180 LysIleProGlyLeuLysArgLysAlaGlu 189

Db 3460 AAAATCCCTGGATTGAAGCGCAAGCAGAA 3489

RESULT 44

AAD01175

ID AAD01175 standard; cDNA; 1568 BP.

XX AC AAD01175;

XX DT 02-NOV-2000 (first entry)

XX DE Rat neurite growth inhibitor Nogo C cDNA.

XX KW Rat; neurite growth inhibitor; Nogo C; neural cell; myelin; CNS;

XX KW central nervous system; neoplastic disease; antiproliferative; glioma;

XX KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;

XX KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;

XX KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;

XX KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;

XX KW structural plasticity; screening; ss.

XX OS Rattus sp.

XX FH Key

XX CDS

FT 1. .1566

FT Location/Qualifiers

FT \*tag= a

FT /product= "Nogo C protein (residues 40-238) flanked by 1-

FT 39 residues at the N-terminal and 239-522 residues at the

FT C-terminal"

FT /transl\_except= (pos:7. .9, aa:Xaa)

FT /transl\_except= (pos:85. .87, aa:Xaa)

FT /transl\_except= (pos:787. .789, aa:Xaa)

FT /transl\_except= (pos:826. .828, aa:Xaa)

FT /transl\_except= (pos:841. .843, aa:Xaa)

FT /transl\_except= (pos:883. .885, aa:Xaa)

FT /transl\_except= (pos:889. .891, aa:Xaa)

FT /transl\_except= (pos:940. .942, aa:Xaa)

FT /transl\_except= (pos:952. .954, aa:Xaa)

FT /transl\_except= (pos:1003. .1005, aa:Xaa)

FT /transl\_except= (pos:1111. .1113, aa:Xaa)

FT /transl\_except= (pos:1120. .1122, aa:Xaa)

FT /transl\_except= (pos:1138. .1140, aa:Xaa)

FT /transl\_except= (pos:1216. .1218, aa:Xaa)

FT /transl\_except= (pos:1222. .1224, aa:Xaa)

FT /transl\_except= (pos:1228. .1230, aa:Xaa)

FT /transl\_except= (pos:1264. .1266, aa:Xaa)

FT /transl\_except= (pos:1297. .1299, aa:Xaa)

FT /transl\_except= (pos:1318. .1320, aa:Xaa)

FT /transl\_except= (pos:1357. .1359, aa:Xaa)

FT /transl\_except= (pos:1393. .1395, aa:Xaa)

FT /transl\_except= (pos:1444. .1446, aa:Xaa)

FT /transl\_except= (pos:1537. .1539, aa:Xaa)

FT /note= "Xaa corresponds to in-frame stop codon; the CNS

FT does not end in a stop codon"

FT /partial

FT 118. .120

FT misc\_feature

FT \*tag= b

FT /note= "Start codon of Nogo C coding region"

FT 715. .717

FT misc\_feature

FT \*tag= c

FT /note= "Stop codon of Nogo C coding region"

XX

PN WO200031235-A2.

XX 02-JUN-2000.

XX PF 05-NOV-1999; 99WO-US026160.

XX PR 06-NOV-1998; 98US-0107446P.

XX PA (SCHW/) SCHWAB M E.

XX CHEN M S.

XX PI Schwab ME, Chen MS;

XX DR WPI; 2000-400052/34.

XX P-PSDB; AAY71312.

XX Nogo proteins and nucleic acids useful for treating neoplastic disorders

XX of the central nervous system and inducing regeneration of neurons.

XX Claim 23; Fig 14; 122pp; English.

XX The present sequence is a cDNA encoding rat Nogo C protein which is a

XX potent neural cell growth inhibitor and is free of all central nervous

XX system (CNS) myelin material with which it is natively associated. Nogo

XX proteins and fragments displaying neurite growth inhibitory activity are

XX used in the treatment of neoplastic disease of the CNS e.g. glioma,

XX glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma,

XX haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma,

XX neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.

XX Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo

XX activity can be used to treat or prevent hyperproliferative or benign

XX dysproliferative disorders e.g. psoriasis and tissue hypertrophy.

XX Ribozymes or antisense Nogo nucleic acids can be used to inhibit

XX production of Nogo protein to induce regeneration of neurons or to

XX promote structural plasticity of the CNS in disorders where neurite

XX growth, regeneration or maintenance are deficient or desired. The animal

XX models can be used in diagnostic and screening methods for predisposition

XX to disorders and to screen for or test molecules which can treat or

XX prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are

XX referred in claim 32 and SEQ ID NO: 29 in disclosure of the

XX specification. However the specification does not include sequences for

XX these SEQ ID numbers

XX SQ Sequence 1568 BP; 435' A; 274 C; 375 G; 484 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6.27e-100 Length: 1568

Score: 904.00 Matches: 183

Percent Similarity: 98.94% Conservative: 3

Best Local Similarity: 97.34% Mismatches: 2

Query Match: 97.10% Indels: 0

DB: 3 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAD01175 (1-1568)

Qy 2 ValValAspLeuLeuTyrTyrArgAspIleLysLysTyrGlyValValPheGlyAlaSer 21

Db 151 GTTGTGGACCTCCCTCTACTGAGAGACATTAAAGAGACTGGAGTGGTGTGGTCCAGC 210

Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

Db 211 TTATTCCTGCTGCTCTCTGACAGTGTTCAGCATTTGTCAGTGAACGGCTACATTGCC 270

Qy 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

Db 271 TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGGTATCCAGGCTATC 330

Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81

Db 331 CAGAAATCAGATGAGGCGCCACCCATTTCAGGCGCATTTTAGAATCTGAAGTGTCTATATCA 390

Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101

Db 391 GAGGAATTGGTTCAGAAATACAGTAATTCCTGCTCTGGTCATGTGAACAGCAATAA 450  
 Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 451 GAACCTCAGCGCGCTTCTTCTAGTTGATGATTTAGTTGATTCCTGAAGTTTGCAGTGTG 510  
 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 511 ATGTGGGTGTTTACTTATGTGTGGTGGCTTGTTCATATGGTCTGCACACTACTGATTTAGCT 570  
 Qy 142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 571 CTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCAATCAGTGCAGATAGATCAT 630  
 Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 631 TATCTAGGACTTGCAACAAGAGTGTTAAGGATGCCATGGCCAAATCCAAAGCAAAATC 690  
 Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
 Db 691 CCTGGATTGAAGCGCAAGCAGAT 714

## RESULT 45

AAV30920  
 ID AAV30920 standard; cDNA; 2386 BP.

XX AAV30920;

AC 14-SEP-1998 (first entry)

DT Human secreted protein BG160\_1 cDNA.

DE BG160\_1; secreted protein; protein factor; human; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 102..2030

FT /\*tag= a

FT sig\_peptide 1863..1899

FT /\*tag= b

FT /\*note= "putative leader/signal peptide"

FT mat\_peptide 1900..2027

FT /\*tag= c

XX WO9817687-A2.

PN 30-APR-1998.

PD 24-OCT-1997; 97WO-US019590.

XX 25-OCT-1996; 96US-00740274.

PR 24-OCT-1997; 97US-00740274.

XX (GEMY ) GENETICS INST INC.

PA Jacobs K, McCoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;

XX Spaulding V, Agostino MJ;

PI WPI; 1998-261426/23.

DR P-PSDB; AAW58383.

XX Nucleic acid encoding secreted protein from human cells - useful, e.g. as

PT immuno-modulators, anti-tumour agents, promoters of tissue growth,

PT haemostatic and thrombolytic agents etc.

XX Claim 20; Page 74-75; 114pp; English.

PS This cDNA clone, designated BG160\_1, codes for a novel human secreted

XX protein (see AAW58383). It was isolated from a human adult brain cDNA

CC library using methods selective for cDNAs that encode secreted proteins.

CC The clone is deposited in composite clone ATCC 98232; an oligonucleotide

CC (see AAT99725) is designed to isolate the clone from the composite. The

CC predicted AT415\_4 amino acid sequence shows homology to neuroendocrine-  
 CC specific proteins. Novel cDNA clones (see AAV30916-32) coding for human  
 CC secreted proteins (see AAW58580-90) are claimed. These can be used for  
 CC recombinant production of the secreted proteins for analysis,  
 CC characterisation, diagnostic or therapeutic use. They can also be used as  
 CC tissue or mol.wt. markers, for chromosome identification, to identify  
 CC genetic disorders, to isolate new related DNA, as sources of primers for  
 CC PCR, to generate antibodies, and in interaction trap assays. The secreted  
 CC proteins may also have many biological activities, e.g. cytokine,  
 CC immunomodulator, haematopoiesis regulating activity, tissue growth  
 CC activity, activin or inhibin activity, chemotactic or chemokinetic  
 CC activity, haemostatic and thrombolytic activity, receptor/ligand  
 CC activity, antiinflammatory, cadherin and tumour invasion suppressor  
 CC activity, and tumour inhibition activity. The proteins can be expressed  
 CC in vivo from DNA, introduced in gene therapy vectors  
 XX  
 SQ Sequence 2386 BP; 756 A; 450 C; 494 G; 686 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.63e-98 Length: 2386  
 Score: 894.50 Matches: 184  
 Percent Similarity: 97.35% Conservative: 0  
 Best Local Similarity: 97.35% Mismatches: 0  
 Query Match: 96.08% Indels: 5  
 DB: Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAV30920 (1-2386)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
 Db 1476 TCAGTTGTTGACCTCTCTACTGGAGACATTAAGAGACTGGAGTGGTGGTGGCC 1535  
 Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 1536 AGCTATTCTCTGCTTTTCATTGACAGTATTTCAGCATTTGTGAGCGTACAGCCTACAT 1595  
 Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 1596 GCCTTGGCGCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGCTGTGATCCAGCT 1655  
 Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 1656 ATCCAGAAATCAGATGAGCGCCACCCATTCAGG-----GAAGTTGCTATA 1700  
 Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 Db 1701 TCTGAGGAGTTGGTTTCAGAAGTACAGTAAATTCCTCTTTGGTTCATGTGAACGCACATA 1760  
 Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 1761 AAGGAACCTCAGCGCGCTCTTCTTAGTATGATTTAGTTGATTTCTCTGAAGTTGCGATG 1820  
 Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 Db 1821 TTGATGTGGGTATTTACCTATGTTGGTGGCTTTGTTTAAATGGTCTGCACACTACTGATTTTG 1880  
 Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 Db 1881 GCTCTCATTTTCATCTTTCAGTGTTCCTGTTTATGAAACGGCATCAGGCACACATAGAT 1940  
 Qy 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 1941 CATTTATCTAGGACTTGCAAAATAGAAATGTTTAAAGATGCTATGGCTAAATCCAAAGCAAA 2000  
 Qy 181 IleProGlyLeuLysArgLysAlaGlu 189  
 Db 2001 ATCCCTGGATTGAAGCGCAAGCTGAA 2027

## RESULT 46

ABK90135

ID ABK90135 standard; DNA; 1798 BP.

XX

AC ABK90135;

XX 21-OCT-2002 (first entry)

XX DNA encoding human NogoC protein.

XX Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;

XX stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;

XX neuroblastoma; hyperproliferative disorder; dysproliferative disorder;

XX cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;

XX tissue hypertrophy; central nervous system; axon regeneration; NogoC;

XX Nogo-associated disease; metastasis; gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 215..814

XX /\*tag= a

XX /product= "Human NogoC protein"

XX WO200257483-A2.

XX 25-JUL-2002.

XX 18-JAN-2002; 2002WO-GB000228.

XX 18-JAN-2001; 2001GB-00001312.

XX (GLAXO ) GLAXO GROUP LTD.

XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Blackstock WP, Hale RS, Prinjha R, Rowley A;

XX WPI; 2002-599722/64.

XX P-PSDB; ABG30939.

XX Identifying modulators of Nogo or BACE activity for treating acute

XX neuronal injuries, neoplastic or dysproliferative disorders, comprises

XX providing and monitoring interaction between Nogo and BACE polypeptides.

XX Disclosure; Page 62-64; 68pp; English.

XX The present invention relates to a new method of identifying modulators

XX of Nogo function or BACE activity. The method involves providing Nogo and

XX BACE polypeptides capable of binding with each other, monitoring the

XX interaction between these polypeptides, and determining if the test agent

XX is a modulator of Nogo or BACE activity. The method is useful in treating

XX acute neuronal injuries, such as spinal or head injury, stroke,

XX peripheral nerve damage, and in neoplastic (e.g. glioblastomas,

XX neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.

XX cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue

XX hypertrophy) of the central nervous system. The BACE polypeptide is

XX useful in screening methods to identify agents that may act as modulators

XX of BACE activity and in particular agents that may be useful in treating

XX Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,

XX and the polynucleotide encoding the BACE polypeptide are useful in

XX manufacturing a medicament for the treatment or prevention of disorders

XX responsive to the modulation of Nogo activity, in alleviating the

XX symptoms or improving the condition of a patient suffering from this

XX disorder, in axon regeneration, or in preventing metastasis or spreading

XX of a cancer. The polynucleotide may also be an essential component in

XX assays, a probe, in recombinant protein synthesis, and in gene therapy

XX techniques. The present nucleic acid sequence encodes the human NogoC

XX protein of the invention

XX Sequence 1798 BP; 540 A; 314 C; 392 G; 552 T; 0 U; 0 Other;

XX

Alignment Scores:

Pred. No.: 1, 19e-97 Length: 1798

Score: 886.00 Matches: 187

Percent Similarity: 98.94% Conservative: 0

Best Local Similarity: 98.94% Mismatches: 1

Query Match: 95.17% Indels: 2

DBs: 6 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ABK90135 (1-1798)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21

DB 248 GTTGTGACCTCCCTGTACTCGAGAGACATTAAAGAACTGGAGTGGTGTGTTGGTCCACG 307

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

DB 308 CTATTCCTGCTGCTTTCATTGACAGATTCAGCAATTGACGCTTAACAGCTACATTGCC 367

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleAlaIle 61

DB 368 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 427

QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81

DB 428 CAGAAATCAGATGAAGGCCACCCCATTCAGGGCATATCTGGAAATCTGAAGTTGCTATATCT 487

QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101

DB 488 GAGGAGTTGGTTTCAAGAGTACAGTAATTTCTGCTCTTGGTCAATGTAAGTGCAGTAAG 547

QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121

DB 548 GAACCTCAGGGCGCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTCAGTGTG 607

QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141

DB 608 ATGTGGGTATTTACCTATGTTGGTGGCTTGTAAATGCTCTGACACTACTGATTTGGCT 667

QY 142 LeuIleSerLeu-PheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHi 161

DB 668 CTCAATTCACCTCTTCAGTGTCTCTGTTATTTA-GAACGGCATCAGGCACAGATAGATCA 726

QY 161 sTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

DB 727 TTAATCTAGGACTTCGAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAGCAAAAT 786

QY 181 eProGlyLeuLysArgLysAlaGlu 189

DB 787 CCCTGGATTGAAGCGCAAAAGCTGAA 811

RESULT 47

AAF98399

ID AAF98399 standard; cDNA; 2386 BP.

XX AAF98399;

XX 07-JUN-2001 (first entry)

XX Human cDNA clone BG160\_1 sequence SEQ ID 41.

DE Human; secreted protein; nutrient; cytokine modulator; proliferation;

XX differentiation; immune system modulator; tissue growth; chemotactic;

XX haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;

XX haematopoiesis.

XX Homo sapiens.

OS WO200119988-A1.

XX 22-MAR-2001.

XX 14-SEP-2000; 2000WO-US025135.

XX 17-SEP-1999; 99US-00398829.

XX (GEM ) GENETICS INST INC.

XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;

XX Merberg D, Treacy M, Bowman MR, Spaulding V, Agostino MJ;

DR WPI; 2001-244801/25.  
 DR P-PSDB; AAB90682.  
 XX Isolated nucleic acids encoding polypeptides, useful for modulating e.g.  
 PT cytokine and cell proliferation/differentiation activity, the immune  
 PT system and hematopoiesis regulating activity.  
 XX Claim 1; Page 408-409; 557pp; English.  
 XX Human cDNA clones represented in AAF98374 - AAF98489 encode secreted  
 CC proteins AAB90667 - AAB90750. The cDNA clones are isolated from various  
 CC tissue types, and may be used in the prevention, treatment and diagnosis  
 CC of diseases associated with inappropriate protein expression. The  
 CC polypeptides and nucleic acids may be used as nutrients or to modulate  
 CC cytokine and cell proliferation/differentiation activity and may also be  
 CC involved in modulation of the immune system. The cDNA sequences,  
 CC proteins, their agonists and/or antagonists exhibit hematopoiesis  
 CC regulating activity; tissue growth activity; activin/inhibin activity;  
 CC chemotactic/chemokinetic activity; haemostatic and thrombolytic activity;  
 CC receptor/ligand activity; anti-inflammatory activity; hematopoiesis  
 CC activity; cadherin/tumour suppressor activity; and/or tumour inhibition  
 CC activity. Included in the invention are probes represented in AAF98490 -  
 CC AAF98572 which are specific for the cDNA clones encoding the secreted  
 CC proteins  
 XX  
 SQ Sequence 2386 BP; 756 A; 448 C; 496 G; 686 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 2,04e-97 Length: 2386  
 Score: 885.50 Matches: 183  
 Percent Similarity: 96.83% Conservative: 0  
 Best Local Similarity: 96.83% Mismatches: 1  
 Query Match: 95.11% Indels: 5  
 DB: Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAF98399 (1-2386)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLeuThyGlyValValPheGlyAla 20  
 DB 1476 TCAGTTGTTGACCTCCTCTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCT 1535  
 QY 21 SerLeuPheLeuLeuSerLeuThyValPheSerIleValSerValThrAlaTyrIle 40  
 DB 1536 AGCCTATTCTGCTGCTTTCTATGACAGTATTGAGCATTTGTGAGCGTAAACGCTACATT 1595  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIlysglyValIleGlnAla 60  
 DB 1596 GCCTTGGCCCTGCTCTCTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCT 1655  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 1656 ATCCAGAAATCAGATCAAGGCCACCCATTCAGG-----GAAGTTGCTATA 1700  
 QY 81 SerGluLeuValGlnIlystYrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 DB 1701 TCTGAGGAGTGGTTCAGAGTACAGTAATTCCTCTTGGTCATGTGAAGTGCAGATA 1760  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 1761 AAGGAATCAGGCGCTCTCTTAGTTGATGATTTAGTTGATTCCTGAGTTGCGAGT 1820  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 DB 1821 TTGATGTGGGTATTTACCTATGTTGTGCTGCTTTAAATGGTGTGACACTACTGATTTTG 1880  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 DB 1881 GCTCTCATTTCTCTCTGAGTGTGTGTATTATGACGGCATCAGGCACAGATAGAT 1940  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 1941 CATTATCTAGGACTTCGAAATAGATGTTAAAGATGCTATGCTAAATCCAGCAAAA 2000

QY 181 lleProGlyLeuLysArgLysAlaGlu 189  
 DB 2001 ATCCCTGGATTGAAGCGCAAGCTGAA 2027  
 RESULT 48  
 ID ABK34580  
 XX ABK34580 standard; cDNA; 1514 BP.  
 AC ABK34580;  
 XX  
 DT 08-MAY-2002 (first entry)  
 XX  
 DE Human cDNA for novel secreted protein, SEQ ID 349.  
 KW Human; ss; gene; secreted protein; immune deficiency; viral infection;  
 KW bacterial infection; fungal infection; autoimmune disorder; burn;  
 KW rheumatoid arthritis; multiple sclerosis; autoimmune thyroiditis;  
 KW diabetes; allergy; asthma; neurodegenerative disease; Crohn's disease;  
 KW Alzheimer's disease; Parkinson's disease; liver fibrosis; tumour;  
 KW coagulation disorder; haemophilia; inflammatory disorder; ulcer;  
 KW tissue regeneration; wound healing; haematopoiesis; myeloid deficiency;  
 KW lymphoid cell deficiency.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177290-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 29-MAR-2001; 2001WO-US010295.  
 XX  
 PR 06-APR-2000; 2000US-0194941P.  
 XX  
 PA (GENY ) GENETICS INST INC.  
 XX  
 PI Wong GG, Clark HF, Fichtel K, Agostino MJ, Howes SH, Resnick RJ;  
 PI Gulukota K, Graham JR;  
 XX  
 DR WPI; 2002-179323/23.  
 XX  
 PT Six hundred and twenty five polynucleotides derived from a variety of  
 PT human tissue sources which encode secreted proteins, useful for treating  
 PT immune deficiencies and disorders such as autoimmune disorders.  
 XX  
 PS Claim 1; Page 173; 339pp; English.  
 XX  
 CC The invention relates to 625 polynucleotides which have been derived from  
 CC a variety of human tissue sources and which encode novel secreted  
 CC proteins, their complements and sequences that hybridise to them. Also  
 CC included are a vector comprising the polynucleotide, a host cell  
 CC transformed with the vector, the proteins encoded by the polynucleotides,  
 CC antibodies that bind to the proteins and identification of modulators of  
 CC the proteins or the expression of the polynucleotide. The polynucleotides  
 CC can be used as probes for the identification and isolation of full length  
 CC cDNA and genomic DNA. The polynucleotides and proteins can also be used  
 CC as nutritional supplements. The protein is useful in the treatment of  
 CC various immune deficiencies and disorders such as viral infections,  
 CC bacterial infections, fungal infections, autoimmune disorders (e.g.  
 CC rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis and  
 CC diabetes) and allergic reactions and conditions (e.g. asthma). They are  
 CC also useful for treating neurodegenerative diseases (e.g. Alzheimer's  
 CC disease, Parkinson's disease), liver fibrosis, coagulation disorders  
 CC (e.g. haemophilia), inflammatory disorders (e.g. Crohn's disease) and  
 CC tumours. They are also useful for tissue regeneration, for wound healing  
 CC and in the treatment of burns, incisions and ulcers. The proteins are  
 CC also useful for regulating haematopoiesis, for treating myeloid or  
 CC lymphoid cell deficiencies. The present sequence is one of the 625 cDNA  
 CC sequences encoding a secreted protein  
 XX  
 SQ Sequence 1514 BP; 455 A; 258 C; 313 G; 488 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1.95e-95 Length: 1514



QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 848 CTATTCCTCTGCTTTTCATGACGATTCAGCATTTGAGCGTAACAGCCCTACATTCGC 907  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 908 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 967  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 968 CAGAAATCAGATCAAGGCCACCCATTGAGGCATATCTGGAATCTGAACTTGTATATCT 1027  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
DB 1028 GAGGAGTTGGTTTTCAGAAATACAGTAATCTGCTCTTGGTCATGTGAAGTGCAGTAAG 1087  
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 1088 GAATCAGGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAGCT----- 1137  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
DB 1137 ----- 1137  
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
DB 1138 CTATTTTCATCTTTCAGTGTCTCTGTTATTTATGAAACGGCATCAGGCACAGATAGATCAT 1197  
QY 162 TyrLeuGlyLeuAlaGlnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 1198 TATCTAGGACTTTCGAATTAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAATC 1257  
QY 182 ProGlyLeuLysArgLysAlaGlu 189  
DB 1258 CTGGGATTAGCGCAAGCTGAA 1281  
RESULT 50  
ID ABX43312  
XX ABX43312 standard; cDNA; 422 BP.  
XX AC ABX43312;  
XX 20-FEB-2003 (first entry)  
XX Bovine EST associated with lactation/muscle/fat deposition #8477.  
XX Bovine; ss; EST; expressed sequence tag; lactation; LMFD;  
XX muscle deposition; fat deposition; genome mapping; gene identification;  
XX gene analysis; cattle breeding.  
XX Bos Taurus.  
XX US2002137139-A1.  
XX 26-SEP-2002.  
XX 24-SEP-2001; 2001US-00960352.  
XX 12-JAN-1999; 99US-0115707P.  
XX 11-JAN-2000; 2000US-00480902.  
XX (BYAT/) BYATT J C.  
XX (MATH/) MATHIALAGAN N.  
XX (TAON/) TAO N.  
XX (WARR/) WARREN W C.  
XX Byatt JC, Mathialagan N, Tao N, Warren WC;  
XX WPI; 2003-110599/10.  
XX New nucleic acid associated with lactation, and muscle and fat  
XX deposition, useful for genome mapping, gene identification and analysis,  
PT

PT cattle breeding, or for genetically improving cattle.  
XX Claim 2; SEQ ID NO 8477; 245pp; English.  
XX The invention relates to a purified nucleic acid molecule associated with  
CC lactation or muscle and fat deposition (designated LMFD), derived from  
CC cattle, and the LMFD nucleic acid can specifically hybridize to a second  
CC nucleic acid molecule comprising any of 15112 nucleotide sequences,  
CC appearing as ABX4336-ABX4997, or complements of them. Also included are  
CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic  
CC acid linked to a promoter and a 3' non-translated sequence that  
CC functions in the cell to cause termination of transcription and addition  
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and  
CC (2) determining a level or pattern of a molecule in a bovine cell or  
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any  
CC of the 15112 nucleic acid sequences or its complement or fragment) with a  
CC complementary nucleic acid molecule obtained from the bovine cell or  
CC tissue, where hybridisation between the marker nucleic acid and the  
CC complementary nucleic acid permits the detection of the molecule; and (b)  
CC detecting the level or pattern of the complementary nucleic acid; where  
CC the detection of the complementary nucleic acid is predictive of the  
CC level or pattern of the molecule. The LMFD nucleic acid is used for  
CC determining a level or pattern of a molecule in a bovine cell or tissue.  
CC It is useful for genome mapping, gene identification and analysis, cattle  
CC breeding, preparation of constructs for use in cattle gene expression, or  
CC for genetically improving cattle. The present sequence is one of the  
CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The  
CC present sequence was not shown in the specification but was obtained in  
CC electronic format from the USPTO web site:  
CC seqdata.uspto.gov/sequence.html?DocID=20020137139  
XX  
SQ Sequence 422 BP; 109 A; 79 C; 94 G; 140 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 3,14e-75 Length: 422  
Score: 695.00 Matches: 140  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 74.65% Indels: 0  
DB: 8 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ABX43312 (1-422)

QY 37 ThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGly 56  
DB 2 ACGGCTACATTCGCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGT 61  
QY 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76  
DB 62 GTGATCCAGGCTATCCAGAAATCTGATGAAGCCACCCATTCCAGGCATATTTGGAATCT 121  
QY 77 GluValAlaIleSerGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal 96  
DB 122 GAAGTTGCTATATCTGAGGAGTTGGTTCAAGAGTACAGCAATTCCTCTGCTCATGTT 181  
QY 97 AsnCysThrIleLysGluLeuArgLeuPheLeuValAspLeuValAspSerLeu 116  
DB 182 AACTGCACAATAAAGAACTCAGACGCCCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTG 241  
QY 117 LysPheAlaValLeuMetTrpValPheThrTyrValGlyValAlaLeuPheAsnGlyLeuThr 136  
DB 242 AAGTTTGCACTGTGATGTTGGGTATTTACTATGTTGGTCCCTTTGTTCAATGGTCTGACA 301  
QY 137 LeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGln 156  
DB 302 CTACTAATTTTGGCTCTGATTTTCACTTTTCACTTTTCTGTTTATTTATGAAGGCATCAG 361  
QY 157 AlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLys 176  
DB 362 GCGCAATAGATCATTTATCTGGACTTGCATAAAGATGTTAAAGATGCTATGGCTAAA 421  
RESULT 51  
ADJ56527



ADJ56527 standard; cDNA; 1520 BP.  
 AC ADJ56527;  
 XX  
 XX  
 XX 06-MAY-2004 (first entry)  
 DT  
 XX  
 DE Rat cDNA differentially expressed in MYCN activated cells SeqID 333.  
 XX  
 XX rat; differential expression; transactivator; proto-oncogene;  
 KW neuroblastoma; small cell lung cancer; cytostatic; gene therapy; ss;  
 KW MYCN activated cell.  
 XX  
 XX Rattus norvegicus.  
 OS  
 XX  
 XX US2003119009-A1.  
 PN  
 XX  
 XX 26-JUN-2003.  
 PD  
 XX  
 XX 25-FEB-2002; 2002US-00084817.  
 PF  
 XX  
 XX 23-FEB-2001; 2001US-0270784P.  
 PR  
 XX  
 XX (STUA//) STUART S G.  
 PA (NUCH//) NUCHTERN J G.  
 PA (PLON//) PLON S E.  
 PA (SHOH//) SHOHET J M.  
 XX  
 XX  
 PI Stuart SG, Nuchtern JG, Plon SE, Shohet JM;  
 XX  
 XX WPI; 2003-635698/60.  
 DR  
 XX  
 XX New genes regulated by MYCN activation, useful in gene therapy,  
 PT particularly for treating a subject with e.g. neuroblastoma or other  
 PT cancers, or for diagnosing, staging or monitoring the treatment of the  
 PT cancer.  
 XX  
 XX  
 PS Claim 1; SEQ ID NO 333; 27pp; English.  
 XX  
 XX This invention relates to novel isolated cDNAs that are differentially  
 CC expressed in MYCN activated cells. Specifically, it refers to  
 CC polynucleotide sequences that exhibit differential expression patterns in  
 CC cells activated by the transactivator MYCN, where MYCN is a proto-  
 CC oncogene that is amplified in neuroblastoma cells and is common in small  
 CC cell lung cancers. The present invention describes these cDNA molecules  
 CC as useful for in hybridisation assays to detect expression of nucleic  
 CC acids (or complementary nucleic acids) in a present in a given sample, as  
 CC well as for screening assays by identifying molecules or compounds that  
 CC specifically bind the cDNA as a ligand and modulate function or activity.  
 CC Accordingly, these compositions exhibit cytostatic activity and can also  
 CC be used for gene therapy purposes. This polynucleotide sequence is a cDNA  
 CC that is differentially expressed in MYCN activated cells, given in an  
 CC exemplification of the invention. NOTE: This sequence does not appear in  
 CC the printed specification but has been obtained in electronic format from  
 CC the US Patent Office at  
 XX ftp.segdata.uspto.gov/sequence.html?docID=20030119009.  
 XX  
 XX  
 SQ Sequence 1520 BP; 398 A; 354 C; 336 G; 432 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 7.31e-73 Length: 1520  
 Score: 682.00 Matches: 128  
 Percent Similarity: 85.03% Conservative: 31  
 Best Local Similarity: 68.45% Mismatches: 28  
 Query Match: 73.25% Indels: 0  
 DB: 10 Gaps: 0  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADJ56527 (1-1520)  
 Qy 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValAlaPheGlyAlaSerLeu 22  
 DB 176 ATTGACCTGTTGTATTTGGCGGACATCAAGCAGACGCGCATCGTGTGTTGGAGTTCTCTG 235  
 Qy 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerIleValThrAlaTyrIleAlaLeu 42

Db 236 CTGCTGCTCTCTCTCCCTCAGCCAGTTTCCAGCGTGGTGGAGCGTCTGCTGGCCCTACCTGGCCCTG 295  
 Qy 43 AlaleuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
 Db 296 GCGGCACTCTCAGCCACCATCAGTTTCCGCATCTACAAGTCTGTTTTCACAGCAGTGCAG 355  
 Qy 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
 Db 356 AANACCGACGAGGCCACCTTTCAAGCCCTACTTTGGAGCTTGAGATCACCTTTCTCAG 415  
 Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102  
 Db 416 GAGCAGATTCAAGAGTACACGAGCTCCTCGAGTTCTACGTGACACGACACTTAAGGAA 475  
 Qy 103 LeuArgArgLeuPheLeuValAspIleValAspSerLeuLysPheAlaValLeuMet 122  
 Db 476 CTGAGGAGGCTCTTCTTGTCCAGGACCTGTGGATTCTTTAAATTTGTCAGTCTCTGATG 535  
 Qy 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeu 142  
 Db 536 TGGCTCTGACCTAGCTTGGGCTCTCTTCAATGGCTGACCTGCTGCTCATGGCTGTG 595  
 Qy 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162  
 Db 596 GTTTCATGTTTACTCTACTCTACCTAGTGTATGTTAAGCACCAGGCACAGATTGACCAATAT 655  
 Qy 163 LeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
 Db 656 CTGGGACTTGTGAGGACTTCACATAAATGCTGTGTGGCAAGATTTCAGGCTAAATCCCA 715  
 Qy 183 GlyLeuLysArgLysAlaGlu 189  
 Db 716 GCGCTAAGAGGCACGCTGAG 736  
 RESULT 52  
 ADO07887  
 ID ADO07887 standard; cDNA; 2331 BP.  
 XX  
 AC ADO07887;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Human polynucleotide #66.  
 XX  
 KW Human; gene; ss; fat cell number; fat cell size; obesity; diabetes;  
 KW anorectic; antidiabetic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004071700-A1.  
 XX  
 PD 15-APR-2004.  
 XX  
 PF 09-OCT-2002; 2002US-00267502.  
 XX  
 PR 09-OCT-2002; 2002US-00267502.  
 XX  
 PA (LIFE-) LIFE SCI DEV CORP.  
 XX  
 PI Kim J, Galant R;  
 XX  
 DR WPI; 2004-328526/30.  
 DR P-FSDB; ADO08104.  
 XX  
 PT Identifying compounds that influence fat cell number or size for treating  
 PT or preventing obesity or diabetes by exposing the cell to the agent and  
 PT identifying fat cell number or size relative to cells not exposed to the  
 PT agent.  
 XX  
 PS Claim 1; SEQ ID NO 213; 275pp; English.  
 XX  
 XX The invention relates to a method of identifying compounds that influence

CC fat cell number or size comprising providing a cell that expresses a gene  
CC and an agent, exposing the cell to the agent and identifying fat cell  
CC number or size relative to cells not exposed to the agent. The method  
CC also comprises providing an expression vector and an agent, exposing the  
CC vector to the agent, detecting a change in expression of the gene  
CC relative to expression of the gene in an expression vector not exposed to  
CC the agent, treating a subject with the agent and identifying fat cell  
CC number or size in the subject. The agent comprises an antisense  
CC oligonucleotide. The subject comprises a mammal, preferably a human. The  
CC method also comprises providing a polypeptide and an agent, exposing the  
CC polypeptide to the agent, detecting binding of the agent to the  
CC polypeptide or a change in an activity of the polypeptide, treating a  
CC subject with the agent and identifying fat cell number or size in the  
CC subject. The agent comprises an antibody. A method of regulating fat cell  
CC number or size comprises providing a subject containing fat cells and an  
CC agent that changes the expression of a gene, and treating the subject  
CC with the agent under conditions so that fat cell size or number in the  
CC subject is altered. The method is useful for identifying compounds that  
CC influence fat cell number or size, for preparing a composition for  
CC treating or preventing obesity or diabetes. This sequence represents  
CC human cDNA used in the scope of the invention.  
XX  
SQ Sequence 2331 BP; 552 A; 698 C; 649 G; 432 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.33e-72 Length: 2331  
Score: 682.00 Matches: 128  
Percent Similarity: 85.03% Conservative: 31  
Best Local Similarity: 68.45% Mismatches: 28  
Query Match: 73.25% Indels: 0  
DB: 12 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADO07887 (1-2331)

QY 3 ValAspLeuLeuThrTrpArgSepIleLysThrGlyValValPheGlyAlaSerLeu 22  
DB 1768 ATTGACCTGTGATTGGCGGACATCAAGCAGCGGCATCGTGTGGAGATTCTCG 1827  
QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
DB 1828 CTGCTGCTCTCTCCCTGACCCAGTTCAGCGTGTGAGCGTCTGCGCTACCTGGCCCTG 1887  
QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaLeu 62  
DB 1888 GCGGCATCTCCAGCCACCATCATGTTTCGCGCATCTACAAGTCTGTTTACAAGCAGTGCAG 1947  
QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
DB 1948 AAMACCGACGAGCCACCCCTTCAAGGCTACTTGAGCTTGAGATCACTTCTCTAG 2007  
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102  
DB 2008 GAGCAGATTTCAGAGTACAGGACTCGCTGACCTTCTACGTGAACGACACTTAAGGAA 2067  
QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
DB 2068 CTGAGGAGGCTCTCTCTGTCAGGACCTGGTGGATTCCTTAAATTTGAGTCTCTGATG 2127  
QY 123 TrpValPheThrTrpValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeu 142  
DB 2128 TGCTCTGACCTACCTGTTGGCGCTCTCTCAATGGCTGACCTGCTGCTGCTGCTGCTG 2187  
QY 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162  
DB 2188 GTTTCATGTTTACTCTACCTGTAGTGTATGTTAAGCAGCCAGGACAGATTGACCAATAT 2247  
QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
DB 2248 CTGGGACTTGTGAGGACTCATATAATGCTGTGTCGCAAGATTTCAGGCTAAATCCCA 2307  
QY 183 GlyLeuLysArgLysAlaGlu 189  
DB 2308 GCGGCTAAGGACGCTGAG 2328

RESULT 53  
AAX75770

ID AAX75770 standard; DNA; 3202 BP.  
XX  
AC AAX75770;  
XX  
DT 22-JUL-1999 (first entry)  
XX  
DE Human neuroendocrine-specific protein NSP-A DNA.  
XX  
KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;  
KW frameshift mutation; age-related disease; neurodegenerative disorder;  
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;  
KW Huntington's disease; multiple sclerosis; alcoholic liver disease;  
KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;  
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;  
KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;  
KW glial fibrillary acidic protein; GFAP; p33; semaphorin III; HUPF-1;  
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;  
KW high mobility group protein-C; neuroendocrine specific protein A; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO9845322-A2.  
XX  
PD 15-OCT-1998.  
XX  
PF 02-APR-1998; 98WO-IB000705.  
XX  
PR 10-APR-1997; 97US-0043163P.  
XX  
PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.  
PA (UYRO-) UNIV ROTTERDAM ERASMUS.  
PA (UYUT-) RIJKSUNIV UTRECHT.  
XX  
PI Van Leeuwen FW, Grosveld FG, Burbach JPH;  
XX  
WPI; 1998-609901/51.  
XX  
PT Diagnosing disease by detecting frameshift mutations in RNA or  
PT corresponding protein mutations - used to diagnose cancer and  
PT neurological diseases, particularly Alzheimer's disease, and also for  
PT treatment and prevention with specific ribozymes or wild-type RNA.  
PS Disclosure; Fig 19; 258pp; English.  
XX  
CC This invention describes a novel method for the diagnosis of a disease  
CC caused by, or associated with, an RNA molecule that has a frameshift  
CC mutation. The method is used to diagnose age-related diseases, especially  
CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's  
CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,  
CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II  
CC and many others listed) or susceptibility to these disorders. The method  
CC allows a definitive diagnosis of Alzheimer's disease in living patients,  
CC at an early stage. It is based on the observation that disease may be  
CC caused by mutations in RNA rather than DNA. The invention describes the  
CC use of neuronal system RNA molecules, specifically microtubule associated  
CC beta-amyloid precursor protein (beta-APP), the microtubule associated  
CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule  
CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,  
CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic  
CC protein (GFAP), the cellular tumour antigen p33, B-cell leukemia/lymphoma  
CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group  
CC protein-C (HMGP-C) and neuroendocrine specific protein A. This sequence  
CC encodes the wild type and mutant protein fragments represented in  
CC AAY21434-Y21520  
XX  
SQ Sequence 3202 BP; 784 A; 891 C; 825 G; 702 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 2.08e-72 Length: 3202  
Score: 682.00 Matches: 128

Percent Similarity: 85.03% Conservative: 31  
Best Local Similarity: 68.45% Mismatches: 28  
Query Match: 73.25% Indels: 0  
DB: 2 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAX75770 (1-3202)

Qy 3 ValaspLeuLeuTyrTrpArgaspIleLysLysThrGlyValValPheGlyAlaSerLeu 22  
Db 1890 ATTGACCTGTTGTTATGGGGGACATCAAGCAGCGGCATCGTGTGGGAGTTCTCTG 1949

Qy 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
Db 1950 CTGCTGCTCTTCTCCCTCACCAGTTCAAGCGTGTGAGCGTGTGGCTCTACCTGCGCCCTG 2009

Qy 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
Db 2010 GCCGCACCTTCAGCCACCATCATGTTCCGATCTCAAGTCTGTTTAAAGCAGTGCAG 2069

Qy 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
Db 2070 AAAACCGAGGAGGCCACCTTTCAAGCCTACTTGGAGCTTGAGATCACCTTCTCTAG 2129

Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCyThrIleLysGlu 102  
Db 2130 GAGCAGATTCAAGTACAGGACTCCCTGCGAGTTCTAGTGAACAGCAGCAGCTTAAGGAA 2189

Qy 103 LeuArgArgLeuPheLeuValAspPheLeuValAspSerLeuLysPheAlaValLeuMet 122  
Db 2190 CTGAGGAGCTCTTCTCTTGTCCAGACCTGGTGGATTCCTTAAATTTTGCAGTCTCATG 2249

Qy 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeu 142  
Db 2250 TGGCTCTGACCTAGTGGGCTCTCTTCAATGAGCTGACCTGCTGCTCATGCTGTG 2309

Qy 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162  
Db 2310 GTTTCATGTTTACTCTACTCTAGTGTATGTTAAGCAGCAGGACGACGATGACCAATAT 2369

Qy 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
Db 2370 CTGGGACTTGTGAGGACTCACATAAATGCTGTGTGGCAAGATTTCAGGCTAAATCCCA 2429

Qy 183 GlyLeuLysArgLysAlaGlu 189  
Db 2430 GCGGCTAAGGACGCTGAG 2450

RESULT 54  
ID ABL64900 standard; DNA; 3202 BP.  
XX ABL64900;  
AC ABL64900;  
XX  
XX  
DT 15-MAY-2002 (first entry)  
XX  
DE Lung cancer related gene sequence SEQ ID NO:3237.  
XX  
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;  
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;  
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;  
KW gene; ds.  
XX  
OS Homo sapiens.  
XX  
XX WO200194629-A2.  
XX  
PD 13-DEC-2001.  
XX  
XX 30-MAY-2001; 2001WO-US010838.  
XX  
PR 05-JUN-2000; 2000US-0209473P.  
PR 05-JUN-2000; 2000US-0209531P.  
PR 18-SEP-2000; 2000US-0233133P.

PR 18-SEP-2000; 2000US-0233617P.  
PR 20-SEP-2000; 2000US-0234009P.  
PR 20-SEP-2000; 2000US-0234034P.  
PR 20-SEP-2000; 2000US-0234052P.  
PR 22-SEP-2000; 2000US-0234509P.  
PR 22-SEP-2000; 2000US-0234567P.  
PR 25-SEP-2000; 2000US-0234923P.  
PR 25-SEP-2000; 2000US-0234924P.  
PR 25-SEP-2000; 2000US-0235077P.  
PR 25-SEP-2000; 2000US-0235082P.  
PR 25-SEP-2000; 2000US-0235134P.  
PR 26-SEP-2000; 2000US-0235637P.  
PR 26-SEP-2000; 2000US-0235638P.  
PR 27-SEP-2000; 2000US-0235711P.  
PR 27-SEP-2000; 2000US-0235720P.  
PR 27-SEP-2000; 2000US-0235840P.  
PR 27-SEP-2000; 2000US-0235863P.  
PR 28-SEP-2000; 2000US-0236028P.  
PR 28-SEP-2000; 2000US-0236032P.  
PR 28-SEP-2000; 2000US-0236033P.  
PR 28-SEP-2000; 2000US-0236034P.  
PR 28-SEP-2000; 2000US-0236109P.  
PR 28-SEP-2000; 2000US-0236111P.  
PR 29-SEP-2000; 2000US-0236842P.  
PR 29-SEP-2000; 2000US-0236891P.  
PR 02-OCT-2000; 2000US-0237172P.  
PR 02-OCT-2000; 2000US-0237173P.  
PR 02-OCT-2000; 2000US-0237278P.  
PR 02-OCT-2000; 2000US-0237294P.  
PR 02-OCT-2000; 2000US-0237295P.  
PR 02-OCT-2000; 2000US-0237316P.  
PR 03-OCT-2000; 2000US-0237425P.  
PR 03-OCT-2000; 2000US-0237598P.  
PR 03-OCT-2000; 2000US-0237604P.  
PR 03-OCT-2000; 2000US-0237606P.  
PR 03-OCT-2000; 2000US-0237608P.  
PR 01-NOV-2000; 2000US-0244867P.  
PR 01-NOV-2000; 2000US-0245084P.  
XX (AVAL-) AVALON PHARM.  
XX Young PE, Augustus M, Carter KC, Ebner R, (Enderess G, Horrigan S;  
PI Soppet DR, Weaver Z;  
XX  
XX WPI; 2002-188264/24.  
XX  
PT Screening for anti-neoplastic agent involves exposing cells to a chemical  
PT agent to be tested for anti-neoplastic activity, and determining a change  
PT in expression of a gene of a signature gene set.  
XX  
PS Claim 1; SEQ ID NO 3237; 44pp; English.  
XX  
CC The present invention describes a method (M1) for screening for an anti-  
CC neoplastic agent. The method involves exposing cells to a chemical agent  
CC to be tested for anti-neoplastic activity, determining a change in  
CC expression of at least one gene (I) of a signature gene set, where (I)  
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61654  
CC ABL70110), or is at least 95% identical to (S), where a change in  
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic  
CC activity and can be used in gene therapy. M1 can be used for screening an  
CC anti-neoplastic agent, and can be used for producing a product which is  
CC the data collected with respect to the anti-neoplastic agent as a result  
CC of M1, and the data is sufficient to convey the chemical structure and/or  
CC properties of the agent. M1 can be used in the treatment of cancer such  
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,  
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell  
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous  
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's  
CC tumour  
XX  
SQ Sequence 3202 BP; 784 A; 891 C; 825 G; 702 T; 0 U; 0 Other;



Db 2370 CTGGACCTGTGAGGACTCACATAAATGCTGTGTGGCAAGATTTCAGGCTAAATCCCA 2429  
QY 183 GlyLeuLeuValGlyAlaGlu 189  
Db 2430 GCGCTAAGAGGACGCTGAG 2450

## RESULT 56

ADR24525

ID ADR24525 standard; DNA; 3202 BP.

XX ADR24525;

AC ADR24525;

XX 21-OCT-2004 (first entry)

DT 21-OCT-2004 (first entry)

XX Breast cancer prognosis marker #386.

DE ds; breast cancer; prognosis; gene expression; diagnosis.

KW Homo sapiens.

XX WO2004065545-A2.

XX 05-AUG-2004.

XX 15-JAN-2004; 2004WO-US001100.

XX 15-JAN-2003; 2003US-00342887.

XX (ROSE-) ROSETTA INPHARMATICS LLC.

PA (NECA-) NETHERLANDS CANCER INST.

XX Van't Veer LJ, He Y;

PI WPI; 2004-593473/57.

XX Classifying a breast cancer patient according to prognosis comprises

CC determining the similarity between the level of expression of each of

CC five genes in a cell sample taken from patient, to control levels.

CC Disclosure; SEQ ID NO 386; 226pp; English.

XX The invention relates to a method of classifying a breast cancer patient

CC according to prognosis by determining the similarity between the level of

CC expression of each of five genes for which markers are listed in the

CC specification, in a cell sample taken from the breast cancer patient, to

CC control levels of expression for each respective five genes to obtain a

CC patient similarity value. The methods are useful for classifying a breast

CC cancer patient according to prognosis. Kits and computer program products

CC are useful for data analysis using the diagnostic, prognostic and

CC statistical methods of the invention. This sequence corresponds to a

CC marker used in the method of the invention.

XX Sequence 3202 BP; 784 A; 891 C; 825 G; 702 T; 0 U; 0 Other;

SQ Alignment Scores:

Pred. No.: 2,088-72 Length: 3202

Score: 682.00 Matches: 128

Percent Similarity: 85.03% Conservative: 31

Best Local Similarity: 68.43% Mismatches: 28

Query Match: 73.25% Indels: 0

DB: 13 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADR24525 (1-3202)

QY 3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22

Db 1890 ATTGACCTGTTGTAATGGCGGACATCAAGCAGCGGCGATCGTGTGGGAGTTTCCTG 1949

QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42

Db 1950 CTGCTGCTCTTCTCCCTGACCCAGTTCAGCGGTGGCGCTGCTGCTGCTGCTGCTG 2009

QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleAlaIleGln 62

Db 2010 GCCGACCTCTCAGCCACCACCATCAGTTTCGCATCTACAGTCTGTTTACAAGCAGTGCAG 2069  
QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
Db 2070 AAAACCGCAGCAAGGCCACCCCTTTCAAGGCCTACTTGGAGCTTGAGATCACCCCTTTCTCAG 2129  
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102  
Db 2130 GAGCAGATTCAAGAGTACACGACTGCTGCAGTCTTACGTGACGACACACTTAAGGAA 2189  
QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
Db 2190 CTGAGGAGGCTCTTCTTGTTCAGGACCTGCTGAGTCTCTTAAATTTGCAGTCTCTGATG 2249  
QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeu 142  
Db 2250 TGGCTCTCGACCTACGTTGGCGCTCTCTCAATGGCCCTGACCCCTGCTCATGCTGTG 2309  
QY 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162  
Db 2310 GTTTCATGTTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACT 2369  
QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
Db 2370 CTGGGACTTGTGAGGACTCACATAAATGCTGTGTGGCAAGATTTCAGGCTAAATCCCA 2429  
QY 183 GlyLeuLysArgLysAlaGlu 189  
Db 2430 GCGCTAAGAGGCGCAGCTGAG 2450

## RESULT 57

ADR65814

ID ADR65814 standard; DNA; 3202 BP.

XX ADR65814;

AC ADR65814;

DT 02-DEC-2004 (first entry)

XX Human prostatic carcinoma derived DNA SEQ ID 10 #1.

DE human; cytostatic; diagnosis; prostatic cancer;

KW differential expression analysis; ds.

XX Homo sapiens.

XX WO2004076614-A2.

XX 10-SEP-2004.

XX 22-FEB-2004; 2004WO-DE000433.

XX 27-FEB-2003; 2003DE-01009985.

XX 14-MAY-2003; 2003DE-01022134.

XX (HINZ/) HINZMANN B.

XX (DAHL/) DAHL E.

XX (ROSE/) ROSENTHAL A.

XX (HERM/) HERMANN K.

XX (PILA/) PILARSKY C.

XX Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarczyk C, Specht T;

XX Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;

XX Xinzhang L, Staub E;

XX WPI; 2004-653386/63.

XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,

XX useful for diagnosis, treatment and in screening for specific binding

XX agents.

XX Claim 1; Page 160; 1607pp; German.

CC This invention describes novel cytostatic polynucleotide and polypeptide  
CC sequences which can be used in a method for diagnosing prostatic cancer  
CC or the risk of developing prostatic cancer. Diagnosis is based on  
CC determining over transcription or over expression of the sequences in  
CC prostatic tissue. Screening for inhibitors of the sequences or detection  
CC substances involves a binding assay, any compounds that bind are  
CC selected, optionally after deconvolution of mixtures. Detection of a  
CC predetermined minimum level of the reporter indicates the presence of  
CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,  
CC short-interfering RNA or ribozymes; an organic molecule of molecular  
CC weight below 5000, preferably 300, that binds to the polypeptide; an  
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the  
CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human  
CC (monoclonal) antibody directed against Ab or any of the above derivatised  
CC with a reporter group, cell toxin, immunostimulatory molecules and/or  
CC radioisotope. The polynucleotides are identified in human prostatic  
CC cancer by differential expression analysis, using DNA microarrays,  
CC between normal and tumorous tissues, with (over)expression being detected  
CC by quantitative PCR. Analysis of prostatic cancer samples showed that  
CC CD24 was upregulated in many of them. Sections of tissue, isolated from  
CC prostatic cancer patients, or subjects at risk, were incubated  
CC sequentially with anti-human CD4 murine monoclonal antibodies;  
CC biotinylated second antibody; streptavidin-conjugated horseradish  
CC peroxidase and then diaminobenzidine as colour former (brown). The  
CC samples were counterstained with hemalum (blue). Malignant cells stained  
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of  
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and  
CC lymph node metastases were also stained. ADR65805-ADR65954 represent the  
CC polynucleotide and polypeptide sequences used in the method of the  
CC invention.

XX SQ Sequence 3202 BP; 784 A; 891 C; 825 G; 702 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	2, 08e-72	Length:	3202
Score:	682.00	Matches:	128
Percent Similarity:	85.03%	Conservative:	31
Best Local Similarity:	68.45%	Mismatches:	28
Query Match:	73.25%	Indels:	0
DB:	13	Gaps:	0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADR65814 (1-3202)

QY	3	ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu	22
DB	1890	ATTGACCTGTGTATTTGGCGGACATCAAGCAGCGGCATCGTGTTCGGAGTTCCTCG	1949
QY	23	PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu	42
DB	1950	CTGCTGCTCTTCTCCCTGACCCAGTTCAGCGTGTGCGCTGCTGCTACCTTCGCGCCG	2009
QY	43	AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln	62
DB	2010	GGCGCACTCTCAGCCACCATCAGTTTCGGCATCTACAGTCTGTTTACAGCAGTGCAG	2069
QY	63	LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu	82
DB	2070	AAAACCGCAGAGCCACCCCTTTCAAGGCGCTACTTGGAGCTTGAGATCACCCTTTCTCAG	2129
QY	83	GluLeuValGlnIlystYrSerAenSerAlaLeuGlyHisValAsnCysThrIleLysGlu	102
DB	2130	GACGACATCAGAAAGTACGGAGTTCGCTGCGAGTTCAGTCAAGCAGCAGTCAAGGAA	2189
QY	103	LeuArgGluLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet	122
DB	2190	CTGAGGAGGCTCTTCCTTTGTCAGGACCTGGTGGATTCTTAAATTTGAGTCTCTGATG	2249
QY	123	TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeu	142
DB	2250	TGCGTCTGACCTACGTTGGCGCTCTCTTCAATGGCGCTGACCTGCTGCTGCTGCTG	2309
QY	143	IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr	162

Db	2310	GTTCCTCAATGTTTACTCTACCTGTAGTGTATGTTAAGCACCAGGCACAGATTGACCAATAT	2369
QY	163	LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetalAlaLysIleGlnAlaLysIlePro	182
Db	2370	CTGGGACTTGTGAGGACTCACATAAATGCTGTGTGGCAAGATTGAGCTAAATCCCA	2429
QY	183	GlyLeuLysArgLysAlaGlu	189
Db	2430	GGCGCTAAGAGGCACGCTGAG	2450
RESULT 58			
ADR66747	ID ADR66747 standard; DNA; 3202 BP.		
XX	AC	ADR66747;	
XX	DT	02-DEC-2004 (first entry)	
XX	DE	Human prostatic carcinoma derived DNA SEQ ID 10 #4.	
XX	KW	human; cytostatic; diagnosis; prostatic cancer;	
XX	KW	differential expression analysis; ds.	
XX	OS	Homo sapiens.	
XX	PN	WO2004076614-A2.	
XX	PD	10-SEP-2004.	
XX	PF	22-FEB-2004; 2004WO-DE000433.	
XX	PR	27-FEB-2003; 2003DE-01009985.	
XX	PR	14-MAY-2003; 2003DE-01022134.	
XX	PA	(HINZ/) HINZMANN B.	
XX	PA	(DAHL/) DAHL E.	
XX	PA	(ROSE/) ROSENTHAL A.	
XX	PA	(HERM/) HERMANN K.	
XX	PA	(PILA/) PILARSKY C.	
XX	PI	Hinzmann B, Rosenthal A, Hermann K, Pilarsky C, Specht T;	
XX	PI	Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;	
XX	PI	Xinzhong L, Staub E;	
XX	DR	WPI; 2004-65386/63.	
XX	PT	New nucleic acids, and encoded proteins, from prostatic cancer tissue,	
XX	PT	useful for diagnosis, treatment and in screening for specific binding	
XX	PS	agents.	
XX	PS	Claim 1; Page 1329; 1607pp; German.	
XX	CC	This invention describes novel cytostatic polynucleotide and polypeptide	
XX	CC	sequences which can be used in a method for diagnosing prostatic cancer	
XX	CC	or the risk of developing prostatic cancer. Diagnosis is based on	
XX	CC	determining over transcription or over expression of the sequences in	
XX	CC	prostatic tissue. Screening for inhibitors of the sequences or detection	
XX	CC	substances involves a binding assay, any compounds that bind are	
XX	CC	selected, optionally after deconvolution of mixtures. Detection of a	
XX	CC	predetermined minimum level of the reporter indicates the presence of a	
XX	CC	tumour cells. Inhibitors can be chosen from antisense oligonucleotides,	
XX	CC	short-interfering RNA or ribozymes; an organic molecule of molecular	
XX	CC	weight below 5000, preferably 300, that binds to the polypeptide; an	
XX	CC	aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the	
XX	CC	polypeptide, preferably humanised or human; an anti-idiotypic, non-human	
XX	CC	(monoclonal) antibody directed against Ab or any of the above derivatised	
XX	CC	with a reporter group, cell toxin, immunostimulatory molecules and/or	
XX	CC	radioisotope. The polynucleotides are identified in human prostatic	
XX	CC	cancer by differential expression analysis, using DNA microarrays,	
XX	CC	between normal and tumorous tissues, with (over)expression being detected	
XX	CC	by quantitative PCR. Analysis of prostatic cancer samples showed that	
XX	CC	CD24 was upregulated in many of them. Sections of tissue, isolated from	
XX	CC	prostatic cancer patients, or subjects at risk, were incubated	

CC sequentially with anti-human CD4 murine monoclonal antibodies;  
CC biotinylated second antibody; streptavidin-conjugated horseradish  
CC peroxidase and then diaminobenzidine as colour former (brown). The  
CC samples were counterstained with hemalum (blue). Malignant cells stained  
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of  
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and  
CC lymph node metastases were also stained. ADR65805-ADR66954 represent the  
CC polynucleotide and polypeptide sequences used in the method of the  
CC invention.  
XX  
SQ Sequence 3202 BP; 784 A; 891 C; 825 G; 702 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 2,08e-72 Length: 3202  
Score: 682.00 Matches: 128  
Percent Similarity: 85.03% Conservative: 31  
Best Local Similarity: 68.45% Mismatches: 28  
Query Match: 73.25% Indels: 0  
DB: 13 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADR66747 (1-3202)

Qy 3 ValAspLeuLeuTyTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22  
Db 1890 ATTGACCTGTTGTATTGGCGGACATCAAGCAGCGGCATCGTGTGGAGTTTCCTG 1949  
Qy 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyIleAlaLeu 42  
Db 1950 CTGCTGCTCTTCCCTCACCAGTTACGCGTGGAGCGTCTGCGCTACTGCGCCCTG 2009  
Qy 43 AlaLeuLeuSerValThrIleSerPheArgIleTyLysGlyValIleGlnAlaIleGln 62  
Db 2010 GCCGCACTCTCAGCCACCACATCAGTTCCGCATCTACAGTCTGTTTACAGCAGTGCG 2069  
Qy 63 LysSerAspGluGlyHisProPheArgAlaTyLeuGluSerGluValAlaIleSerGlu 82  
Db 2070 AAAACCGCAGAGCGCCACCTTTCAAGCGCTACTTGGAGCTTGAGATCACCTTTCTCAG 2129  
Qy 83 GluLeuValGlnLysTySerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102  
Db 2130 GAGCAGATTCAAGATGACAGGACTGCTGCAGTTCCTACGTGAACAGCACACTTAAGGAA 2189  
Qy 103 LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
Db 2190 CTGAGAGGCTCTCTTGTTCAGACCTGCTGGATTCCTTAAATTTGCGTCTGATG 2249  
Qy 123 TrpValPheThrTyValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeu 142  
Db 2250 TGGCTCTCAGCCTAGCTGGGCTCTCTTCAATGGCCTGACCTGCTGCTGCTGCTG 2309  
Qy 143 IleSerLeuPheSerValProValIleTyGluArgHisGlnAlaGlnIleAspHisTy 162  
Db 2310 GTTTCATGTTTACTCTACCTGTAGTGTATGTAAGCACCAGGACGACATTGACCAATAT 2369  
Qy 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
Db 2370 CTGGCACTGTGAGGACTCACATAATCTGTTGTGGCAAGATTCAGGCTAAATCCCA 2429  
Qy 183 GlyLeuLysArgLysAlaGlu 189  
Db 2430 GCGCTAAGAGGCGCTGAG 2450

RESULT 59

ADQ23106

ID ADQ23106 standard; DNA; 3305 BP.

XX AC

ADQ23106;

XX DT

26-AUG-2004 (first entry)

XX DE

Human soft tissue sarcoma-upregulated DNA - SEQ ID 5926.

XX XX

soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;

KW ds.

XX Homo sapiens.

XX WO2004048938-A2.

XX 10-JUN-2004.

XX 26-NOV-2003; 2003WO-US038193.

XX 26-NOV-2002; 2002US-0429739P.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Aziz N, Ginsburg WM, Zlotnik A;

XX WPI; 2004-441208/41.

XX Early detection of soft tissue sarcoma comprises determining expression  
XX of a gene in a first soft tissue sample and a normal soft tissue sample  
XX and comparing the gene expression, also useful in treating soft tissue  
XX sarcoma.

XX Example 2; SEQ ID NO 5926; 210pp; English.

XX The invention relates to a novel method for detecting soft tissue sarcoma  
XX which comprises obtaining a first soft tissue sample from an individual,  
XX and a normal soft tissue sample from the same or different individual,  
XX determining the expression of a gene in both samples and comparing the  
XX expression of the gene in both soft tissue samples, where a higher level  
XX of protein expression in the first soft tissue sample indicates the  
XX presence of soft tissue sarcoma. The method of the invention has  
XX cytostatic applications and may be useful for detecting soft tissue  
XX sarcoma, possibly via gene therapy or vaccine production. The nucleic  
XX acid sequences may be useful in diagnostic and screening applications.  
XX The current sequence is that of a human soft tissue sarcoma-upregulated  
XX DNA of the invention. The current sequence is not shown within the  
XX specification per se but was submitted in CD format by the inventor.

XX Sequence 3305 BP; 828 A; 913 C; 843 G; 721 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,17e-72 Length: 3305  
Score: 682.00 Matches: 128  
Percent Similarity: 85.03% Conservative: 31  
Best Local Similarity: 68.45% Mismatches: 28  
Query Match: 73.25% Indels: 0  
DB: 12 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADQ23106 (1-3305)

Qy 3 ValAspLeuLeuTyTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22  
Db 1890 ATTGACCTGTTGTATTGGCGGACATCAAGCAGCGGCATCGTGTGGAGTTTCCTG 1949  
Qy 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyIleAlaLeu 42  
Db 1950 CTGCTGCTCTTCCCTCACCAGTTACGCGTGGAGCGTCTGCGCTACTGCGCCCTG 2009  
Qy 43 AlaLeuLeuSerValThrIleSerPheArgIleTyLysGlyValIleGlnAlaIleGln 62  
Db 2010 GCCGCACTCTCAGCCACCACATCAGTTCCGCATCTACAGTCTGTTTACAGCAGTGCG 2069  
Qy 63 LysSerAspGluGlyHisProPheArgAlaTyLeuGluSerGluValAlaIleSerGlu 82  
Db 2070 AAAACCGCAGAGCGCCACCTTTCAAGCGCTACTTGGAGCTTGAGATCACCTTTCTCAG 2129  
Qy 83 GluLeuValGlnLysTySerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102  
Db 2130 GAGCAGATTCAAGATGACAGGACTGCTGCAGTTCCTACGTGAACAGCACACTTAAGGAA 2189  
Qy 103 LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet 122

Db 2190 CTGAGGAGGCTCTCTGTCAGGACCTGGTGGATTCTTAAATTTGACGCTCTGATG 2249  
QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuLeuAlaLeu 142  
|||:::|||||  
Db 2250 TGGCTCTGACCTACGTTGGCGCTCTCTTCAATGGCTGACCTGCTGCTCATGGCTG 2309  
QY 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162  
|||:::|||||  
Db 2310 GTTTCATGTTTACTCTACCTGAGTGTATGTTAAGCACCGCACAGATTGACCAATAT 2369  
QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
|||:::|||||  
Db 2370 CTGGGACTGTGAGGACTACATAATGCTGTGTGGCAAGATTGAGCTTAATCCCA 2429  
QY 183 GlyLeuLysArgLysAlaGlu 189  
|||:::|||||  
Db 2430 GGGCTAAGAGGCACGCTGAG 2450

## RESULT 60

AD599925  
ID ADS99925 standard; cDNA; 3327 BP.

AC ADS99925;

XX 02-DEC-2004 (first entry)

XX Human reticulon 1 (RTN1), transcript variant 1, cDNA.

XX Human; ss: gene; Bisulphite; metastasis; cancer; cytostatic;  
KW DNA methylation; matrix-assisted laser desorption/ionisation; MALDI;  
KW electrospray; mass spectrometry; CpG dinucleotide; solid tumour.

XX Homo sapiens.

XX US2003148327-A1.

XX 07-AUG-2003.

XX 21-JAN-2003; 2003US-00240485.

XX 06-APR-2000; 2000DE-01019058.

PR 07-APR-2000; 2000DE-01019173.

PR 30-JUN-2000; 2000DE-01032529.

PR 01-SEP-2000; 2000DE-01043826.

PR 06-APR-2001; 2001WO-EP003970.

XX (OLEK/) OLEK A.

PA (PIEP/) PIEPENBROCK C.

PA (BERL/) BERLIN K.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2002-010922/01.

DR GENBANK; NM\_021136.

XX New nucleic acid derived from chemically treated metastasis genes, useful  
PT for diagnosis of cancers by analysis of cytosine methylation, also for  
PT treatment.

XX Claim 2; Page; 9pp; English.

XX The invention relates to a nucleic acid comprising at least 18 bases from  
CC a segment of the chemically pretreated DNA of genes associated with  
CC metastasis, i.e. any of ADS99709-ADS9906 human genomic sequences or any  
CC of the 19 sequences appearing as ADS9911-ADS9929. SEQ ID 2, 4, 6 etc are  
CC the complements of SEQ ID 1, 3, 5, etc. Also included are an oligomer  
CC (particularly an oligonucleotide or peptide nucleic acid) comprising at  
CC least one base sequence of at least 9 bases which hybridises to (or is  
CC identical with) the sequences referred to above, producing an array of  
CC the oligomers on a carrier, obtaining genetic and/or epigenetic  
CC parameters for diagnosis and/or therapy of diseases (or predisposition to  
CC them) by analysis of cytosine methylation and a kit comprising a  
CC bisulphite (disulphite or hydrogen sulphite) and the oligomers. In the

CC method of above 5-unmethylated cytosines in a genomic DNA sample are  
CC converted chemically to uracil, or another base with hybridisation  
CC properties different from those of cytosine, then fragments of the  
CC treated DNA amplified (particularly by polymerase chain reaction) using  
CC the oligomers and a polymerase (preferably heat stable) to produce  
CC labelled amplicons. These are tested for hybridisation to an array of  
CC oligomers and any hybridisation detected. The amplicons are labelled with  
CC fluorescent or radioactive markers, or with a detachable mass marker to  
CC allow their detection by mass spectrometry, specifically using the matrix  
CC -assisted laser desorption/ionisation (MALDI) or electrospray techniques.  
CC To improve detection in the mass spectrometer, fragments formed in the  
CC instrument have only a single net charge (positive or negative). The  
CC genomic DNA is from e.g. a cell line, biopsy sample, blood, or paraffin-  
CC embedded tissue sample. Oligonucleotides or peptide-nucleic acids that  
CC are complementary to (or identical with) parts of the nucleic acids listed  
CC above may be used as primers for amplification of the nucleic acids or  
CC their complements, and for determining cytosine methylation status and/or  
CC single nucleotide polymorphisms in metastasis-related genes. They can be  
CC used for analysis of diseases associated with methylation of CpG  
CC dinucleotides and to determine (epi)genetic parameters for diagnosis  
CC and/or therapy of disease (or predisposition). The genomic DNA sequences  
CC are useful for diagnosis and therapy of solid tumours and cancer. The  
CC present sequence is human gene fragment or cDNA associated with  
CC metastasis. Note: The sequence was not displayed in the specification but  
CC was obtained by the indexer from Genbank.

XX SQ Sequence 3327 BP; 829 A; 907 C; 877 G; 714 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 2, 19e-72 Length: 3327  
Score: 682.00 Matches: 128  
Percent Similarity: 85.03% Conservative: 31  
Best Local Similarity: 68.45% Mismatches: 28  
Query Match: 73.25% Indels: 0  
DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADS99925 (1-3327)

QY 3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22  
|||:::|||||  
Db 1977 ATTGACCTGTTGATTGGCGGACATCAAGCAGACGGCATCGTGTGGAGTTTCTCTG 2036  
QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
|||:::|||||  
Db 2037 CTGCTGCTCTCTCCCTGACCCAGTTCAGCGGTGGAGCGTCTGCGCTTACCTGCGCCCTG 2096  
QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
|||:::|||||  
Db 2097 GCGGCACCTTCAGCCACCACATCAGTTTCCGCATCTACAAGTCTGTTTACAAGCAGTGCAG 2156  
QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
|||:::|||||  
Db 2157 AAAACCGCAGAGGCGCCCTTTCAAGGCTACTTTGGAGCTTGAGATCACCCCTTTCTCAG 2216  
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102  
|||:::|||||  
Db 2217 GAGCAGATTCAAGATACAGGACTGCGCTGCGAGTTCTACGTGACAGACACTTAGGAA 2276  
QY 103 LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
|||:::|||||  
Db 2277 CTGAGGAGGCTCTTCTTGTCCAGGACCTGGTGGATTCTTAAATTTGACGCTCTCTGATG 2336  
QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeu 142  
|||:::|||||  
Db 2337 TGGCTCTGACCTACGTTGGCGCTCTCTTCAATGGCTGACCTGCTGCTCATGGCTG 2396  
QY 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162  
|||:::|||||  
Db 2397 GTTTCATGTTTACTCTACCTGATGATGTTAAGCACCGCACAGATTGACCAATAT 2456  
QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
|||:::|||||  
Db 2457 CTGGGACTTGTGAGGACTCACATAAATGCTGTGTGGCAAGATTGAGCTTAATCCCA 2516



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QY 183 GlyLeuLysArgLysAlaGlu 189
|||
Db 2517 GCGGCTAGAGGACGCTGAG 2537

RESULT 61
ID ADB79854
AC ADB79854;
XX
XX
DT 04-DEC-2003 (first entry)
DE Rat rs-Rex-s human NSP C homolog coding sequence, SEQ ID 94.
KW Analgesic; pain; streptozocin-induced diabetes; rat; gene; ds.
XX
XX OS Rattus norvegicus.
XX
XX PN EP1279744-A2.
XX
XX PD 29-JAN-2003.
XX
XX PF 26-JUL-2002; 2002EP-00255249.
XX
XX PR 27-JUL-2001; 2001GB-00018354.
XX
XX PR 07-FEB-2002; 2002GB-00002910.
XX
XX PA (WARN ) WARNER LAMBERT CO.
XX
XX PI Brooksbank RA, Dixon AK, Lee K, Pincock RD;
XX
XX DR WPI: 2003-395407/38.
XX
XX DR P-PSDB; ADB79853.
XX
XX
XX PT Use of isolated gene sequences and encoded polypeptides that are
XX upregulated in the spinal cord in response to streptozocin-induced
XX diabetes for screening compounds for the treatment of pain, or for
XX diagnosing pain.
XX
XX PS Claim 1; Page 171; 334pp; English.
XX
XX CC The present invention relates to nucleotide sequences which are useful in
XX the screening of compounds for the treatment of pain, or for the
XX diagnosis of pain. The nucleotide sequences are up-regulated in the
XX spinal cord in response to streptozocin-induced diabetes. The present
XX sequence is one such nucleotide sequence.
XX
XX SQ Sequence 1502 BP; 348 A; 392 C; 363 G; 399 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9,528-73 Length: 1502
Score: 681.00 Matches: 127
Percent Similarity: 85.03% Conservative: 32
Best Local Similarity: 67.91% Mismatches: 28
Query Match: 73.15% Indels: 0
DB: 10 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x ADB79854 (1-1502)

QY 3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22
|||
Db 179 ATTGACCTTCTGTACTGGGGGACATCAAGCAGCGGGGATGTGTTCGGGAGCTTCTCG 238

QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
|||
Db 239 CTGCTGCTCTTCCTGCTGACCCAGTTCAGCGTGTGTGAGCGTGTGCTGCTGCTGCTGCTG 298

QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62
|||
Db 299 GCTGCCCTCTCTGCCACCATCATGCTTCGCGATCTCAAGTCGCTTCTCAAGCTGTGCG 358

QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
|||
```

```
Db 359 AAAACAGATGAGGTACCCCTTCAAGSCCTACCTGGAGCTGGAGATCACCCCTGTCCCAG 418
|||
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102
|||
Db 419 GAGCAGATCCAGAAGTACACAGACTGCTGCTGAGCTATACGTATACGTGAACAGCACCTCTGAAGGAG 478
|||
QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122
|||
Db 479 CTACGGAGCTCTTCCTGGTCCAGGACCTGGTGGATTCCTTAAATTTGCAGTCTCATG 538
|||
QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeu 142
|||
Db 539 TGGCTCTGACTACCTGCTGGCGCACTCTTCAATGGCCTGACCTGCTGCTTATGGCTGTG 598
|||
QY 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162
|||
Db 599 GTTTCGATGTTTACTCTACCTGTGTATATGTTAAGCACCGGACACAGGTGACCAATAT 658
|||
QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
|||
Db 659 CTGGGACTTGTGAGGACTCATATAACACCCGTTGTGGCAAGATCCAGGCTAAATCCCC 718
|||
QY 183 GlyLeuLysArgLysAlaGlu 189
|||
Db 719 GCGGCCAAGAGGACGCTGAG 739

RESULT 62
ADO07889
ID ADO07889 standard; cDNA; 2343 BP.
XX
XX AC ADO07889;
XX
XX DT 01-JUL-2004 (first entry)
XX
XX DE Mouse polynucleotide #58.
XX
XX KW Mouse; gene; ss; fat cell number; fat cell size; obesity; diabetes;
XX anorectic; antidiabetic.
XX
XX OS Mus sp.
XX
XX PN US2004071700-A1.
XX
XX PD 15-APR-2004.
XX
XX PF 09-OCT-2002; 2002US-00267502.
XX
XX PR 09-OCT-2002; 2002US-00267502.
XX
XX PA (LIFE-) LIFE SCI DEV CORP.
XX
XX PI Kim J, Galant R;
XX
XX DR WPI: 2004-328526/30;
XX
XX DR P-PSDB; ADO08106.
XX
XX PT Identifying compounds that influence fat cell number or size for treating
XX or preventing obesity or diabetes by exposing the cell to the agent and
XX identifying fat cell number or size relative to cells not exposed to the
XX agent.
XX
XX PS Claim 1; SEQ ID NO 215; 275pp; English.
XX
XX CC The invention relates to a method of identifying compounds that influence
XX fat cell number or size comprising providing a cell that expresses a gene
XX and an agent, exposing the cell to the agent and identifying fat cell
XX number or size relative to cells not exposed to the agent. The method
XX also comprises providing an expression vector and an agent, exposing the
XX vector to the agent, detecting a change in expression of the gene
XX relative to expression of the gene in an expression vector not exposed to
XX the agent, treating a subject with the agent and identifying fat cell
XX number or size in the subject. The agent comprises an antisense
```

CC oligonucleotide. The subject comprises a mammal, preferably a human. The  
 CC method also comprises providing a polypeptide and an agent, exposing the  
 CC polypeptide to the agent, detecting binding of the agent to the  
 CC polypeptide or a change in an activity of the polypeptide, treating a  
 CC subject with the agent and identifying fat cell number or size in the  
 CC subject. The agent comprises an antibody. A method of regulating fat cell  
 CC number or size comprises providing a subject containing fat cells and an  
 CC agent that changes the expression of a gene, and treating the subject  
 CC with the agent under conditions so that fat cell size or number in the  
 CC subject is altered. The method is useful for identifying compounds that  
 CC influence fat cell number or size, for preparing a composition for  
 CC treating or preventing obesity or diabetes. This sequence represents  
 CC mouse cDNA used in the scope of the invention.

XX Sequence 2343 BP; 536 A; 710 C; 646 G; 451 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 1.78e-72 Length: 2343  
 Score: 681.00 Matches: 127  
 Percent Similarity: 85.03% Conservative: 32  
 Best Local Similarity: 67.91% Mismatches: 28  
 Query Match: 73.15% Indels: 0  
 DB: 12 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADO07889 (1-2343)

QY 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22  
 DB 1780 ATTGACCTCTGTACTGCGGACATCAAGCAGACTGGGATGTTGTTCGGAGCTTCCTG 1839  
 QY 23 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
 DB 1840 CTGCTGCTCTCTCCCTGACCCATTTAGCGTTGTGAGGCTGCTTCCTACCTGGCCCTG 1899  
 QY 43 AlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
 DB 1900 GCGGCCCTCTCTGCCACATCAGCTTCGGCACTACAGTCGCTTCTACAGCTGTGCAG 1959  
 QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
 DB 1960 AAAACAGATGAGGCTCACCTTTCAAGGCTTACCTGGAGCTGAGATCACCTGTCCAG 2019  
 QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102  
 DB 2020 GAGCAGATCAGAAGTACACAGACTGCTGCTGCTGATGTGAAACAGACTCTGAAGGAG 2079  
 QY 103 LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
 DB 2080 CTACGGAGGCTTTCTGCTCAGGACCTGGTGGATTCCTTAAATTTGCAGTCTCATG 2139  
 QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAlaLeu 142  
 DB 2140 TGCTCTGACCTACCTGCTGGCGGCTTCTCAATGGCTGACCTGCTGTATGGCTGTG 2199  
 QY 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162  
 DB 2200 GTTTCGATGTTTACTCTACCTGTGTGTAGCTTTAAGCAGCAGCAGGACCAAGTTGACCAATAT 2259  
 QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
 DB 2260 CTGGGACTTGTGAGGACTCAATAACACCGCTGCTGGCAAGATCCAGGCTAATATCCCC 2319  
 QY 183 GlyLeuLysArgLysAlaGlu 189  
 DB 2320 GGGCCCAAGAGGACCGCTGAG 2340  
 RESULT 63  
 ABX46402  
 ID ABX46402 standard; cDNA; 422 BP.  
 XX  
 AC ABX46402;  
 XX  
 DT 21-FEB-2003 (first entry)

XX DE Bovine EST associated with lactation/muscle/fat deposition #11567.  
 XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;  
 KW muscle deposition; fat deposition; genome mapping; gene identification;  
 KW gene analysis; cattle breeding.  
 XX Bos Taurus.  
 XX US2002137139-A1.  
 XX 26-SEP-2002.  
 XX 24-SEP-2001; 2001US-00960352.  
 XX 12-JAN-1999; 99US-0115707P.  
 XX 11-JAN-2000; 2000US-00480902.  
 XX (BYAT/) BYATT J C.  
 XX (MATH/) MATHIALAGAN N.  
 XX (TAON/) TAO N.  
 XX (WARR/) WARREN W C.  
 XX Byatt JC, Mathialagan N, Tao N, Warren WC;  
 XX WPI; 2003-110599/10.  
 XX New nucleic acid associated with lactation, and muscle and fat  
 PT deposition, useful for genome mapping, gene identification and analysis,  
 PT cattle breeding, or for genetically improving cattle.  
 XX Claim 2; SEQ ID NO 11567; 245pp; English.  
 XX The invention relates to a purified nucleic acid molecule associated with  
 CC lactation or muscle and fat deposition (designated LMFD), derived from  
 CC cattle, and the LMFD nucleic acid can specifically hybridise to a second  
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,  
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are  
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic  
 CC acid linked to a promoter and a 3' non-translated sequence that  
 CC functions in the cell to cause termination of transcription and addition  
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and  
 CC (2) determining a level or pattern of a molecule in a bovine cell or  
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any  
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a  
 CC complementary nucleic acid molecule obtained from the bovine cell or  
 CC tissue, where hybridisation between the marker nucleic acid and the  
 CC complementary nucleic acid permits the detection of the molecule; and (b)  
 CC detecting the level or pattern of the complementary nucleic acid, where  
 CC the detection of the complementary nucleic acid is predictive of the  
 CC level or pattern of the molecule. The LMFD nucleic acid is used for  
 CC determining a level or pattern of a molecule in a bovine cell or tissue.  
 CC It is useful for genome mapping, gene identification and analysis, cattle  
 CC breeding, preparation of constructs for use in cattle gene expression, or  
 CC for genetically improving cattle. The present sequence is one of the  
 CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The  
 CC present sequence was not shown in the specification but was obtained in  
 CC electronic format from the USPTO web site:  
 CC seqdata.uspto.gov/sequence.html?DocID=20020137139  
 XX  
 SQ Sequence 422 BP; 99 A; 85 C; 96 G; 142 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 2.01e-72 Length: 422  
 Score: 672.00 Matches: 138  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 99.28% Mismatches: 0  
 Query Match: 72.18% Indels: 0  
 DB: 8 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ABX46402 (1-422)

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40

```

Db 4 AACCTGTTCTCTGCTCTGCTGACAGTATTGAGCATTTGAGTGTAAAGCGCTACATT 63
Qy 41 AlaleuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 64 GCCTTGGCCCTGCTCTCTGCTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGCT 123
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 124 ATCCAGAAATCTGATGAAGGCCACCCATTGAGGCATATTTGGAATCTGAAGTTGCTATA 183
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 184 TCTGAGGAGTTGGTTTCAAGATACAGCAATCTCTGCTCTGCTGATGTTAACTGCACAATA 243
Qy 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 244 AAAGAACTCAGACGCCCTCTCTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAG 303
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 304 TTGATGTGGGTATTTACCTATGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 363
Qy 141 AlaleuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIle 159
Db 364 GCTCTGATTTTCACTTTCAGTGTTCCTGTTATTTATGAAAGCATCAGGCGCAATA 420

```

## RESULT 64

ADB85247

ID ADB85247 standard; DNA; 1473 BP.

XX AC ADB85247;

XX DT 04-DEC-2003 (first entry)

XX DE Rat C1-13 protein neuronal-specific gene SEQ ID NO:128.

XX rat; streptozocin; kinase; phosphatase; ion channel protein; receptor;  
 XX transporter; G-protein coupled receptor; GPCR; DNA-binding proteins;  
 XX protease; enzyme; analgesic; gene therapy; pain; diabetes; ds; gene.  
 XX OS Rattus norvegicus.

XX PN EP1284297-A2.

XX PD 19-FEB-2003.

XX PF 26-JUL-2002; 2002EP-00255228.

XX PR 27-JUL-2001; 2001GB-00018354.

XX PS 07-FEB-2002; 2002GB-00002880.

XX PA (WARN) WARNER LAMBERT CO.

XX PI Brookebank RA, Dixon AK, Lee K, Pincock RD;

XX DR WPI; 2003-364994/35.

XX DR P-PSDB; ADB85246.

XX PT Use of gene sequence that is down-regulated in response to streptozocin-  
 XX induced diabetes, vector, host cell, animal, polypeptide and antibody, in  
 XX screening of compounds for treating or diagnosing pain.  
 XX PS Claim 1; Page 197; 256pp; English.

XX The invention relates to a novel isolated gene sequence that is down-  
 XX regulated in the spinal cord in response to streptozocin-induced  
 XX diabetes, or comprising, hybridising or having at least 80% sequence  
 XX identity to a sequence whose expression products are kinases,  
 XX phosphatases, ion channel proteins, receptors, transporters, G-protein  
 XX coupled receptor proteins, DNA-binding proteins, proteases or enzymes,  
 XX given in the specification. A gene of the invention has analgesic  
 XX activity, and may have a use in gene therapy. The gene sequences, vector,

CC host cell, animal, polypeptide and antibody are useful for screening of  
 CC compounds for diagnosing or treating pain. The kits are useful for  
 CC simultaneous, separate or sequential detecting and/or quantifying down-  
 CC regulation of a gene sequence in the spinal cord of a mammal in response  
 CC to streptozocin-induced diabetes. The compound or pharmaceutical  
 CC composition is useful as a medicament for treating or diagnosing pain.  
 CC The present sequence represents a gene of the invention.

XX SQ Sequence 1473 BP; 357 A; 373 C; 343 G; 400 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 8,29e-71 Length: 1473  
 Score: 665.00 Matches: 127  
 Percent Similarity: 85.03% Conservative: 32  
 Best Local Similarity: 67.91% Mismatches: 28  
 Query Match: 71.43% Indels: 1  
 DB: 10 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADB85247 (1-1473)

```

Qy 3 ValAspLeuLeuTyrTrpArgAspIleLeValysThrGlyValValPheGlyAlaSerLeu 22
Db 146 ATTGACCTTCTGACTTCCGCGGACATCAGCAGACGGGGATTGTTCGGGAGCTTCCTG 205
Qy 23 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
Db 206 CTGCTGCTCTCTCCCTGACCCAGTTCAGCGTTGTGAGCGTCTGCTGCTGCTGCTGCTG 265
Qy 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62
Db 266 GCTGCCCTCTCTGCCACCATCAGCTTCGGCATCTTCAAGTCCGTTCTTACAGCTGTGCAG 325
Qy 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
Db 326 AAAACAGATGAGGTCCACCTTTCAAGGCTTACCTGAGCTGGAGATCACCCTGTCCGAG 385
Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102
Db 386 GAGCAGATCCAGAGTACACAGACTGCTGCAGCTATACGTGACAGACACTCTCGAGGAG 445
Qy 103 LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet 122
Db 446 CTACGGAGGCTCTTCTCTGTCCAGACCTAGTGGATTCTTAAATTTTGCAGTCTCTCATG 505
Qy 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeu 142
Db 506 TGGCTCTGACCTACGTGGCGCACTCTTCAATGGCTGACCTGCTGCTGCTGCTGCTG 565
Qy 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162
Db 566 GTTTCGATGTTTACTCTACTCTGTTATATGTTAAGCACCAGGCACAGGTTGACCAATAT 625
Qy 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
Db 626 CTGGGACTTGTGAGGACTCACATAAACACCCGTTGTGGCAAGATCCAGGCTTAAATCCCC 685
Qy 183 GlyLeuLysArgLysAlaGlu 189
Db 686 GGCAGC-AAGAGGCATGCTGAG 705

```

## RESULT 65

AAH57558

ID AAH57558 standard; cDNA; 3279 BP.

XX AC AAH57558;

XX DT 10-SEP-2001 (first entry)

XX DE Human brain cell specific cDNA sequence SEQ ID NO:398.

XX Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung;  
 XX liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;  
 XX metabolic disease; developmental disease; cytostatic; immunomodulatory;



CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,  
CC cytotactic and tranquiliser activities. This polynucleotide is a full  
CC length human cDNA sequence of the invention. NOTE: This sequence is not  
CC given in the sequence listing of the specification but can be obtained on  
CC CD-ROM from the European Patent Office, Vienna Sub-office.

XX SQ Sequence 4607 BP; 1428 A; 944 C; 945 G; 1290 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1,548-65 Length: 4607  
Score: 627.50 Matches: 116  
Percent Similarity: 81.05% Conservative: 38  
Best Local Similarity: 61.05% Mismatches: 35  
Query Match: 67.40% Indels: 1  
DB: 13 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADR06965 (1-4607)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleTyrLysThrGlyValValPheGlyAla 20  
DB 2353 TCAGTGCAGCATCTGATTTCCTGGAGAGATGGAAGAAGACTGGGTTGTCTTGGCACC 2412  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThraLafTyrIle 40  
DB 2413 ACGCTGATCATGCTCTTCCCTGGCAGCTTTTCAGTGTTCATCAGTGTGGTTCTTACCTC 2472  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
DB 2473 ATCCCTGGCTCTCTCTGTACCATCAGCTTCAGGATCTACAACTCCGTTCATCAAGCT 2532  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
DB 2533 GTACAGAGTCAAGAGAGGATCCATTCAAAGCTACCTGGAGTAGACATCTACTG 2592  
QY 81 SerGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAsnCysThrIle 100  
DB 2593 TCCTCAGAAGCTTTCATTAATACATGAATGCTGCTGATGCAATCAACAGGCGCCCTG 2652  
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
DB 2653 AAATCATATTTCGTCTCTTCTGTGAAGAGATCTGGTGTACTCTTGAAGCTGCTGTC 2712  
QY 121 LeuMetTrpValPheTyrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuIleLeu 140  
DB 2713 TTATGTGCTGATGACCTATGTTGCTGCTTTTAAAGGATCACTCTTAACTTCT 2772  
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
DB 2773 GCTGAACCTGCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAGACCCAGATTGAT 2832  
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
DB 2833 CACTATGTTGGATCGCCCGAGATCAGACCAGTCAATTGTTGAAGATCAAGCAAAA 2892  
QY 181 IleProGlyLeu---LysArgLysAlaGlu 189  
DB 2893 CTCCTCGAATCGCCAAAAGAGGACAGAA 2922

RESULT 67

AAZ38318

ID AAZ38318 standard; cDNA; 708 BP.

XX AC

AC AAZ38318;

XX DT

09-FEB-2000 (first entry)

XX DE

Human transmembrane protein cDNA clone HP02061 coding sequence.

XX KW

HP02061; transmembrane domain; Saos-2; homology;

KW neuroendocrine-specific protein C; antibody; assay reagent;

KW diagnostic marker; primer; probe; antisense; gene therapy; agonist;

KW antagonist; ligand; therapeutic; ds.

XX

OS Homo sapiens.

XX Key Location/Qualifiers  
FT CDS 1..708

FT /\*tag= a

FT /product= "Human transmembrane protein HP02061"

FT /note= "No stop codon given in the specification"

XX PN WO9955862-A2.

XX PD 04-NOV-1999.

XX PF 27-APR-1999; 99WO-JP002226.

XX PR 28-APR-1998; 98JP-00119395.

XX PA (SAGA ) SAGAMI CHEM RES CENT.

XX PA (PROT-) PROTEGENE INC.

XX PI Kato S, Kimura T;

XX WPI; 2000-023358/02.

XX DR P-PSDB; AAY52387.

XX PT Human proteins with transmembrane domains, involved in control of cell

XX PT proliferation and differentiation, useful for treating e.g. cancer or

XX PT inflammation.

XX PS Claim 3; Page 85; 114pp; English.

XX CC This sequence represents the coding sequence of human cDNA clone HP02061

XX CC which encodes a 26 kD protein with two putative transmembrane domains.

XX CC The cDNA was isolated from a Saos-2 (human osteosarcoma cell line) cDNA

XX CC library. The protein has homology with the human neuroendocrine-specific

XX CC protein C (PIR Accession No. I60904), and may have a similar function.

XX CC The protein may be used to raise specific antibodies, as assay reagents,

XX CC as diagnostic tissue markers, for the isolation of cognate receptors,

XX CC ligands and binding proteins, and as biologically active agents.

XX CC Nucleotides encoding the protein may be used as primers and probes or

XX CC antisense molecules, and in gene therapy. Cells transformed with these

XX CC nucleotides may be used to screen for agonists and antagonists which are

XX CC potentially useful therapeutically

XX SQ Sequence 708 BP; 158 A; 195 C; 169 G; 186 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,598-66 Length: 708

Score: 624.50 Matches: 115

Percent Similarity: 81.05% Conservative: 39

Best Local Similarity: 60.53% Mismatches: 35

Query Match: 67.08% Indels: 1

DB: 3 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAZ38318 (1-708)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleTyrLysThrGlyValValPheGlyAla 20

DB 139 CGGTGCAGCATCTGATTTCCTGGAGAGATGGAAGAAGACTGGGTTGTCTTGGCACC 198

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThraLafTyrIle 40

DB 199 ACGCTGATCATGCTCTTCCCTGGCAGCTTTTCAGTGTTCATCAGTGTGGTTCTTACCTC 258

QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60

DB 259 ATCTGGCTCTTCTCTGTCCATCAGCTTCAGGATCTACAAAGTCCGTTCATCAAGCT 318

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80

DB 319 GTACAGAGTCAAGAGAGGCCATCCATTCAAAGCTACCTGGAGTAGACATCTACTG 378

QY 81 SerGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAsnCysThrIle 100

DB 81 SerGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAsnCysThrIle 100

Db 379 TCCTCAGAGCTTTCATTAATACATGAATGCTGCCATCAACAGGCGCCCTG 438  
 QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 439 AAATCATTAATTCGCTCTCTCTGTTGGTGAAGATCTGTTGACTCTCTTGAAGCTGGCTGC 498  
 QY 121 LeuMetTTPValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 Db 499 TTCATGTGGCTGATGACCTATGTTGGTGTCTGTTTAAACGGAATCAACCTTCTAATTC 558  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 Db 559 GCTGAACCTCATTTTCAGTGTCCGATGCTATGAGAAGTACAGACCAGATTGAT 618  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 619 CACTATGTTGGCATCGCCGAGATCAGACCAAGTCAATGTTGAAAAGATCCAAGCAAAA 678  
 QY 181 IleProGlyLeu---LysArgLysAlaGlu 189  
 Db 679 CTCCTGGAATCGCCAAAAAAGGCAGAA 708

## RESULT 68

ADK67496  
 ID ADK67496 standard; cDNA; 711 BP.

XX AC ADK67496;

XX DT 06-MAY-2004 (first entry)

XX DE Human RTN-3 cDNA sequence.

XX KW ds; neuroprotective; gene therapy; BACE1 activity; RTN4; RTN3;

XX KW amyloidosis; Alzheimer's disease.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 1..711

XX FT FT /\*tag= a

XX FT FT /product= "RTN-3 protein"

XX PN WO2003088926-A2.

XX PD 30-OCT-2003.

XX PF 08-APR-2003; 2003WO-US008829.

XX PR 17-APR-2002; 2002US-0373284P.

XX PA (PHAA ) PHARMACIA & UPJOHN CO.

XX PI Yan R, Lu Y;

XX DR WPI; 2003-854033/79.

XX DR F-PSDB; ADK67497.

XX PT New polypeptide having BACE1 activity, useful in preparing a composition for treating amyloidosis or Alzheimer's disease.

XX PS Claim 2; SEQ ID NO 1; 42pp; English.

XX CC The invention relates to an isolated polypeptide having BACE1 activity. The protein is RTN4 or RTN3 protein. The polypeptide is useful in preparing a composition for treating amyloidosis or Alzheimer's disease. This sequence corresponds to the RTN-3 gene.

SQ Sequence 711 BP; 161 A; 196 C; 168 G; 186 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 2,61e-66 Length: 711  
 Score: 624.50 Matches: 115  
 Percent Similarity: 81.05% Conservative: 39

Best Local Similarity: 60.53% Mismatches: 35  
 Query Match: 67.08% Indels: 1  
 DB: 10 Gaps: 1  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADK67496 (1-711)

QY 1 SerValValAspLeuLeuTyrTTPArgAspIleLysLysThrGlyValValPheGlyAla 20  
 Db 139 GCGGTGCAGATCTCATTTCTTGGAGAGATGTGAAGAAGCTGGGTGTCTTTGGCACC 198  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 199 AGCGTGATCATGCTGCTTTCCTGCGAGCTTTCAGTGTCACTCAGGTGTGTTTCTTACCTC 258  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 259 ATCTCGGCTCTTCTCTGTCCATCAGTTCAGGATCTACAGTCCGCTCATCCAAGCT 318  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 319 GTACAGAAGTCAGAAAGGCGCATCCATTCAAAGCTTACCTGGAGTAGACATTACTCTG 378  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 Db 379 TCCTCAGAAGCTTTCATTAATTTACATGAATGCTGCCATGTCACATCAACAGGCGCCCTG 438  
 QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 439 AAATCATTAATTCGCTCTCTCTGTTGAGAAGATCTGTTGACTCTCTTGAAGCTGGCTGC 498  
 QY 121 LeuMetTTPValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
 Db 499 TTCATGTGGCTGATGACCTATGTTGGTGTCTGTTTAAACGGAATCACCTTCTAATTC 558  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 Db 559 GCTGAACCTCATTTTCAGTGTCCGATGCTATGAGAAGTACAGACCAGATTGAT 618  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 619 CACTATGTTGGCATCGCCGAGATCAGACCAAGTCAATGTTGAAAAGATCCAAGCAAAA 678  
 QY 181 IleProGlyLeu---LysArgLysAlaGlu 189  
 Db 679 CTCCTGGAATCGCCAAAAAAGGCAGAA 708

## RESULT 69

AAH34853

ID AAH34853 standard; cDNA; 1330 BP.

XX AC AAH34853;

XX DT 03-SEP-2001 (first entry)

XX DE Human colon cancer antigen encoding cDNA SEQ ID NO:1935.

XX KW Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma; chromosome 11; ss.

XX OS Homo sapiens.

XX PN WO200122920-A2.

XX PD 05-APR-2001.

XX PF 28-SEP-2000; 2000WO-US026524.

XX PR 29-SEP-1999; 99US-0157137P.

XX PR 03-NOV-1999; 99US-0163280P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Barash SC, Birse CE, Rosen CA;



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DB: 2 Gaps: 1
US-09-830-972-29_COPY_990_1178 (1-189) x AAX60810 (1-1656)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
DB 165 GCGGTGCAGATCTGATTTCTGGAGAGATGGAAGACAGCTGGTTGCTCTTGGCACC 224
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 225 ACGCTGATCATGCTGCTTTCCCTGGCAGCTTTTCAGTGTTCATCAGTGTGGTTCTTACCTC 284
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
DB 285 ATCTCGGCTCTTCTCTGTCCACATCAGTTCAGATCTACAGTCCGTCATCCAGCT 344
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 345 GTACAGAGTCAGAGAAGCCATCCATTCAAGCCCTACTGGACGTAGACATTACTCTG 404
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
DB 405 TCTCAGAAAGCTTTCATAATTACATGAATGCTGCCATGTCACATCAACAGGGCCCTG 464
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
DB 465 AAACATCATATTGCTCTCTTCTGGTAGAAGATCTGGTTGATCTCCTTGAAGCTGGCTGC 524
QY 121 LeuMetTrpValPheTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
DB 525 TTCATGTGCTGATGACCTATGTTGGTGTCTGTTTAAAGGATCACTCTTATTTCT 584
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
DB 585 GCTGAATCTGCTCATTTTCAGTGTCCGATTTCTATGAGAGTACAAAGCCAGATTGAT 644
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
DB 645 CACTATGTGGTATGCCCGCAGATCAGACCAAGTCAATTGTTGAAAGATCCAAAGCAAA 704
QY 181 IleProGlyLeu---LysArgLysAlaGlu 189
DB 705 CTCCTCGAATCGCCAAAGAGGAGAA 734
RESULT 71
ID AAS59216 standard; cDNA; 1656 BP.
AC AAS59216;
XX 16-JAN-2002 (first entry)
DE Human cDNA encoding a secreted protein yb8_1.
XX
KW Human; secreted protein; ss; antiinflammatory; immunosuppressive;
KW neurotropic; neuroprotective; antiarthritic; antimicrobial; vulnerary;
KW cytostatic; antidiabetic; virucide; antiinfertility; anticonvulsant;
KW vasotropic; antiparkinsonian; immunostimulant; dermatological;
KW antirheumatic; antitumor; antiulcer; osteopathic; tranquiliser;
KW cerebroprotective; cytokine; cell proliferation; cell differentiation;
KW immune deficiency; severe combined immunodeficiency; SCID; tumour;
KW autoimmune disorder; multiple sclerosis; rheumatoid arthritis;
KW graft-versus-host disease; myeloid deficiency; wound healing; ulcer;
KW periodontal disease; osteoporosis; osteoarthritis; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; infection; cardiac disease;
KW stroke; sepsis; inflammatory bowel disease; contraceptive; immunogen;
KW food supplement.
XX
OS Homo sapiens.
XX
PN WO200175068-A2.
XX
XX 11-OCT-2001.
PD
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XX PF 22-MAR-2001; 2001WO-US009369.  
XX PR 30-MAR-2000; 2000US-00539330.  
XX PR 04-DEC-2000; 2000US-00729674.  
XX PA (GENY ) GENETICS INST INC.  
XX PI Jacobs K, Mccoy JM, Lavallie E, Collins-Racie LA, Evans C;  
PI Treacy M, Agostino MJ, Steininger RJ, Spaulding V, Wong GG, Clark H;  
PI Fechtel K, Merberg D;  
XX WPI: 2001-639363/73.  
DR P-PSDB; AAU38998.  
PT Secreted human proteins, useful as vaccine for treating various diseases  
PT such as autoimmune disorders (e.g. multiple sclerosis), and nervous  
PT system disorders (e.g. stroke).  
XX Claim 13; Page 471; 61pp; English.  
PS The invention relates to novel human secreted proteins, the nucleic acids  
CC encoding them. The protein may exhibit cytokine, cell proliferation or  
CC cell differentiation activity or may induce production of other cytokines  
CC in certain cell populations and may exhibit immune stimulating or immune  
CC suppressing activity, which is useful for the treatment of various immune  
CC deficiencies and disorders e.g. multiple sclerosis, systemic lupus  
CC autoimmune disorders e.g. severe combined immunodeficiency (SCID),  
CC erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation.  
CC The proteins are also useful in the treatment of diseases and disorders  
CC including tissue, skin and organ transplantation and in graft-versus-host  
CC diseases (GVHD), in the induction of tumour immunity, myeloid or lymphoid  
CC cell deficiencies, wound healing and tissue repair, in the treatment of  
CC burns, incisions and ulcers; as well as in treatment of periodontal  
CC disease, osteoporosis or osteoarthritis, mediated by inflammatory  
CC processes, diseases of the peripheral nervous system, Alzheimer's,  
CC Parkinson's disease, Huntington's disease, amyotrophic lateral  
CC sclerosis, and Shy-Drager syndrome, infections, infarction of cardiac and  
CC central nervous system vessel e.g. stroke, sepsis, inflammatory bowel  
CC disease, ulcers, bone regeneration. The protein, having activin- or  
CC inhibin-related activities is useful as a contraceptive based on the  
CC ability of inhibins to decrease fertility in female mammals and decrease  
CC spermatogenesis in male mammals. The proteins and nucleic acids are also  
CC useful as food supplements. The present sequence encodes a secreted  
CC protein of the invention  
XX SQ Sequence 1656 BP; 473 A; 389 C; 340 G; 454 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8,54e-66 Length: 1656  
Score: 624.50 Matches: 115  
Percent Similarity: 81.05% Conservative: 39  
Best Local Similarity: 60.53% Mismatches: 35  
Query Match: 67.08% Indels: 1  
DB: Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAS59216 (1-1656)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
DB 165 GCGGTGCAGATCTGATTTCTGGAGAGATGGAAGACAGCTGGTTGCTCTTGGCACC 224  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 225 ACGCTGATCATGCTGCTTTCCCTGGCAGCTTTTCAGTGTTCATCAGTGTGGTTCTTACCTC 284  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
DB 285 ATCTCGGCTCTTCTCTGTCCACATCAGTTCAGATCTACAGTCCGTCATCCAGCT 344  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
DB 345 GTACAGAGTCAGAGAAGCCATCCATTCAAGCCCTACTGGACGTAGACATTACTCTG 404





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QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 405 TCCTCAGAAAGCTTTCATTAATACATGAATGTCGCATGCGTGCATCAACAGGGCCCTG 464
QY 101 LysGluLeuArgGluPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 465 AAACATCAATTATTCGTCCTCTTCTGGTGAAGATCTGGTTCCTTGAAGTGGCTGTC 524
QY 121 LeuMetTyrPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db 525 TTCAATGCTGCTGATGACCTATGTTGGTGTCTTTTAAACGGAATCACCTCTTAATCTT 584
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 585 GCTGAACCTGCTCATTTTCAGTGTCCGATGTCTATGAGAACTCAAGACCCAGATTGAT 644
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 645 CACTATGTGGTATCGCCGAGATCAGACCAAGTCAATTTGTAAGAAAGATCCAGCAAAA 704
QY 181 IleProGlyLeu---LysArgLysAlaGlu 189
Db 705 CTCCTCGAATCGCCAAAGAAAGGCAGAA 734
RESULT 73
AAZ36240
ID AAZ36240 standard; cDNA; 1668 BP.
AC
AC AAZ36240;
XX
XX 22-FEB-2000 (first entry)
DE
DE cDNA encoding a bone marrow secreted protein designated BMS240.
XX
KW Bone marrow secreted protein; bone marrow stromal cell; cytokine;
KW cell proliferation; cell differentiation; hematopoiesis; anaemia;
KW myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;
KW erythroid progenitor cell; colony stimulating factor; granulocyte;
KW monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;
KW platelet disorder; thrombocytopenia; hematopoietic stem cell;
KW stem cell disorder; aplastic anaemia; bone differentiation;
KW paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon;
KW ligament; nerve; wound healing; tissue repair; burn; incision; ulcer;
KW bone fracture; cartilage damage; artificial joint; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 99..809
FT /*tag= a
FT /*product= "bone marrow secreted protein"
FT poly_a_signal 1626..1631
FT /*tag= b
XX
XX WO9933979-A2.
XX
XX 08-JUL-1999.
XX
XX 18-DEC-1998; 98WO-US027008.
XX
XX 30-DEC-1997; 97US-0068958P.
XX 24-SEP-1998; 98US-0101603P.
XX 30-SEP-1998; 98US-0102540P.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Lin H, Cao L;
XX
XX WPI; 2000-038344/03.
XX P-PSDB; AAY53634.
XX
XX New isolated human polynucleotide and secreted proteins can induce
```

PT production of other cytokines in certain cell populations.

XX Claim 11; Page 98-100; 120pp; English.

XX AAZ36228-49 encode bone marrow secreted proteins of human bone marrow stromal cells. The proteins can exhibit cytokine, cell proliferation, or cell differentiation activity (either inducing or inhibiting). They can be used to support colony forming cells or factor-dependent cell lines, to regulate hematopoiesis, and to treat myeloid or lymphoid cell deficiencies. In addition, they may be used to support the growth and proliferation of erythroid progenitor cells, and to treat various anaemias. They can have colony stimulating factor (CSF) activity and can be used to support the growth and proliferation of myeloid cells such as granulocytes, monocytes or macrophages, to prevent or treat myelo-suppression, to support the growth and proliferation of megakaryocytes and platelets, thereby allowing prevention or treatment of platelet disorders such as thrombocytopenia, to support the growth and proliferation of hematopoietic stem cells, either in place of or in conjunction with platelet transfusions, to treat stem cell disorders, such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to repopulate the stem cell compartment after irradiation or chemotherapy. They can be used for growth or differentiation of bone, cartilage, tendon, ligament, or nerve tissue, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers, to induce cartilage and/or bone growth in circumstances where bone is not normally formed and thus have an application in healing bone fractures and cartilage damage or defects, prophylactic use in fracture reduction and also in the improved fixation of artificial joints

XX SQ Sequence 1668 BP; 435 A; 414 C; 349 G; 470 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 8.63e-66 Length: 1668  
Score: 624.50 Matches: 115  
Percent Similarity: 81.05% Conservative: 39  
Best Local Similarity: 60.53% Mismatches: 35  
Query Match: 67.08% Indels: 1  
DB: 3 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAZ36240 (1-1668)

QY 1 SerValValAspLeuLeuTyrTyrArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 237 GCGGTGACGATCTGATTTCTGGAGAGATGTGACAGAGACTGGGTGTCTTTGGCACC 296  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 297 ACGCTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTTCATGCTGTGTTCTTACCTC 356  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 357 ATCTCGGCTCTTCTCTCTGTCACCATCAGTTCAGGATCTCAAGTCCGTTCATCAAGCT 416  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 417 GTACAGAAAGTCAAGAAAGGCCATCCATTCAAGCTACCTGGAGCTAGACATTAATCTG 476  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 477 TCCTCAGAAAGCTTTCATAATTTACATGAATGTCGCATGTCATCAACAGGGCCCTG 536  
QY 101 LysGluLeuArgGluPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 537 AAACATCAATTATTCGTCCTCTTCTGGTGAAGATCTGGTTCCTTGAAGTGGCTGTC 596  
QY 121 LeuMetTyrPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
Db 597 TTCAATGCTGCTGATGACCTATGTTGGTGTCTTTTAAACGGAATCACCTCTTAATCTT 656  
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db 657 GCTGAACCTGCTCATTTTCAGTGTCCGATTTGTCTATGAGAAAGTCAAGACCCAGATTGAT 716

QY 161 HistTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 717 CACTATGTGGATCGCCGAGATCAGACCAAGTCAATTGTTGAAGAAGATCCAGCAAAA 776

QY 181 IleProGlyLeu---LysArgLysAlaGlu 189  
 Db 777 CTCCTGGAATCGCCCAAAAAAAGGCAGAA 806

## RESULT 74

AAZ38319  
 ID AAZ38319 standard; cDNA; 1759 BP.

XX

AC AAZ38319;

DT 09-FEB-2000 (first entry)

XX Human transmembrane protein cDNA clone HP02061.

DE HP02061; transmembrane domain; Saos-2; homology;

KW neuroendocrine-specific protein C; antibody; assay reagent;

KW diagnostic marker; primer; probe; antisense; gene therapy; agonist;

KW antagonist; ligand; therapeutic; ds.

XX Homo sapiens.

OS

XX Key

PH Location/Qualifiers

FT 142..852

FT /\*tag= a

FT /product= "Human transmembrane protein HP02061"

XX WO9955862-A2.

XX 04-NOV-1999.

XX 27-APR-1999; 99WO-JP002226.

XX 28-APR-1998; 98JP-00119395.

XX (SAGA ) SAGAMI CHEM RES CENT.

XX (PROT-) PROTEGENE INC.

XX Kato S, Kimura T;

XX WPI; 2000-023358/02.

XX P-PSDB; AAY52387.

XX Human proteins with transmembrane domains, involved in control of cell

XX proliferation and differentiation, useful for treating e.g. cancer or

XX inflammation.

XX Claim 4; Page 92-94; 114pp; English.

XX This sequence represents the human cDNA clone HP02061 which encodes a 26

XX kD protein with two putative transmembrane domains. The cDNA was isolated

XX from a Saos-2 (human osteosarcoma cell line) cDNA library. The protein

XX has homology with the human neuroendocrine-specific protein C (PIR

XX Accession No. I6904), and may have a similar function. The protein may

XX be used to raise specific antibodies, as assay reagents, as diagnostic

XX tissue markers, for the isolation of cognate receptors, ligands and

XX binding proteins, and as biologically active agents. Nucleotides encoding

XX the protein may be used as primers and probes or antisense molecules, and

XX in gene therapy. Cells transformed with these nucleotides may be used to

XX screen for agonists and antagonists which are potentially useful

XX therapeutically

XX SQ Sequence 1759 BP; 454 A; 433 C; 376 G; 496 T; 0 U; 0 Other;

XX Alignment Scores:

XX Pred. No.: 9,29e-66 Length: 1759

XX Score: 624.50 Matches: 115

XX Percent Similarity: 81.05% Conservatve: 39

XX Best Local Similarity: 60.53% Mismatches: 35

XX Query Match: 67.08% Indels: 1

DB: 3 Gaps: 1  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAZ38319 (1-1759)  
 QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 Db 280 GCGGTGCACGATCTGATTTCTGGAGAGATGTGAAGAAGATGGGTTTGTCTTTGGCACC 339  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThraLalaTyrIle 40  
 Db 340 ACGCTGATCATGCTGCTTTCCCTGGCAGCTTTTCAGTGTGCATCAGTGTGTTCTTACCTC 399  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 400 ATCTGGCTCTTCTCTGTCCATCAGCTTCAGATCTACAGTCCGTTCATCCAGCT 459  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 460 GTACAGAAGTCAGAAGAAGGCCATCCATTCAAGGCTACCTGGACGTAGACATTACTCTG 519  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 Db 520 TCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGTCGCATCAACAGGCCCTG 579  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 580 AAATCATATTGCTCTCTTCTGTGGTGAAGATCTGGTGGACTCTCTTGAAGCTGGCTGTC 639  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 Db 640 TTCAITGGTGTGATGACCTATGTTGGTCTGTTTAAACGGAATCACCTCTTAATCTT 699  
 QY 141 AlaLeuLysSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 Db 700 GCTGAACCTGCTCAATTTTCAGTGTCCCGATGCTCTATGAGAAGTACAGACCCAGATTGAT 759  
 QY 161 HistTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 760 CACTATGTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAGAAGATCCAGCAAAA 819  
 QY 181 IleProGlyLeu---LysArgLysAlaGlu 189  
 Db 820 CTCCTGGAATCGCCCAAAAAAAGGCAGAA 849  
 RESULT 75  
 AAV59748  
 ID AAV59748 standard; DNA; 1766 BP.  
 XX  
 AC AAV59748;  
 XX  
 DT 19-JAN-1999 (first entry)  
 XX Human secreted protein gene 92 clone HAUBL57.  
 DE Human; secreted protein; fusion protein; gene therapy; protein therapy;  
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
 KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;  
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9839448-A2.  
 XX  
 XX 11-SEP-1998.  
 XX  
 XX 06-MAR-1998; 98WO-US004493.  
 XX  
 XX 07-MAR-1997; 97US-0038621P.  
 XX  
 XX 07-MAR-1997; 97US-0040161P.

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PR 07-MAR-1997; 97US-0040162P.
PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040336P.
PR 07-MAR-1997; 97US-0040626P.
PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043568P.
PR 11-APR-1997; 97US-0043569P.
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043578P.
PR 11-APR-1997; 97US-0043580P.
PR 11-APR-1997; 97US-0043669P.
PR 11-APR-1997; 97US-0043670P.
PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.
PR 11-APR-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047492P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047503P.
PR 23-MAY-1997; 97US-0047581P.
PR 23-MAY-1997; 97US-0047582P.
PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
PR 23-MAY-1997; 97US-0047585P.
PR 23-MAY-1997; 97US-0047586P.
PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048644P.
PR 06-JUN-1997; 97US-0048974P.
PR 13-JUN-1997; 97US-0049610P.
PR 16-JUL-1997; 97US-0051926P.
PR 18-AUG-1997; 97US-0055724P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056636P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
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PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
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PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.
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PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057669P.
PR 05-SEP-1997; 97US-0057761P.
PR 12-SEP-1997; 97US-0058785P.
PR 02-OCT-1997; 97US-0061060P.

XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
PI Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PB, Greene JM;
PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX WPI; 1998-506364/43.
DR P-PSDB; AAW74963.
XX
XX New isolated human genes and the secreted polypeptide(s) they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX Claim 1; Page 473-474; 721pp; English.
XX
XX This sequence represents a nucleic acid molecule designated Gene 92 from
CC the human cDNA clone HAUBL57 (deposited as clone ATCC 97897 and ATCC
CC 209043) which encodes a secreted human protein. The gene can be used to
CC generate fusion proteins by linking to the gene to a human immunoglobulin
CC Fc portion (e.g. AAV59502) for increasing the stability of the fused
CC protein as compared to the human protein only. The invention relates to
CC 186 novel genes and their fragments (nucleic acid sequences: AAV59511-
CC V59812; amino acid sequences AAW74731-W5026) which are useful for
CC preventing, treating or ameliorating medical conditions e.g. by protein
CC or gene therapy. Also, pathological conditions can be diagnosed by
CC determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 186 polynucleotides, based on
CC which tissues they are most highly expressed in (see AAV59511 for
CC described uses)
XX
XX Sequence 1766 BP; 463 A; 437 C; 383 G; 481 T; 0 U; 2 Other;
SQ
Alignment Scores:
Pred. No.: 9.34e-66 Length: 1766
Score: 624.50 Matches: 115
Percent Similarity: 81.05% Conservative: 39
Best Local Similarity: 60.53% Mismatches: 35
Query Match: 67.08% Indels: 1
DB: 2 Gaps: 1
US-09-830-972-29_COPY_990_1178 (1-189) x AAV59748 (1-1766)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 287 GCGGTGCACGATCTGATTTCTTGGAGAGATGTGAAGAGACTGGTGTCTTTGGACC 346
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PR 22-AUG-1997; 97US-0056884P.  
 PR 22-AUG-1997; 97US-0056886P.  
 PR 22-AUG-1997; 97US-0056887P.  
 PR 22-AUG-1997; 97US-0056888P.  
 PR 22-AUG-1997; 97US-0056889P.  
 PR 22-AUG-1997; 97US-0056892P.  
 PR 22-AUG-1997; 97US-0056893P.  
 PR 22-AUG-1997; 97US-0056894P.  
 PR 22-AUG-1997; 97US-0056903P.  
 PR 22-AUG-1997; 97US-0056908P.  
 PR 22-AUG-1997; 97US-0056909P.  
 PR 22-AUG-1997; 97US-0056910P.  
 PR 22-AUG-1997; 97US-0056911P.  
 PR 05-SEP-1997; 97US-0057669P.  
 PR 05-SEP-1997; 97US-0057761P.  
 PR 12-SEP-1997; 97US-0058785P.  
 PR 02-OCT-1997; 97US-0061060P.  
 PR 06-MAR-1998; 98WO-US004493.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC;  
 PI Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;  
 PI Ferrite AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;  
 PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;  
 XX  
 DR WPI; 2002-634796/68.  
 DR P-PSDB; ABG95423.  
 XX  
 PT New isolated human secreted protein for diagnosing, preventing, treating  
 PT or ameliorating medical conditions and used as a food additive or  
 PT preservative.  
 XX  
 PS Example 1; SEQ ID NO 254; 129pp; English.  
 XX  
 CC The invention relates to an isolated protein that is one of 186 human  
 CC secreted proteins, given in the specification, encoded by one of 309 cDNA  
 CC sequences also given in the specification. The protein is used in a  
 CC pharmaceutical composition used to prevent, treat or ameliorate a medical  
 CC condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs,  
 CC chickens or sheep. Disorders which are diagnosed or treated include  
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders  
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,  
 CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,  
 CC infections caused by bacteria, viruses and fungi and ocular disorders  
 CC e.g. corneal infection. The polypeptides can also be used to aid wound  
 CC healing and epithelial cell proliferation, to prevent skin aging due to  
 CC sunburn, to maintain organs before transplantation, for supporting cell  
 CC culture of primary tissues, to regenerate tissues and in chemotaxis. The  
 CC polypeptides can also be used as a food additive or preservative to  
 CC increase or decrease storage capabilities, fat content, lipid, protein,  
 CC carbohydrate, vitamins, minerals, cofactors and other nutritional  
 CC components. The present sequence represents a cDNA derived from a gene  
 CC encoding one of the novel human secreted proteins of the invention. Note:  
 CC This sequence did not form part of the printed specification, but was  
 CC obtained in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=6420526B1  
 XX  
 SQ Sequence 1766 BP; 463 A; 437 C; 383 G; 481 T; 0 U; 2 Other;  
 Alignment Scores:  
 Pred. No.: 9.34e-66 Length: 1766  
 Score: 624.50 Matches: 115  
 Percent Similarity: 81.05% Conservative: 39  
 Best Local Similarity: 60.53% Mismatches: 35  
 Query Match: 67.08% Indels: 1  
 DB: Gaps: 6

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ABS73741 (1-1766)

QY 1 SerValValAspLeuLeuTyrTTPArgAspIleLysLysThrGlyValPheGlyAla 20

Db 287 GCGGTGCAGATCTGATTTCTGGAGAGATGTGAAGAGACTGGGTGTTCTTTGGCACC 346  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 Db 347 ACGCTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTTCATCAGTGTGTTCTTACCTC 406  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 Db 407 ATCTTGGCTCTTCTCTGTCCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCT 466  
 QY 61 IleGlnLysSerAspGluLysHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 Db 467 GTACAGAAGTCAGAGAAGGCCATCATTTCAAGGCTACCTGGACGTAGACATTACTCTG 526  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 Db 527 TCTTCAGAAGCTTTCATATTAATGATGCTGCCATGGTGCACATCAACAGGCCCTG 586  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 Db 587 AAACATATTATTGCTCTCTTCTGGTAGAAGATCTGGTTGACTCTCTTGAAGCTGGCTGC 646  
 QY 121 LeuMetTTPValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIle 140  
 Db 647 TTCATGTGGCTGATGACCTATGTTGGTCTGTTTTTAACGGAATCACCTCTTAATCTT 706  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 Db 707 GCTGAAGTCTCATTTTCAGTGTCCCGATTGCTATGAGAAGTACAAGACCCAGATTGAT 766  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 Db 767 CACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGTTAAAGAGATCCAAGCAAA 826  
 QY 181 IleProGlyLeu--LysArgLysAlaGlu 189  
 Db 827 CTCCTTGGATCGCCAAAAAAGGAGAA 856  
 RESULT 77  
 ACD82884  
 ID ACD82884 standard; cDNA; 1766 BP.  
 XX ACD82884;  
 AC ACD82884;  
 XX  
 DT 22-SEP-2003 (first entry)  
 DE  
 DE cDNA sequence #244 containing coding region of a human secreted protein.  
 KW Human; secreted protein; hyperproliferative disorder; leukaemia;  
 KW breast cancer; wound; reproductive disorder; blood-related disorder;  
 KW haemophilia; thrombocytopaenia; immunodeficiency; thymic hypoplasia;  
 KW Wiskott-Aldrich syndrome; autoimmune disorder; multiple sclerosis;  
 KW graft-versus-host disease; Hashimoto's thyroiditis; allergy; asthma;  
 KW viral infection; bacterial infection; fungal infection; AIDS; sepsis;  
 KW renal disorder; kidney failure; cardiovascular disorder; cytostatic;  
 KW angina pectoris; cerebral ischaemia; congenital heart defect;  
 KW respiratory disorder; neurological disorder; Alzheimer's disease;  
 KW Parkinson's disease; inflammation; Crohn's disease; vulvovaginitis;  
 KW immunosuppressive; antibacterial; haemostatic; thrombolytic;  
 KW anticoagulant; neuroprotective; thyromimetic; antiallergic;  
 KW antiasthmatic; virucide; fungicide; anti-HIV; nephrotropic; antianginal;  
 KW cerebroprotective; cardiant; nootropic; antiparkinsonian;  
 KW antiinflammatory; gene; ss.  
 XX Homo sapiens.  
 OS  
 XX US2003049618-A1.  
 PN  
 XX 13-MAR-2003.  
 PD  
 XX 16-MAR-2001; 2001US-00809391.  
 XX

PR 07-MAR-1997; 97US-0038621P.  
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PR 09-OCT-1997; 97US-0061660P.  
PR 06-MAR-1998; 98WO-US004493.  
PR 08-SEP-1998; 98US-00149476.  
PR 17-MAR-2000; 2000US-0190068P.  
XX  
PA (RUBE//) RUBEN S M.  
PA (ROSE//) ROSEN C A.  
PA (SOPP//) SOPPET D R.  
PA (CART//) CARTER K C.  
PA (BEDN//) BEDNARIK D P.  
PA (ENDR//) ENDRESS G A.  
PA (YUGG//) YU G.  
PA (NIJJ//) NI J.  
PA (FENG//) FENG P.  
PA (YOUN//) YOUNG P E.  
PA (GREE//) GREENE J M.  
PA (FERR//) FERRIE A M.  
PA (DUAN//) DUAN D R.  
PA (HUJJ//) HU J.  
PA (FLOR//) FLORENCE K A.  
PA (OLSE//) OLSEN H S.  
PA (FISC//) FISCHER C L.  
PA (EBNE//) EBNER R.  
PA (BREW//) BREWER L A.  
PA (MOOR//) MOORE P A.  
PA (SHIY//) SHI Y.  
PA (LAPL//) LAFLEUR D W.  
PA (LIYY//) LI Y.  
PA (ZENG//) ZENG Z.  
PA (KYAW//) KYAW H.  
XX  
PI Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;  
PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;  
PI Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;  
PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;  
XX  
MPI; 2003-521800/49.  
DR P-PSDB; ABO34617.  
XX  
PT New genes and its encoded prostate cancer antigen proteins, useful for  
PT preventing, treating, ameliorating or diagnosing e.g. prostate cancers,  
PT thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral  
PT ischemia.  
XX  
PS Claim 4; SEQ ID NO 254; 260pp; English.  
XX  
CC The present invention relates to the isolation of novel human secreted  
CC proteins and the polynucleotide sequences encoding them. The invention

CC also discloses vectors, host cells, antibodies, and recombinant methods  
CC for producing human secreted proteins. The polypeptide and polynucleotide  
CC sequences for the secreted proteins are useful for preventing, treating,  
CC ameliorating or diagnosing medical conditions such as hyperproliferative  
CC disorders (e.g. leukemia or breast cancers), wounds, reproductive  
CC disorders, blood-related disorders (e.g. haemophilia or  
CC thrombocytopenia), immunodeficiencies (e.g. Wiskott-Aldrich syndrome or  
CC thymic hypoplasia), autoimmune disorders (e.g. graft-versus-host disease,  
CC multiple sclerosis or Hashimoto's thyroiditis), allergies (e.g. asthma),  
CC viral or bacterial or fungal infections (e.g. AIDS or sepsis), renal  
CC disorders (e.g. kidney failure), cardiovascular disorders (e.g. angina  
CC pectoris, cerebral ischaemia or congenital heart defects), respiratory  
CC disorders, neurological disorders (e.g. Alzheimer's disease or  
CC Parkinson's disease), and inflammations (e.g. Crohn's disease). The  
CC polynucleotide or polypeptide may also be used as vaccine adjuvants.  
CC ACD82641-ACD82950 encode human secreted proteins or their fragments.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from the  
CC USPTO web site at [seqdata.uspto.gov/paipdIDEntry.html](http://seqdata.uspto.gov/paipdIDEntry.html)

XX SQ Sequence 1766 BP; 463 A; 437 C; 383 G; 481 T; 0 U; 2 Other;

## Alignment Scores:

Prod. No.:	9.34e-66	Length:	1766
Score:	624.50	Matches:	115
Percent Similarity:	81.05%	Conservative:	39
Best Local Similarity:	60.53%	Mismatches:	35
Query Match:	67.08%	Indels:	1
DB:	9	Gaps:	1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ACD82884 (1-1766)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLeuThrGlyValValPheGlyAla 20  
Db 287 GCGGTGCACATCTGATTTTCGAGAGATGTGAAGAGACTGGTGTCTTTGTCACCC 346  
QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 347 ACCTCATCATCTGCTGCTTCCCTGGCAGCTTTCAGTGTTCATCAGTGTGTTCTTACCTC 406  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 407 ATCTGCTGCTTCTCTCTGTCCACATCAGCTTCAGATCTACAGTCCGTCATCCAGCT 466  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleGluSerGluValAlaIle 80  
Db 467 GTACAGAAGTCAGAGAAGGCCATCCATCAAGCCCTACCTGGCAGTAGACATTACTCTG 526  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 527 TCCTCAGAAGCTTTCATTAATATACATGAATGCTGCCATGTGCACATCAACAGGCCCTG 586  
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 587 AAATCATTAATTCCTCTCTCTGTGAGAGATCTGTTGACTTCCTTGAAGCTGGCTGC 646  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 647 TTCATGTGGCTGATGACCTATGTTGTGCTGTTTAAACGGAATCACCTTCTTAATCTT 706  
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db 707 GCTGAATGCTCATTTTCAGTGTCCCGATTTGCTATGAGAGAGTACAGACCCAGATTGAT 766  
QY 161 HisTyrIleGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 767 CATATGTTGGCATGCCCGAGATCAGACCAATCAATCTTGAAGAAGTCCAGCAAA 826  
QY 181 IleProGlyLeu---LysArgLysAlaGlu 189  
Db 827 CTCCTCGAATCGCAAAAAAAGGAGAA 856

RESULT 78

ADI22969  
ID ADI22969 standard; cDNA; 1766 BP.  
XX ADI22969;  
XX ADI22969;  
DT 22-APR-2004 (first entry)  
XX cDNA encoding novel human secreted protein seq id 254.  
KW cytostatic; gene therapy; cancer; human; secreted protein; gene; ss.  
XX Homo sapiens.  
XX US2003175858-A1.  
PD 18-SEP-2003.  
XX 18-JUN-2001; 2001US-00882171.  
XX 07-MAR-1997; 97US-0038621P.  
PR 07-MAR-1997; 97US-0040162P.  
PR 07-MAR-1997; 97US-0040163P.  
PR 07-MAR-1997; 97US-0040333P.  
PR 07-MAR-1997; 97US-0040334P.  
PR 07-MAR-1997; 97US-0040336P.  
PR 07-MAR-1997; 97US-0040626P.  
PR 11-APR-1997; 97US-0043311P.  
PR 11-APR-1997; 97US-0043312P.  
PR 11-APR-1997; 97US-0043313P.  
PR 11-APR-1997; 97US-0043314P.  
PR 11-APR-1997; 97US-0043315P.  
PR 11-APR-1997; 97US-0043568P.  
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PR 06-JUN-1997; 97US-0048974P.
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PR 09-OCT-1997; 97US-0061660P.
PR 06-MAR-1998; 98WO-US004453.
PR 08-SEP-1998; 98US-00149476.
PR 17-MAR-2000; 2000US-0190068P.
PR 16-MAR-2001; 2001US-00809391.
XX
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREEN/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAPL/) LAPLEUR D W.
PA (LIY/) LI Y.

PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
XX
PI Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;
PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
PI Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX
WPI: 2003-898535/82.
DR P-PSDB; ADI23278.
XX
PT New nucleic acid molecule, useful for preparing a medicament for
PT diagnosing, preventing, treating or ameliorating a medical condition
PT e.g., cancer.
XX
PS Claim 1; SEQ ID NO 254; 256pp; English.
XX
CC The invention describes an isolated nucleic acid comprising a sequence
CC having 95 % identity with: a polynucleotide fragment of a sequence not
CC given in the specification, or its allelic variant; a polynucleotide
CC fragment of the cDNA sequence; a polynucleotide sequence encoding a
CC polypeptide, or its fragment, domain, epitope or species homologue; or a
CC polynucleotide that hybridises under stringent conditions to any one of
CC the sequences of (a)-(c). The nucleic acid is useful for preparing a
CC medicament for diagnosing, preventing, treating or ameliorating a medical
CC condition e.g., cancer. The sequence encodes a novel human secreted
CC protein of the invention.
XX
SQ Sequence 1766 BP; 463 A; 437 C; 383 G; 481 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.: 9,34e-66 Length: 1766
Score: 624.50 Matches: 115
Percent Similarity: 81.05% Conservative: 39
Best Local Similarity: 60.53% Mismatches: 35
Query Match: 67.08% Indels: 1
DB: 10 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x ADI22969 (1-1766)
QY 1 SerValValAspLeuLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
Db 287 CGCGTGCACGATCTGATTTCTTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCACC 346
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 347 ACGCTGATCATCTGCTGCTTCCCTGGCAGCTTCAGTGTTCATCAGTGGTGTTCCTACCTC 406
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 407 ATCTGGCTCTTCTCTGTCCATCCATCAGCTTCAGGATCTACAGTCCGTCATCCAGCT 466
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 467 GTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCTACCTGCGAGCTAGACATTACTCTG 526
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCyethrIle 100
Db 527 TCCTCAGAAGGCTTCCCATTAATACATGAATGCTCCATGGTGCACTCAACAGGGCCCTG 586
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 587 AAACATCATATTGCTCTCTTCTGGTAGAAGATCTGGTTGACTCTCTTGAAGCTGGCTGTC 646
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 647 TTCATGTGGCTGATGACCTATGTTGGTCTGTTTTTAACGGAATCACCTCTCTAATTCCT 706
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 707 GCTGAACCTGCATTTTCAGTGTCCCGATTTCTATGAGAAGTACAAACACCCAGCTTGAAT 766
QY 161 HistTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaIleGlnAlaLys 180

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PS Claim 3; SEQ ID NO 254; 142pp; English.

XX The invention relates to isolated nucleic acid molecules and the human  
CC secreted proteins (SPs) they encode. The proteins and nucleic acids may  
CC be used in the prevention, diagnosis and treatment of diseases associated  
CC with inappropriate SP expression e.g. cancer, haematopoietic disorders,  
CC endocrine disorders, diseases of the immune system, inflammatory  
CC disorders and many others. Full details of disorders that may be  
CC prevented, diagnosed and/or treated by the above methods are given in the  
CC specification. The nucleic acid molecules may be used to produce their  
CC proteins. The nucleic acid and its complementary sequences may also be  
CC used as DNA probes in diagnostic assays to detect and quantitate the  
CC presence of similar nucleic acids in samples, and therefore which  
CC patients may be in need of restorative therapy. The SPs may also be used  
CC as antigens in the production of antibodies against the proteins and in  
CC assays to identify modulators of SP expression and activity. The anti-SP  
CC antibodies and antagonists may also be used to down regulate expression  
CC and activity. The anti-SP antibodies may also be used as diagnostic  
CC agents for detecting the presence of the proteins in samples (e.g. by  
CC enzyme linked immunosorbent assay (ELISA)). The present sequence  
CC represents a human secreted protein cDNA.

XX SQ Sequence 1766 BP; 463 A; 437 C; 383 G; 481 T; 0 U; 2 Other;

#### Alignment Scores:

Pred. No.:	9,346-66	Length:	1766
Score:	624.50	Matches:	115
Percent Similarity:	81.05%	Conservative:	39
Best Local Similarity:	60.53%	Mismatches:	35
Query Match:	67.08%	Indels:	1
DB:	12	Gaps:	1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADH73971 (1-1766)

Qy	1	SerValValAspLeuLeuTyrTrpArgAspLeuLysThrGlyValValPheGlyAla	20
Db	287	CGCGTGCCAGCATCTGATTTCTGGAGAGATGTGAAGAAGCTGGGTTTGTCTTGGCACC	346
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	347	ACGCTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTCACTACAGTGTGTTCTTACCTC	406
Qy	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
Db	407	ATCTGGCTCTCTCTGTCCATCATCAGTTCAGGATCTACAGTCCGTATCCAGCT	466
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
Db	467	GTACAGAAGTCAGAGAAGGCCATCCATTCAAAGCCTACCTGGAGCTAGACATTACTCTG	526
Qy	81	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle	100
Db	527	TCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGACATCAACAGGCGCCTG	586
Qy	101	LysGluLeuLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal	120
Db	597	AAACTCATATTGCTCTCTTCTGGTAGAAGATCTGGTTGACTCTTGAAGCTGGCTGTC	646
Qy	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
Db	647	TTCATGTGGCTGATGACCTATGTTGGTGTCTGTTTAAACGGAATCACCTTCTAATCTT	706
Qy	141	AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp	160
Db	707	GCTGAACCTGCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAACCCAGATTGAT	766
Qy	161	HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys	180
Db	767	CACATATGGTCATGCCCGAGATCAGACCAGTCAATTGTTGAAGAAGATCCAGCAAAA	826
Qy	181	IleProGlyLeu---LysArgLysAlaGlu	189
Db	827	CTCCCTGGAATCGCCCAAAAAAAGGACGAA	856

#### RESULT 80

ADM36177  
ID ADM36177 standard; DNA; 1911 BP.  
AC ADM36177;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Human RTN3 isoform VI coding sequence, SEQ ID 60.  
XX  
KW Neuroprotective; Myotropic; neuromuscular disease; RTN3; reticulon 3;  
XX amytrophic lateral sclerosis; ALS; myopathy; human; gene; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
CDS 124..834  
FT /\*tag= a  
FT /product= "RTN3 isoform VI"  
XX

W02004001069-A2.

31-DEC-2003.

20-JUN-2003; 2003WO-FR001910.

25-JUN-2002; 2002FR-00007846.

(UYPA-) UNIV PASTEUR LOUIS.

Dupuis L, Di Scala F, De Tapia M, Larmet Y, Loeffler J;  
Gonzales De Aguilar J, Boutillier AL, Gaidon C, Rene F;

WPI; 2004-071743/07.

P-ESDB; ADM36178.

Diagnosing, prognosing and monitoring neuromuscular disease, particularly  
amyotrophic lateral sclerosis, comprises detecting modulation of the  
reticulon 3 gene.

Claim 17; SEQ ID NO 60; 116pp; French.

The present invention relates to a method for diagnosing, or evaluating  
progression of, a neuromuscular disease. The method comprises detecting  
modulation of the expression of a product (I) of the RTN (reticulon)3  
gene. Differential expression of RTN3 is a specific marker of  
neuromuscular disease, allowing early diagnosis from readily available  
muscle biopsies. The method is also useful for determining the efficacy  
of treatment. The method is used to diagnose (also to evaluate  
progression or therapy of) neuromuscular disorders, specifically  
amyotrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies  
specific for isoforms of RTN3 or oligonucleotides (antisense sequences or  
small interfering RNA) that can block/reduce expression of these isoforms  
are useful for treating neuromuscular diseases and (ii) cells that  
express RTN3 are useful in screening for therapeutic agents. The present  
sequence is a RTN3 DNA sequence used to illustrate the invention.

Sequence 1911 BP; 488 A; 463 C; 406 G; 554 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.:	1,046-65	Length:	1911
Score:	624.50	Matches:	115
Percent Similarity:	81.05%	Conservative:	39
Best Local Similarity:	60.53%	Mismatches:	35
Query Match:	67.08%	Indels:	1
DB:	12	Gaps:	1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADM36177 (1-1911)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspLeuLysThrGlyValValPheGlyAla 20

Db 262 CGCGTGCCAGCATCTGATTTCTGGAGAGATGTGAAGAAGCTGGGTTTGTCTTGGCACC 321



QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 467 GTACAGAGTCAAGAGAGCCATTCATCAAGGCTACCTGGAGCTAGACATTAATCTGTG 526  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 DB 527 TCCTCAGAAGCTTTCCATAATACATGAATGTCGTCATGTCACATCAACAGGCGCTG 586  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 587 AAATCATATTGCTCTCTCTGTGAGAGATCTGGTGTGACTCTCTGAAGCTGGCTGTC 646  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 DB 647 TTCATGTGGCTGATGACCTATGTTGCTGCTGTTTAAACGGAATCACCCTCTTAATCTT 706  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 DB 707 GCTGAATGCTCATTTTCAGTGTCCGATTTGCTATGAGAAAGTACAGACCCAGATTGAT 766  
 QY 161 HistyLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 767 CACTATGTGGCATGCCCGAGATCAGACCAAGTCAATTTGTGAAGAAAGATCCAGCAAAA 826  
 QY 181 IleProGlyLeu---LysArgLysAlaGlu 189  
 DB 827 CTCCTCGAATCGCCAAAAGGAGCAAA 856

RESULT 82  
 ID AAF93902 standard; cDNA; 2530 BP.  
 XX AAF93902;  
 AC AAF93902;  
 DT 23-MAY-2001 (first entry)  
 XX Human cDNA encoding a membrane or secretory protein clone PSE0103.  
 DE Human; secretory protein; membrane protein; vaccine; gene therapy;  
 KW rheumatoid arthritis; diabetes; ss.  
 XX Homo sapiens.  
 XX EP1067182-A2.  
 XX 10-JAN-2001.  
 XX 07-JUL-2000; 2000EP-00114090.  
 XX 08-JUL-1999; 98JP-00194179.  
 PR 11-JAN-2000; 2000JP-00118775.  
 PR 02-MAY-2000; 2000JP-00183766.  
 XX (HELI-) HELIX RES INST.  
 XX Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;  
 XX WPI; 2001-093989/11.  
 DR P-PSDB; AAB88475.  
 XX Nucleic acids encoding secretory proteins/membrane proteins, useful in  
 PT gene therapy or as candidate target molecules in drug development.  
 XX Claim 1; SEQ ID NO 317; 609pp + Sequence Listing; English.  
 XX This invention relates to nucleic acid sequences AAF93744 - AAF93916  
 CC which encode human secretory or membrane proteins represented by AAB88317  
 CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and  
 CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the  
 CC invention. The invention also includes methods for the production of  
 CC antibodies directed against the proteins, and cDNA sequences, which can  
 CC be used in vaccines. The polynucleotide sequences can be used in gene

CC therapy. The polynucleotide sequences and the proteins they encode may be  
 CC used in the prevention, treatment and diagnosis of diseases associated  
 CC with inappropriate secretory protein/membrane protein expression. The  
 CC nucleic acids and complementary sequences may also be used as DNA probes  
 CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect  
 CC and quantitate the presence of similar nucleic acid sequences in samples.  
 CC They may also be used to study the expression and function of secretory  
 CC proteins/membrane polypeptides and their role in metabolism. The  
 CC polypeptides may be used as antigens in the production of antibodies  
 CC against them and in assays to identify modulators (agonists and  
 CC antagonists) of expression and activity. The antibodies and antagonists  
 CC may also be used as therapeutic agents to down regulate expression and  
 CC activity. The antibodies may also be used as diagnostic agents for  
 CC detecting the presence of the polypeptides in samples (e.g. by enzyme  
 CC linked immunosorbent assay (ELISA)). Examples of diseases which may be  
 CC treated include rheumatoid arthritis and diabetes

XX  
 SQ Sequence 2530 BP; 665 A; 577 C; 534 G; 754 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.55e-65 Length: 2530  
 Score: 624.50 Matches: 115  
 Percent Similarity: 81.05% Conservative: 39  
 Best Local Similarity: 60.53% Mismatches: 35  
 Query Match: 67.08% Indels: 1  
 DB: 5 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AAF93902 (1-2530)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
 DB 276 GCGGTGCAGCATCTGATTTCTCGAGAGATGCTGAAGAAGACTGGGTTTGTCTTTGGCACC 335  
 QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 336 ACGTGTATCATGTGCTTCTCCCTGGCAGCTTTCAGTGTGCATCAGTGTGTTCTTACCTC 395  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 396 ATCTGGCTCTCTCTCTGTCCATCATCAGCTTCAGATCTACAGTCCGTATCCAGCT 455  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 456 GTACAGAAGTCAGAAGAAGGCCATCCATTTCAAGCTACCTGGACGTAGACATTAATCTCTG 515  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 DB 516 TCCTCAGAAGCTTTCCATAATTAATGATGCTGCCATGTCGACATCAACAGGCGCCCTG 575  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 576 AAATCATATTGCTCTCTCTGTGAGAGATCTGGTGTGACTCTCTGAAGCTGGCTGTC 635  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 DB 636 TTCATGTGGCTGATGACCTATGTTGCTGCTTTTAAACGGAATCACCCTTCTTAATCTT 695  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 DB 696 GCTGAATGCTCATTTTCAGTGTCCGATTTCTATGAGAAAGTACAGACCCAGATTGAT 755  
 QY 161 HistyLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 756 CACTATGTGGCATGCCCGAGATCAGACCAAGTCAATTTGTGAAGAAAGATCCAGCAAAA 815  
 QY 181 IleProGlyLeu---LysArgLysAlaGlu 189  
 DB 816 CTCCTCGAATCGCCAAAAGGAGCAAA 845

RESULT 83  
 ID ADL02184 standard; cDNA; 2559 BP.  
 XX











PR 11-APR-1997; 97US-0043672P.  
 PR 11-APR-1997; 97US-0043674P.  
 PR 23-MAY-1997; 97US-0047492P.  
 PR 23-MAY-1997; 97US-0047500P.  
 PR 23-MAY-1997; 97US-0047501P.  
 PR 23-MAY-1997; 97US-0047502P.  
 PR 23-MAY-1997; 97US-0047503P.  
 PR 23-MAY-1997; 97US-0047581P.  
 PR 23-MAY-1997; 97US-0047582P.  
 PR 23-MAY-1997; 97US-0047583P.  
 PR 23-MAY-1997; 97US-0047584P.  
 PR 23-MAY-1997; 97US-0047585P.  
 PR 23-MAY-1997; 97US-0047586P.  
 PR 23-MAY-1997; 97US-0047587P.  
 PR 23-MAY-1997; 97US-0047588P.  
 PR 23-MAY-1997; 97US-0047589P.  
 PR 23-MAY-1997; 97US-0047590P.  
 PR 23-MAY-1997; 97US-0047592P.  
 PR 23-MAY-1997; 97US-0047593P.  
 PR 23-MAY-1997; 97US-0047594P.  
 PR 23-MAY-1997; 97US-0047595P.  
 PR 23-MAY-1997; 97US-0047596P.  
 PR 23-MAY-1997; 97US-0047597P.  
 PR 23-MAY-1997; 97US-0047598P.  
 PR 23-MAY-1997; 97US-0047599P.  
 PR 23-MAY-1997; 97US-0047600P.  
 PR 23-MAY-1997; 97US-0047601P.  
 PR 23-MAY-1997; 97US-0047612P.  
 PR 23-MAY-1997; 97US-0047613P.  
 PR 23-MAY-1997; 97US-0047614P.  
 PR 23-MAY-1997; 97US-0047615P.  
 PR 23-MAY-1997; 97US-0047617P.  
 PR 23-MAY-1997; 97US-0047618P.  
 PR 23-MAY-1997; 97US-0047632P.  
 PR 23-MAY-1997; 97US-0047633P.  
 PR 06-JUN-1997; 97US-0048964P.  
 PR 06-JUN-1997; 97US-0048974P.  
 PR 13-JUN-1997; 97US-0049610P.  
 PR 08-JUL-1997; 97US-0051926P.  
 PR 16-JUL-1997; 97US-0052874P.  
 PR 18-AUG-1997; 97US-0055724P.  
 PR 22-AUG-1997; 97US-0056630P.  
 PR 22-AUG-1997; 97US-0056631P.  
 PR 22-AUG-1997; 97US-0056632P.  
 PR 22-AUG-1997; 97US-0056636P.  
 PR 22-AUG-1997; 97US-0056637P.  
 PR 22-AUG-1997; 97US-0056662P.  
 PR 22-AUG-1997; 97US-0056664P.  
 PR 22-AUG-1997; 97US-0056845P.  
 PR 22-AUG-1997; 97US-0056862P.  
 PR 22-AUG-1997; 97US-0056864P.  
 PR 22-AUG-1997; 97US-0056872P.  
 PR 22-AUG-1997; 97US-0056874P.  
 PR 22-AUG-1997; 97US-0056875P.  
 PR 22-AUG-1997; 97US-0056876P.  
 PR 22-AUG-1997; 97US-0056877P.  
 PR 22-AUG-1997; 97US-0056878P.  
 PR 22-AUG-1997; 97US-0056879P.  
 PR 22-AUG-1997; 97US-0056880P.  
 PR 22-AUG-1997; 97US-0056881P.  
 PR 22-AUG-1997; 97US-0056882P.  
 PR 22-AUG-1997; 97US-0056884P.  
 PR 22-AUG-1997; 97US-0056886P.  
 PR 22-AUG-1997; 97US-0056887P.  
 PR 22-AUG-1997; 97US-0056888P.  
 PR 22-AUG-1997; 97US-0056889P.  
 PR 22-AUG-1997; 97US-0056892P.  
 PR 22-AUG-1997; 97US-0056893P.  
 PR 22-AUG-1997; 97US-0056894P.  
 PR 22-AUG-1997; 97US-0056903P.  
 PR 22-AUG-1997; 97US-0056908P.  
 PR 22-AUG-1997; 97US-0056909P.  
 PR 22-AUG-1997; 97US-0056910P.  
 PR 22-AUG-1997; 97US-0056911P.  
 PR 05-SEP-1997; 97US-0057650P.  
 PR 05-SEP-1997; 97US-0057669P.  
 PR 05-SEP-1997; 97US-0057761P.  
 PR 12-SEP-1997; 97US-0058785P.  
 PR 09-OCT-1997; 97US-0061660P.  
 PR 06-MAR-1998; 98WO-US004493.  
 PR 08-SEP-1998; 98US-00149476.  
 PR 17-MAR-2000; 2000US-0190068P.  
 XX (RUBE/) RUBEN S M.  
 PA (ROSE/) ROSEN C A.  
 PA (SOPP/) SOPPET D R.  
 PA (CART/) CARTER K C.  
 PA (BEDN/) BEDNARIK D P.  
 PA (ENDR/) ENDRESS G A.  
 PA (YUGG/) YU G.  
 PA (NIJU/) NI J.  
 PA (FENG/) FENG P.  
 PA (YOUN/) YOUNG P E.  
 PA (GREE/) GREENE J M.  
 PA (FERR/) FERRIE A M.  
 PA (DUAN/) DUAN D R.  
 PA (HUJU/) HU J.  
 PA (FLOR/) FLORENCE K A.  
 PA (OLSE/) OLSEN H S.  
 PA (FISC/) FISCHER C L.  
 PA (EBNE/) EBNER R.  
 PA (BREW/) BREWER L A.  
 PA (MOOR/) MOORE P A.  
 PA (SHIY/) SHI Y.  
 PA (LAFU/) LAFLEUR D W.  
 PA (LIYU/) LI Y.  
 PA (ZENG/) ZENG Z.  
 PA (KYAW/) KYAW H.  
 XX Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;  
 PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;  
 PI Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;  
 PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;  
 XX WPI: 2003-521800/49.  
 DR P-PSDB; ABO34618.  
 DR  
 XX  
 PT New genes and its encoded prostate cancer antigen proteins, useful for  
 PT preventing, treating, ameliorating or diagnosing e.g. prostate cancers,  
 PT thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral  
 PT ischemia.  
 XX  
 PS Claim 4; SEQ ID NO 255; 260pp; English.  
 XX  
 CC The present invention relates to the isolation of novel human secreted  
 CC proteins and the polynucleotide sequences encoding them. The invention  
 CC also discloses vectors, host cells, antibodies, and recombinant methods  
 CC for producing human secreted proteins. The polypeptide and polynucleotide  
 CC sequences for the secreted proteins are useful for preventing, treating,  
 CC ameliorating or diagnosing medical conditions such as hyperproliferative  
 CC disorders (e.g. leukaemia or breast cancers), wounds, reproductive  
 CC disorders, blood-related disorders (e.g. haemophilia or  
 CC thrombocytopaenia), immunodeficiencies (e.g. Wiskott-Aldrich syndrome or  
 CC thymic hypoplasia), autoimmune disorders (e.g. graft-versus-host disease,  
 CC multiple sclerosis or Hashimoto's thyroiditis), allergies (e.g. asthma),  
 CC viral or bacterial or fungal infections (e.g. AIDS or sepsis), renal  
 CC disorders (e.g. kidney failure), cardiovascular disorders (e.g. angina  
 CC pectoris, cerebral ischaemia or congenital heart defects), respiratory  
 CC disorders, neurological disorders (e.g. Alzheimer's disease or  
 CC Parkinson's disease), and inflammations (e.g. Crohn's disease). The  
 CC polynucleotide or polypeptide may also be used as vaccine adjuvants.  
 CC ACD82641-ACD82950 encode human secreted proteins or their fragments.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from the  
 CC USPTO web site at [seqdata.uspto.gov/psipdb/entry.html](http://seqdata.uspto.gov/psipdb/entry.html)  
 XX

SQ Sequence 2664 BP; 707 A; 605 C; 566 G; 779 T; 0 U; 7 Other;

Alignment Scores:	1.66e-65	Length:	2684
Pred. No.:	Score: 624.50	Matches:	115
Percent Similarity:	81.05%	Conservative:	39
Best Local Similarity:	60.53%	Mismatches:	35
Query Match:	67.08%	Indels:	1
DB:	9	Gaps:	1

US-09-830-972-29 COPY 990 1178 (1-189) x ACD82885 (1-2664)

Qy	20	1	SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla	20
Db	262	CGCGTGCACGATCTGATTTTTTCTGGAGAGATGTGAGAAAGACTGGGGTTTGTCTTTGGCACC	321	
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40	
Db	322	ACGCTGATCATGCTGCTTCCCTGGCAGCTTTACGTGTCATCAGTGGTGTCTTCACTC	381	
Qy	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60	
Db	382	ATCCTGGCTTCTCTCTGTACCATCAGTTCAGGATCTACAGTCCGTATCCCAAGCT	441	
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80	
Db	442	GTACAGAAGTCAAGAAAGGCCATCCATTCAAAGCTACTCTGGACGTAGACATTA	501	
Qy	81	SerGluGluLeuValGlnLysTyrSerIleSerAlaLeuGlyHisValAsnCysThrIle	100	
Db	502	TCCTCAGAAGCTTCCATTAATACATGAATGCTGCCATGGTGCAATCAACAGGGCCCTG	561	
Qy	101	LysGluLeuArgGluLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal	120	
Db	562	AAACTATTATTCTGCTCTCTCTGGTGAAGATCTGGTTGACTCCTTGAAGCTGGCTGTC	621	
Qy	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140	
Db	622	TTCAATGGCTGATGACCTPATGTTGGTGTGTTTTTAACGGAAATCACCCCTTCTA	681	
Qy	141	AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp	160	
Db	682	GCTGAACCTGCTCATTTTCAGTGTCCGATTGTCTATGAGAAGTACAGACCAGATTGAT	741	
Qy	161	HisTyrLeuGlyLeuAlaAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys	180	
Db	742	CACATGTTGGCATGCCCGCAGATCAGACCAAGTCAATTGTTGAAAGATCCCAAGCAAA	801	
Qy	181	IleProGlyLeu---LysArgLysAlaGlu	189	
Db	802	CTCCCTGGAAATCGCCAAAAAAGGCAGAA	831	

RESULT 87

ADI22970

ID ADI22970 standard; cDNA; 2664 BP.

XX  
XX

AC ADI22970;

XX  
DT 22-APR-2004 (first entry)

XX DE CPNA encoding novel human secreted protein seq id 255.

XX  
KW

cytostatic; gene therapy; cancer; human; secreted protein; gene; ss.

XX Homo sapiens.

XX  
PN  
US2003175858-A1.

XX  
PD 18-SEP-2003.

18 JUN-2001: XX PF

PR 07-MAR-1997: 97US-0038621P: XX

PR	07-MAR-1997	97US-004016129
PR	07-MAR-1997	97US-004016139
PR	07-MAR-1997	97US-004033339
PR	07-MAR-1997	97US-004033349
PR	07-MAR-1997	97US-004033369
PR	07-MAR-1997	97US-004052629
PR	07-MAR-1997	97US-004331119
PR	11-APR-1997	97US-004331129
PR	11-APR-1997	97US-004331339
PR	11-APR-1997	97US-004331349
PR	11-APR-1997	97US-004331559
PR	11-APR-1997	97US-004356899
PR	11-APR-1997	97US-004356999
PR	11-APR-1997	97US-004357699
PR	11-APR-1997	97US-004357899
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PR	11-APR-1997	97US-004750099
PR	23-MAY-1997	97US-004750199
PR	23-MAY-1997	97US-004750299
PR	23-MAY-1997	97US-004750399
PR	23-MAY-1997	97US-004758199
PR	23-MAY-1997	97US-004758299
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PR	23-MAY-1997	97US-004758999
PR	23-MAY-1997	97US-004759099
PR	23-MAY-1997	97US-004759299
PR	23-MAY-1997	97US-004759399
PR	23-MAY-1997	97US-004759499
PR	23-MAY-1997	97US-004760099
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PR	23-MAY-1997	97US-004761299
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PR	23-MAY-1997	97US-004761499
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PR	23-MAY-1997	97US-004761799
PR	23-MAY-1997	97US-004761899
PR	23-MAY-1997	97US-004763299
PR	23-MAY-1997	97US-004763399
PR	06-JUN-1997	97US-004896499
PR	06-JUN-1997	97US-004897499
PR	13-JUN-1997	97US-004961099
PR	08-JUL-1997	97US-005132699
PR	16-JUL-1997	97US-005287499
PR	18-AUG-1997	97US-005572499
PR	22-AUG-1997	97US-005663099
PR	22-AUG-1997	97US-005663199
PR	22-AUG-1997	97US-005663299
PR	22-AUG-1997	97US-005663699
PR	22-AUG-1997	97US-005663799
PR	22-AUG-1997	97US-005666299
PR	22-AUG-1997	97US-005666499
PR	22-AUG-1997	97US-005686299
PR	22-AUG-1997	97US-005686499
PR	22-AUG-1997	97US-005687299
PR	22-AUG-1997	97US-005687499
PR	22-AUG-1997	97US-005687599



XX OS Homo sapiens.  
XX PN US2003225248-A1.  
XX PD 04-DEC-2003.  
XX PF 10-JUN-2002; 2002US-00164861.  
XX PR 07-MAR-1997; 97US-0038621P.  
XX PR 07-MAR-1997; 97US-0040161P.  
XX PR 07-MAR-1997; 97US-0040162P.  
XX PR 07-MAR-1997; 97US-0040163P.  
XX PR 07-MAR-1997; 97US-0040333P.  
XX PR 07-MAR-1997; 97US-0040334P.  
XX PR 07-MAR-1997; 97US-0040336P.  
XX PR 07-MAR-1997; 97US-0040626P.  
XX PR 11-APR-1997; 97US-0043311P.  
XX PR 11-APR-1997; 97US-0043312P.  
XX PR 11-APR-1997; 97US-0043313P.  
XX PR 11-APR-1997; 97US-0043314P.  
XX PR 11-APR-1997; 97US-0043315P.  
XX PR 11-APR-1997; 97US-0043568P.  
XX PR 11-APR-1997; 97US-0043569P.  
XX PR 11-APR-1997; 97US-0043576P.  
XX PR 11-APR-1997; 97US-0043578P.  
XX PR 11-APR-1997; 97US-0043580P.  
XX PR 11-APR-1997; 97US-0043669P.  
XX PR 11-APR-1997; 97US-0043670P.  
XX PR 11-APR-1997; 97US-0043671P.  
XX PR 11-APR-1997; 97US-0043672P.  
XX PR 11-APR-1997; 97US-0043674P.  
XX PR 23-MAY-1997; 97US-0047492P.  
XX PR 23-MAY-1997; 97US-0047500P.  
XX PR 23-MAY-1997; 97US-0047501P.  
XX PR 23-MAY-1997; 97US-0047502P.  
XX PR 23-MAY-1997; 97US-0047503P.  
XX PR 23-MAY-1997; 97US-0047581P.  
XX PR 23-MAY-1997; 97US-0047582P.  
XX PR 23-MAY-1997; 97US-0047583P.  
XX PR 23-MAY-1997; 97US-0047584P.  
XX PR 23-MAY-1997; 97US-0047585P.  
XX PR 23-MAY-1997; 97US-0047593P.  
XX PR 23-MAY-1997; 97US-0047594P.  
XX PR 23-MAY-1997; 97US-0047595P.  
XX PR 23-MAY-1997; 97US-0047596P.  
XX PR 23-MAY-1997; 97US-0047597P.  
XX PR 23-MAY-1997; 97US-0047598P.  
XX PR 23-MAY-1997; 97US-0047599P.  
XX PR 23-MAY-1997; 97US-0047600P.  
XX PR 23-MAY-1997; 97US-0047601P.  
XX PR 23-MAY-1997; 97US-0047612P.  
XX PR 23-MAY-1997; 97US-0047613P.  
XX PR 23-MAY-1997; 97US-0047614P.  
XX PR 23-MAY-1997; 97US-0047615P.  
XX PR 23-MAY-1997; 97US-0047617P.  
XX PR 23-MAY-1997; 97US-0047618P.  
XX PR 23-MAY-1997; 97US-0047632P.  
XX PR 23-MAY-1997; 97US-0047633P.  
XX PR 06-JUN-1997; 97US-0048964P.  
XX PR 06-JUN-1997; 97US-0048974P.  
XX PR 13-JUN-1997; 97US-0049610P.  
XX PR 08-JUL-1997; 97US-0051926P.  
XX PR 16-JUL-1997; 97US-0052874P.  
XX PR 18-AUG-1997; 97US-0055724P.  
XX PR 22-AUG-1997; 97US-0056630P.  
XX PR 22-AUG-1997; 97US-0056631P.  
XX PR 22-AUG-1997; 97US-0056632P.  
XX PR 22-AUG-1997; 97US-0056636P.  
XX PR 22-AUG-1997; 97US-0056637P.  
XX PR 22-AUG-1997; 97US-0056642P.  
XX PR 22-AUG-1997; 97US-0056644P.  
XX PR 22-AUG-1997; 97US-0056845P.  
XX PR 22-AUG-1997; 97US-0056862P.  
XX PR 22-AUG-1997; 97US-0056864P.  
XX PR 22-AUG-1997; 97US-0056872P.  
XX PR 22-AUG-1997; 97US-0056874P.  
XX PR 22-AUG-1997; 97US-0056875P.  
XX PR 22-AUG-1997; 97US-0056876P.  
XX PR 22-AUG-1997; 97US-0056877P.  
XX PR 22-AUG-1997; 97US-0056878P.  
XX PR 22-AUG-1997; 97US-0056879P.  
XX PR 22-AUG-1997; 97US-0056880P.  
XX PR 22-AUG-1997; 97US-0056881P.  
XX PR 22-AUG-1997; 97US-0056882P.  
XX PR 22-AUG-1997; 97US-0056884P.  
XX PR 22-AUG-1997; 97US-0056886P.  
XX PR 22-AUG-1997; 97US-0056887P.  
XX PR 22-AUG-1997; 97US-0056888P.  
XX PR 22-AUG-1997; 97US-0056889P.  
XX PR 22-AUG-1997; 97US-0056892P.  
XX PR 22-AUG-1997; 97US-0056893P.  
XX PR 22-AUG-1997; 97US-0056894P.  
XX PR 22-AUG-1997; 97US-0056903P.  
XX PR 22-AUG-1997; 97US-0056908P.  
XX PR 22-AUG-1997; 97US-0056909P.  
XX PR 22-AUG-1997; 97US-0056910P.  
XX PR 05-SEP-1997; 97US-0056911P.  
XX PR 05-SEP-1997; 97US-0057650P.  
XX PR 05-SEP-1997; 97US-0057669P.  
XX PR 12-SEP-1997; 97US-0057761P.  
XX PR 12-SEP-1997; 97US-0058785P.  
XX PR 02-OCT-1997; 97US-0061060P.  
XX PR 06-MAR-1998; 98WO-US004493.  
XX PR 08-SEP-1998; 98US-00149476.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;  
PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;  
PI Duan R, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;  
PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;  
XX WPI; 2004-131264/13.  
XX P-PSDB; ADH74281.  
XX Isolated nucleic acid molecules encoding human secreted proteins, useful  
PT for preventing, diagnosing and treating disorders associated with  
PT aberrant expression and activity.  
XX Claim 3; SEQ ID NO 255; 142pp; English.  
XX The invention relates to isolated nucleic acid molecules and the human  
CC secreted proteins (SPs) they encode. The proteins and nucleic acids may  
CC be used in the prevention, diagnosis and treatment of diseases associated  
CC with inappropriate SP expression e.g. cancer, haematopoietic disorders,  
CC endocrine disorders, diseases of the immune system, inflammatory  
CC disorders and many others. Full details of disorders that may be  
CC prevented, diagnosed and/or treated by the above methods are given in the  
CC specification. The nucleic acid molecules may be used to produce their  
CC proteins. The nucleic acid and it's complementary sequences may also be  
CC used as DNA probes in diagnostic assays to detect and quantitate the  
CC presence of similar nucleic acids in samples, and therefore which  
CC patients may be in need of restorative therapy. The SPs may also be used  
CC as antigens in the production of antibodies against the proteins and in  
CC assays to identify modulators of SP expression and activity. The anti-SP  
CC antibodies and antagonists may also be used to down regulate expression  
CC and activity. The anti-SP antibodies may also be used as diagnostic  
CC agents for detecting the presence of the proteins in samples (e.g. by  
CC enzyme linked immunosorbant assay (ELISA)). The present sequence

CC represents a human secreted protein cDNA.

Sequence 2664 BP: 707 A; 605 C; 566 G; 779 T; 0 U; 7 Other; XX

Alignment Scores:	1.66e-65	Length:	2664
Pred. No.:	624.50	Matches:	115
Score:	81.0%	Conservative:	39
Percent Similarity:	60.53%	Mismatches:	35
Best Local Similarity:	67.08%	Indels:	1
Query Match:	12	Gaps:	1
DB:			

US-09-830-972-29 COPY 990 1178 (1-189) X ADH73972 (1-2664)

Qy	1	SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla	20
Db	262	CGCGTGCCAGATCTGATTTCCTGGAGAGATGTGAAGAAGACCTGGGTTCCTTTGGCACC	321
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThraLaTyrlle	40
Db	322	ACGCTGATCATGCTGCTTCCTCGCAGCTTTCAGTGTGCATCAGTGTGGTTTCCTTACCTTC	381
Qy	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyTLysGlyValIleGlnAla	60
Db	392	ATCTGGGCTCTTCCTCTGTCACCATCAGCTTCAGAGTCTACAAGTCCGTCATCCAAGCT	441
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyLeuGluSerGluValaLarIe	80
Db	442	GTCAGAAAGTCAGAAAGGCCATCCATTCAAGAGCTACTCGAGCTAGACATTACTCTG	501
Qy	81	SerGluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValasnCystrIle	100
Db	502	TCCTCAGAAGCTTTCATAATTACATGAATGTCGCATGTCACATCAACAGGGCCCTG	561
Qy	101	LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal	120
Db	562	AAACTCATTATTCGTCTCTCTCTGTAGAAGATCTGGTTGACTCTCTTGAAGCTGGCTGTC	621
Qy	121	LeuMetTrpValPheThrTyrrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuleLeu	140
Db	622	TTCATGTGGCTGATGACCTATGTTGGTGTGTTTTTAACGGAAATCACCTTCTTAATCTTT	681
Qy	141	AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp	160
Db	692	GCTGAACCTGCTCATTTTCAGTGTCCGATGTCTATGAGAGATACAAAGCCAGATTGAT	741
Qy	161	HisTyrrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlalysileGlnAlaLys	180
Db	742	CACATATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCAACAGCAA	801
Qy	181	IleProGlyLeu---LysArgLysAlaGlu	189
Db	802	CTCCCTCGAATTCGCCAAAAAAGGCAGAA	831

RESULT 89

ADO24047

ID ADO24047 standard: DNA: 2768 BP.

[illegible]

AC ADO24047:

[illegible]

DT 26-AUG-2004 (first entry)

Human soft tissue sarcoma-upregulated DNA - SEQ ID 6867.  
Human soft tissue sarcoma; cytotstatic; gene therapy; vaccine; screening; human; ds.

26-NOV-2003; 2003WO-US038193.  
26-NOV-2002; 2002US-0429739P.  
(PROT-) PROTEIN DESIGN LABS INC.  
Aziz N, Ginsburg WM, Zlotnik A;  
WPI; 2004-441208/41.  
Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue sarcoma.

Example 2: S

XX CC The invention relates to a novel method for detecting  
CC CC which comprises obtaining a first soft tissue sample  
CC CC and a normal soft tissue sample from the same or different  
CC CC determining the expression of a gene in both samples  
CC CC expression of the gene in both soft tissue samples, with

CC presence of soft tissue sarcoma. The method of the in

CC	cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications.
CC	The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
XX	
SQ	Sequence 2768 BP; 748 A; 635 C; 586 G; 794 T; 0 U; 5 Other;
 Alignment Scores:	
Pred. No.:	1.76e-65 Length: 2768
Score:	624.50 Matches: 115
Percent Similarity:	81.05% Conservative: 39
Best Local Similarity:	60.53% Mismatches: 35
Query Match:	67.08% Indels: 1
DB:	12 Gaps: 1
 US-09-830-972-29_COPY_990_1178 (1-189) x ADQ24047 (1-2768)	
Qy	1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20 ::    ::    ::    ::    ::    ::    ::    ::    ::    ::
Db	320 GCGGTGCAGCATCTGATTTCTGGAGACATGTGAAGAAGACTGGTGTTGCTTTTGGCACC 379 ::    ::    ::    ::    ::    ::    ::    ::    ::    ::
Qy	21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40 ::    ::    ::    ::    ::    ::    ::    ::    ::    ::
Db	380 ACGCTGATCATGTCGTCTTCCTGGCACGTTTCAGTGCATCATCAGTGTGTTTCTTACCTC 439 ::    ::    ::    ::    ::    ::    ::    ::    ::    ::
Qy	41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60 ::    ::    ::    ::    ::    ::    ::    ::    ::    ::
Db	440 ATCTGTGCTCTCTCTGTGTCAACCATCAGCTTCAGAGCTACAAGTCGTCATCCAAGCT 499 ::    ::    ::    ::    ::    ::    ::    ::    ::    ::
Qy	61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80 ::    ::    ::    ::    ::    ::    ::    ::    ::    ::
Db	500 GTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCCTACCTGGACGTACACATTACTCTG 559 ::    ::    ::    ::    ::    ::    ::    ::    ::    ::
Qy	81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100 ::    ::    ::    ::    ::    ::    ::    ::    ::    ::
Db	560 TCCTCAGAAGCTTTCACATAAATCATGTAATGCTGCCATGCTGCATCAACAGGGCCCTG 619 ::    ::    ::    ::    ::    ::    ::    ::    ::    ::
Qy	101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120 ::    ::    ::    ::    ::    ::    ::    ::    ::    ::
Db	620 AAACCTCATATTGCTCTCTTCTGGTAGAAGATCTGGTTGACTCTCTTGAAGCTGGCTGTC 679 ::    ::    ::    ::    ::    ::    ::    ::    ::    ::
Qy	121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140 ::    ::    ::    ::    ::    ::    ::    ::    ::    ::
Db	680 TTCATGTGGCTGTATGACCTATGTGGTGCTGTGTTTTAACGGAATCACCTTCTTAATCTT 739 ::    ::    ::    ::    ::    ::    ::    ::    ::    ::
Qy	141 AlaLeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160 ::    ::    ::    ::    ::    ::    ::    ::    ::    ::

Db 740 GCTGAACGCTCTCATTTTCAGTGTCCCGATGTCTATGAGAGTACAGACCCAGATTGAT 799  
Qy 161 HistTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysTleGlnAlaLys 180  
Db 800 CACTATGTGGATCGCCGAGATCAGACCAAGTCAATTGTGTGAAGAGATCAAGCAAAA 859  
Qy 181 lleProGlyLeu---LysArgLysAlaGlu 189  
Db 860 CTCCTCGAATCGCCCAAAAAAAGGCAGAA 889

## RESULT 90

ID ADM36171 standard; DNA; 1968 BP.

AC ADM36171;

DT 03-JUN-2004 (first entry)

DE Human RTN3 isoform III coding sequence, SEQ ID 54.

DE Neuroprotective; Myotrophic; neuromuscular disease; RTN3; reticulon 3;

KW amyotrophic lateral sclerosis; ALS; myopathy; human; gene; ds.

XX Homo sapiens.

FH Key Location/Qualifiers

FT CDS 124..891

FT /\*tag= a

FT /product= "RTN3 isoform III"

XX WO2004001069-A2.

XX 31-DEC-2003.

XX 20-JUN-2003; 2003WO-FR001910.

XX 25-JUN-2002; 2002FR-00007846.

XX (UYPA-) UNIV PASTEUR LOUIS.

PI Dupuis L, Di Scala F, De Tapia M, Larmet Y, Loeffler J;

PI Gonzales De Aguilar J, Boutillier AL, Gaidon C, Rene F;

XX WPI; 2004-071743/07.

DR P-PSDB; ADM36172.

XX Diagnosing, prognosing and monitoring neuromuscular disease, particularly  
PT amyotrophic lateral sclerosis, comprises detecting modulation of the  
PT reticulon 3 gene.

XX Claim 35; SEQ ID NO 54; 116pp; French.

XX The present invention relates to a method for diagnosing, or evaluating  
CC progression of, a neuromuscular disease. The method comprises detecting  
CC modulation of the expression of a product (I) of the RTN (reticulon)3  
CC gene. Differential expression of RTN3 is a specific marker of  
CC neuromuscular disease, allowing early diagnosis from readily available  
CC muscle biopsies. The method is also useful for determining the efficacy  
CC of treatment. The method is used to diagnose (also to evaluate  
CC progression or therapy of) neuromuscular disorders, specifically  
CC amyotrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies  
CC specific for isoforms of RTN3 or oligonucleotides (antisense sequences or  
CC small interfering RNA) that can block/reduce expression of these isoforms  
CC are useful for treating neuromuscular diseases and (ii) cells that  
CC express RTN3 are useful in screening for therapeutic agents. The present  
CC sequence is a RTN3 DNA sequence used to illustrate the invention.

XX Sequence 1968 BP; 496 A; 482 C; 411 G; 579 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.44e-65 Length: 1968  
Score: 623.50 Matches: 115  
Percent Similarity: 80.95% Conservative: 38

Best Local Similarity: 60.85% Mismatches: 35  
Query Match: 66.97% Indels: 1  
DB: 12 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADM36171 (1-1968)

Qy 2 ValValAspLeuLeuTyrTrrArgAspIleLysLysThrGlyValValPheGlyAlaSer 21

Db 322 GTGCACGATCTGATTTCTCGAGAGAGTGTGAAGAACTGGGTTTGTCTTTGGCACCCAGC 381

Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

Db 382 CTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTTCATCAGTGTGGTTTCTTACCTCATC 441

Qy 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

Db 442 CTGGCTCTTCTCTGTGCACCATCAGCTTACAGGATCTACAAGTCGTCATCAAGCTGTA 501

Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81

Db 502 CAGAAGTCAGAGAAGGCCATCCATTCAAGGCCTACCTGGACGTAGACATTACTCTGTCC 561

Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101

Db 562 TCAGAAGCTTTCCATAAATTACATGATGCTGCCATGGTGCCACATCAACAGGGCCCTGAAA 621

Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121

Db 622 CTCATTATTCTGCTCTTCTGTGTAGAAGATCTGGTTGACTCTCTTGAAGCTGGCTGCTTC 681

Qy 122 MetTrrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeuAla 141

Db 682 ATGTGGCTGATGACCTATGTTGGTGTCTGTTTAAACGGAATCACCTTCTTAATCTTGT 741

Qy 142 LeuLysSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161

Db 742 GAACCTGCTCATTTTTCAGTGTCCCGATTGCTATGAGAAGTACAAGACCCAGATTGATCAC 801

Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

Db 802 TATGTTGGCATFCGCCCGAGATCAGACCAAGTCAATTGTTGAAGAAGATCCAAGCAAACTC 861

Qy 182 ProGlyLeu---LysArgLysAlaGlu 189

Db 862 CCTGGAATCGCCAAAAAAGGCAGAA 888

## RESULT 91

ID ADM36171

XX ADQ84465 standard; cDNA; 2250 BP.

XX AC ADQ84465;

XX DT 07-OCT-2004 (first entry)

XX Human tumour-associated antigenic target (TAT) cDNA sequence #1279.

XX human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;  
XX cancer; cell proliferative disorder; gene; ss.

XX Homo sapiens.

XX WO2004060270-A2.

XX PD 22-JUL-2004.

XX 15-OCT-2003; 2003WO-US029126.

XX 18-OCT-2002; 2002US-0418988P.

XX (GETH ) GENENTECH INC.

XX PA (WUTD/) WU T D.

XX PA (ZHOU/) ZHOU Y.

XX XX

PI Wu TD, Zhou Y;  
 XX WPI; 2004-534300/51.  
 XX New nucleic acid molecule and encoded polypeptide, for diagnosing,  
 PT preventing or treating cell proliferative disorders such as cancer.  
 XX  
 XX Claim 1; SEQ ID NO 1279; 5504pp; English.  
 XX  
 CC The present invention describes an isolated tumour-associated antigenic  
 CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide  
 CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of  
 CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%  
 CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-  
 CC (c). Also described: (1) an expression vector comprising the above  
 CC nucleic acid; (2) a host cell comprising the above expression vector; (3)  
 CC a process for producing a polypeptide; (4) an isolated polypeptide  
 CC comprising: (a) an amino acid sequence encoded by any of the above  
 CC nucleotide sequences; (b) an amino acid sequence encoded by the full-  
 CC length coding region of the above nucleotide sequences; or (c) a sequence  
 CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide  
 CC comprising the above polypeptide fused to a heterologous polypeptide; (6)  
 CC an isolated antibody that binds to the above polypeptide; (7) a process  
 CC for producing the antibody; (8) an isolated oligopeptide that binds to  
 CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)  
 CC binding organic molecule that binds to the above polypeptide; (10) a  
 CC composition of matter comprising the above (chimeric) polypeptide,  
 CC antibody, oligopeptide or TAT binding organic molecule, in combination  
 CC with a carrier; (11) an article of manufacture comprising a container and  
 CC the composition of matter contained within the container; (12) methods of  
 CC inhibiting the growth of a cell that expresses the above protein, where  
 CC the growth of the cell is at least in part dependent upon a growth  
 CC potentiating effect of the above protein; (13) a method of  
 CC therapeutically treating a mammal having a cancerous tumour comprising  
 CC cells that express the above protein; (14) a method of determining the  
 CC presence of a protein in a sample suspected of containing the protein  
 CC described above; (15) methods of diagnosing the presence of a tumour in a  
 CC mammal; (16) a method for treating or preventing a cell proliferative  
 CC disorder associated with increased expression or activity of the above  
 CC protein; and (17) a method of binding an antibody, oligopeptide or  
 CC organic molecule to a cell that expresses the protein described above.  
 CC The TAT sequences have cytostatic activities, and can be used in gene  
 CC therapy. The composition and methods are useful for diagnosing,  
 CC preventing or treating cancer. The composition is also used for preparing  
 CC a medicament for the therapeutic treatment or diagnostic detection of a  
 CC cell proliferative disorder or cancer. The present sequence represents a  
 CC human TAT cDNA sequence from the present invention.  
 XX  
 SQ Sequence 2250 BP; 629 A; 469 C; 456 G; 696 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.74e-65 Length: 2250  
 Score: 623.50 Matches: 115  
 Percent Similarity: 80.95% Conservative: 38  
 Best Local Similarity: 60.85% Mismatches: 35  
 Query Match: 66.97% Indels: 1  
 DB: 12 Gaps: 1  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADQ84465 (1-2250)  
 QY 2 ValValAspLeuLeuTyrrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 DB 1 GTGCACGATCTGATTTCTGGAGAGATGTGAAGACATCGGTTGCTTGGCACCAGC 60  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 DB 61 CTGATCATGCTGCTTCTCCCTGGCAGCTTTTCAGTGTCTATCAGTGTGTTCTTACTCTATC 120  
 QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 DB 121 CTGGCTTCTCTCTCTACCATCATCAGTCTCAGATCTACAGTCCGTCCTCAAGCTGTA 180  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 181 CAGAACTCAGAGAGAGCCCATCCATTCAAGCTACCTGGAGCTAGACATTAATCTGTCTC 240  
 QY 82 GluGluLeuValGlnLysTyrrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 241 TCAGAAAGCTTTCATTAATTAATGATGATGCTGCGTGTGCATCAACAGGCGCCCTGAAA 300  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 301 CTCATTATTCGCTCTCTTTCTGGTAGAAGATCTGGTTGACTCTTGAAGCTGGCTGTCTTC 360  
 QY 122 MetTppValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
 Db 361 AATGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
 QY 142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 421 GAACCTGCTCATTTTCAGTGTCCGATTTCTATGAGAAGTACAGACCCAGATTGATCAC 480  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 481 TATGTTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 Db 541 CCTGGAATGCCCAAAAAGGCGAGAA 567  
 RESULT 92  
 ADQ86409  
 ID ADQ86409 standard; cDNA; 2250 BP.  
 XX  
 AC ADQ86409;  
 XX  
 DT 07-OCT-2004 (first entry)  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #3281.  
 XX  
 KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;  
 KW cancer; cell proliferative disorder; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004060270-A2.  
 XX  
 PD 22-JUL-2004.  
 XX  
 PF 15-OCT-2003; 2003WO-US029126.  
 XX  
 PR 18-OCT-2002; 2002US-0418989P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 PI Wu TD, Zhou Y;  
 XX  
 DR WPI; 2004-534300/51.  
 XX  
 PT New nucleic acid molecule and encoded polypeptide, for diagnosing,  
 PT preventing or treating cell proliferative disorders such as cancer.  
 XX  
 PS Claim 1; SEQ ID NO 3281; 5504pp; English.  
 XX  
 CC The present invention describes an isolated tumour-associated antigenic  
 CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide  
 CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of  
 CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%  
 CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-  
 CC (c). Also described: (1) an expression vector comprising the above  
 CC nucleic acid; (2) a host cell comprising the above expression vector; (3)  
 CC a process for producing a polypeptide; (4) an isolated polypeptide  
 CC comprising: (a) an amino acid sequence encoded by any of the above  
 CC nucleotide sequences; (b) an amino acid sequence encoded by the full-  
 CC length coding region of the above nucleotide sequences; or (c) a sequence  
 CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide  
 CC comprising the above polypeptide fused to a heterologous polypeptide; (6)  
 CC an isolated antibody that binds to the above polypeptide; (7) a process  
 CC for producing the antibody; (8) an isolated oligopeptide that binds to  
 CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)  
 CC binding organic molecule that binds to the above polypeptide; (10) a  
 CC composition of matter comprising the above (chimeric) polypeptide,  
 CC antibody, oligopeptide or TAT binding organic molecule, in combination  
 CC with a carrier; (11) an article of manufacture comprising a container and  
 CC the composition of matter contained within the container; (12) methods of  
 CC inhibiting the growth of a cell that expresses the above protein, where  
 CC the growth of the cell is at least in part dependent upon a growth  
 CC potentiating effect of the above protein; (13) a method of  
 CC therapeutically treating a mammal having a cancerous tumour comprising  
 CC cells that express the above protein; (14) a method of determining the  
 CC presence of a protein in a sample suspected of containing the protein  
 CC described above; (15) methods of diagnosing the presence of a tumour in a  
 CC mammal; (16) a method for treating or preventing a cell proliferative  
 CC disorder associated with increased expression or activity of the above  
 CC protein; and (17) a method of binding an antibody, oligopeptide or  
 CC organic molecule to a cell that expresses the protein described above.  
 CC The TAT sequences have cytostatic activities, and can be used in gene  
 CC therapy. The composition and methods are useful for diagnosing,  
 CC preventing or treating cancer. The composition is also used for preparing  
 CC a medicament for the therapeutic treatment or diagnostic detection of a  
 CC cell proliferative disorder or cancer. The present sequence represents a  
 CC human TAT cDNA sequence from the present invention.  
 XX  
 SQ Sequence 2250 BP; 629 A; 469 C; 456 G; 696 T; 0 U; 0 Other;



length coding region of the above nucleotide sequences; or (c) a sequence having at least 80% identical to (a) or (b); (5) a chimeric polypeptide comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (9) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth potentiating effect of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAT cDNA sequence from the present invention.

XX SQ Sequence 2250 BP; 629 A; 469 G; 456 C; 696 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.:	1,74e-65	Length:	2250
Score:	623.50	Matches:	115
Percent Similarity:	80.95%	Conservative:	38
Best Local Similarity:	60.85%	Mismatches:	35
Query Match:	66.97%	Indels:	1
DB:	12	Gaps:	1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADQ86409 (1-2250)

Qy	2	ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer	21
Db	1	GTGCACGATCTGATTTCTCGAGAGATGTCGAAGAGACTGGGTTGTCTTTGGCCACACG	60
Qy	22	LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla	41
Db	61	CTGATCATGCTGCTTCCCTCGCAGCTTTCAGTGTCTCATGCTGGTTCCTTACTCATC	120
Qy	42	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle	61
Db	121	CTGGCTCTCTCTCTGTCACCATCATGCTTCAGATCTCAAGTCTCATCAAGCTGTA	180
Qy	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer	81
Db	181	CAGAAGTCAGAAGAGGCCATCCATTCAAAGCTACCTGGACGTAGACATTAATCTGTCC	240
Qy	82	GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCyThrIleLys	101
Db	241	TCAGAAGCTTCCATAATTACATGAATGCTGCCATGTCGTCATCAACAGGGCCCTGAAA	300
Qy	102	GluLeuArgAlaLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu	121
Db	301	CTCATTTATTCGTCTCTTTCTGTGATGAAGATCTGGTTGACTCTCTTGAAGCTGGCTGTC	360
Qy	122	MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla	141
Db	361	ATGTGGCTGATCACCATTATGTTGGTCTGCTTTTAAAGGAATCACCCTCTTAATCTTGT	420
Qy	142	LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis	161
Db	421	GAATGCTCATTTTTCAGTGTCCGATTTCTATGATGAGAGTCAACAGCCAGATGATCAC	480

Qy	162	TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetalAlaLysIleGlnAlaLysIle	181
Db	481	TATGTTGGCATCGCCGAGATCAGACACCAAGTCATTGTTGAAGATCCAGCAAACTC	540
Qy	182	ProGlyLeu---LysArgLysAlaGlu	189
Db	541	CCTGGAATCGCCAAAAAAGGCAGAA	567

#### RESULT 93

ADQ85262

ID ADQ85262 standard; cDNA; 2250 BP.

XX AC ADQ85262;

DT 07-OCT-2004 (first entry)

XX Human tumour-associated antigenic target (TAT) cDNA sequence #2076.

DE human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;

KW cancer; cell proliferative disorder; gene; ss.

XX Homo sapiens.

XX WO2004060270-A2.

XX 22-JUL-2004.

XX 15-OCT-2003; 2003WO-US029126.

XX 18-OCT-2002; 2002US-0418988P.

PA (GETH ) GENENTECH INC.

PA (WUTD/) WU T D.

XX (ZHOU/) ZHOU Y.

XX Wu TD, Zhou Y;

XX WPI; 2004-534300/51.

PT New nucleic acid molecule and encoded polypeptide, for diagnosing,

PT preventing or treating cell proliferative disorders such as cancer.

XX Claim 1; SEQ ID NO 2076; 5504pp; English.

XX The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; or (c) a sequence having at least 80% identical to (a) or (b); (5) a chimeric polypeptide comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (9) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth potentiating effect of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative

CC disorder associated with increased expression or activity of the above  
CC protein; and (17) a method of binding an antibody, oligopeptide or  
CC organic molecule to a cell that expresses the protein described above.  
CC The TAT sequences have cytostatic activities, and can be used in gene  
CC therapy. The composition and methods are useful for diagnosing,  
CC preventing or treating cancer. The composition is also used for preparing  
CC a medicament for the therapeutic treatment or diagnostic detection of a  
CC cell proliferative disorder or cancer. The present sequence represents a  
CC human TAT cDNA sequence from the present invention.

XX  
SQ Sequence 2250 BP; 629 A; 469 C; 456 G; 696 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.74e-65 Length: 2250  
Score: 623.50 Matches: 115  
Percent Similarity: 80.95% Conservatives: 38  
Best Local Similarity: 60.85% Mismatches: 35  
Query Match: 66.97% Indels: 1  
DB: 13 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADQ85262 (1-2250)

QY 2 ValValAspLeuLeuThrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 1 GTGCAGATCTGATTTCTGGAGAGATGTGAAGACACTGGTGTCTTTGGCACCAG 60  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 61 CTGATCATGCTGTTTCCCTGGCAGCTTTTCAGTGTCTCATGCTGGTTCCTTACCTCATC 120  
QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 121 CTGGCTCTTCTCTCTGTCACCATCATGCTTCAGATCTACAGTTCAGCTCAAGCTGA 180  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 181 CAGAGTCAAGAGAGGCCATCATTTCAAGGCTTACTGGACGTAGACATTAATCTGTCC 240  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 241 TCAGAGAGCTTCCATTAATACATGAATGCTGCATGTCACATCAACAGGCGCTGAA 300  
QY 102 GluLeuArgLeuPheLeuValAspLeuValAspLeuValAspLeuLysPheAlaValLeu 121  
Db 301 CTCATTATTCGTCCTCTTCTGGTAGAAGATCTGGTTCCTTGAAGCTGCTGCTTC 360  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuAla 141  
Db 361 ATGTGCTCATGACCTATGTTGGTGTGTTTAAAGGAATCACCTTCTTAATCTTGT 420  
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 421 GAAGTCTCATTTTCAGTGTCCGATGTCTATGAGAGTACAGACCCAGATTCATCAC 480  
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 481 TATGTTGGCATGCCCGCAGATCAGACCAAGTCAATTTGTTGAAAGATCAAGCAAACTC 540  
QY 182 ProGlyLeu---LysArgLysAlaGlu 189  
Db 541 CCTGGAATGCCAAAAGAGGAGAA 567

RESULT 94

ID ADQ83313 standard; cDNA; 2250 BP.

XX AC ADQ83313;

XX DT 07-OCT-2004 (first entry)

XX DE Human tumour-associated antigenic target (TAT) cDNA sequence #127.

XX KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;

KW cancer; cell proliferative disorder; gene; ss.

XX Homo sapiens.

XX WO2004060270-A2.

XX 22-JUL-2004.

XX 15-OCT-2003; 2003WO-US029126.

XX 18-OCT-2002; 2002US-0418988P.

XX (GETH) GENENTECH INC.

XX (WUTD/) WU T D.

XX (ZHOU/) ZHOU Y.

XX Wu TD, Zhou Y;

XX WPI; 2004-534300/51.

PT New nucleic acid molecule and encoded polypeptide, for diagnosing,  
PT preventing or treating cell proliferative disorders such as cancer.

XX Claim 1; SEQ ID NO 127; 5504pp; English.

CC The present invention describes an isolated tumour-associated antigenic  
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide  
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of  
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%  
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-  
CC (c). Also described: (1) an expression vector comprising the above  
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)  
CC a process for producing a polypeptide; (4) an isolated polypeptide  
CC comprising: (a) an amino acid sequence encoded by any of the above  
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-  
CC length coding region of the above nucleotide sequences; or (c) a sequence  
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide  
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)  
CC an isolated antibody that binds to the above polypeptide; (7) a process  
CC for producing the antibody; (8) an isolated oligopeptide that binds to  
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)  
CC binding organic molecule that binds to the above polypeptide; (10) a  
CC composition of matter comprising the above (chimeric) polypeptide,  
CC antibody, oligopeptide or TAT binding organic molecule, in combination  
CC with a carrier; (11) an article of manufacture comprising a container and  
CC inhibiting the growth of a cell that expresses the above protein, where  
CC the growth of the cell is at least in part dependent upon a growth  
CC potentiating effect of the above protein; (13) a method of  
CC therapeutically treating a mammal having a cancerous tumour comprising  
CC cells that express the above protein; (14) a method of determining the  
CC presence of a protein in a sample suspected of containing the protein  
CC described above; (15) methods of diagnosing the presence of a tumour in a  
CC mammal; (16) a method for treating or preventing a cell proliferative  
CC disorder associated with increased expression or activity of the above  
CC protein; and (17) a method of binding an antibody, oligopeptide or  
CC organic molecule to a cell that expresses the protein described above.  
CC The TAT sequences have cytostatic activities, and can be used in gene  
CC therapy. The composition and methods are useful for diagnosing,  
CC preventing or treating cancer. The composition is also used for preparing  
CC a medicament for the therapeutic treatment or diagnostic detection of a  
CC cell proliferative disorder or cancer. The present sequence represents a  
CC human TAT cDNA sequence from the present invention.

XX SQ Sequence 2250 BP; 629 A; 469 C; 456 G; 696 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.74e-65 Length: 2250  
Score: 623.50 Matches: 115  
Percent Similarity: 80.95% Conservatives: 38  
Best Local Similarity: 60.85% Mismatches: 35  
Query Match: 66.97% Indels: 1  
DB: 13 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADQ83313 (1-2250)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 1 GTGCAGCATCTGATTTCTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCACCACG 60

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 61 CTGATCATGCTGCTTCTCCCTGGCAGCTTTCAGTGTCACTAGTGGTTCTTACTCATC 120

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 121 CTGGCTCTCTCTCTGTCACCATCAGCTTCCAGATCTCAAGTCGTCATCAAGCTGTA 180

QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 181 CAGAAAGTCAGAAAGAGCCCATCCATTCAAGCCTACCTGGAGCTAGACATTACTCTGTCC 240

QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 241 TCAGAGCTTCCATAATATCATGATGCTGCGCATGTCACATCAAGCGCCCTGAAA 300

QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 301 CTCATTATTCGTCTCTCTGTCAGAGATCTGTTGACTCTCTTGAAGCTGGCTGTCTTC 360

QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAlaSerGlyLeuThrLeuLeuAla 141  
Db 361 ATGTGGCTGATGACCATATGTTGGTCTCTTTTAAACGGAATCACCCCTTCTAATTTGCT 420

QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 421 GAATGCTCATTTTCAGTGTCCGATGCTATGAGAAGTACAGACCCAGATGATCAC 480

QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 481 TATGTTGGCATCGCCGAGATCAGACCAAGTCAATGTTGAAAGATCAAGCAAAATC 540

QY 182 ProGlyLeu---LysArgLysAlaGlu 189  
Db 541 CCTGGAATCGCCAAAAGGAGCAGAA 567

RESULT 95  
ADB5889  
ID ADB5889 standard; DNA; 2773 BP.

XX  
AC ADB5889;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Toxicity-related gene, SEQ ID 3915.  
XX  
KW Toxic; toxin; gene expression profile; hepatotoxicity; liver;  
XX  
KW drug screening; toxicity assay; db.  
XX  
OS Unidentified.  
XX  
FN WO2003064624-A2.  
XX  
PD 07-AUG-2003.  
XX  
PF 31-JAN-2003; 2003WO-US0003194.  
XX  
PR 31-JAN-2002; 2002US-00060087.  
XX  
PR 15-MAR-2002; 2002US-0364045P.  
XX  
PR 15-MAR-2002; 2002US-0364055P.  
XX  
PR 30-DEC-2002; 2002US-0436643P.  
XX  
PA (GENE-) GENE LOGIC INC.  
XX  
PI Mendrick D, Porter M, Johnson K, Higgins B, Castle A, Elashoff M;  
XX

DR WPI; 2003-689530/65.  
XX  
PT Predicting a toxic effect of a compound, useful in identifying toxicity  
PT markers in liver tissues or cells for drug screening and toxicity assays,  
PT comprises preparing gene expression profile of tissue or cells exposed to  
PT the compound.  
XX  
PS Claim 1; SEQ ID NO 3915; 1156pp; English.  
XX  
CC The present invention relates to a method for predicting a toxic effect  
CC of a compound. The method comprises preparing a gene expression profile  
CC of a tissue or cell sample exposed to the compound, and comparing the  
CC gene expression profile to a database comprising SEQ ID 1-4925, where  
CC differential expression of the gene indicates at least one toxic effect.  
CC The method is useful for predicting at least one toxic effect of a  
CC compound, predicting hepatotoxicity or the progression of a toxic effect  
CC of a compound, identifying an agent that modulates the onset or  
CC progression of a toxic response, predicting the cellular pathways that a  
CC compound modulates in a cell, and identifying an agent that modulates at  
CC least one activity of a protein. The method and compositions of the  
CC present invention using a database of genes having liver toxin-induced  
CC differential expression, are useful in identifying toxicity markers in  
CC liver tissues or cells for drug screening and toxicity assays. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 2773 BP; 699 A; 653 C; 632 G; 789 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 2,33e-65 Length: 2773  
Score: 623.50 Matches: 115  
Percent Similarity: 81.05% Conservative: 39  
Best Local Similarity: 60.53% Mismatches: 35  
Query Match: 66.97% Indels: 1  
DB: 10 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADB5889 (1-2773)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
Db 267 GCGGTGCATGATCTGATTTCTGGCGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCACC 326

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 327 ACGTGATCATGCTGCTCTCTCTGGCAGCTTTCAGTGTATCAGTGGTCTCTTACTCTC 386

QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 387 ATCTGGCTCTACTCTCTGTCCACCATCAGCTTCAGAGTCTACAAGTCTGTCTATCCAAGCT 446

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 447 GTGCAGAAGTCAGAAGAAGGACATCCATTCAAGCCTACCTGGATGTGGACATTACACTG 506

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 507 TCCTCAGAAGCTTCCACAGCTACATGAATGCTCAATGGTGCATGTCAACAGGCCCTC 566

QY 101 LysGluLeuLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
Db 567 AAACCTATTATTCGTCTCTCTCTGTAGAGACATTTGGTTGACTCCTTGAAGCTGCTGTC 626

QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAlaGlnIleLeuLeu 140  
Db 627 TTCAATGTGGCTGATGACCTACGTCGTCTCTTTTAAACGGAATTACCTTCTGATTTCTC 686

QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db 687 GCCAGCTGTGGTTTTCAGCGTCCCAATGCTATGAGAAGTATAGACACATTTGAC 746

QY 161 HistTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180

Db 747 CACTATGTTGGATTCCCGGATCAGACCAAGTCAATTGTTCAAAAGATCCAGCAAG 806

Qy 181 IleProGlyLeu---LysArgLysAlaGlu 189

Db 807 CTTCTGGAATCCCAAAAGGCGAGAA 836

# RESULT 96

ADM36175  
ID ADM36175 standard; DNA; 3231 BP.

XX AC ADM36175;

XX DT 03-JUN-2004 (first entry)

XX Human RTN3 isoform V coding sequence, SEQ ID 58.

XX Neuroprotective; Myotrophic; neuromuscular disease; RTN3; reticulon 3;

XX amytrophic lateral sclerosis; ALS; myopathy; human; gene; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 124..2154

XX FT /\*tag= a

XX FT /product= "RTN3 isoform V"

XX WO2004001069-A2.

XX PD 31-DEC-2003.

XX PF 20-JUN-2003; 2003WO-FR001910.

XX PR 25-JUN-2002; 2002FR-00007846.

XX XX (UYPA-) UNIV PASTEUR LOUIS.

XX PI Dupuis L, Di Scala F, De Tapia M, Larmet Y, Loeffler J;

XX PI Gonzales De Aguilar J, Boutillier AL, Gaiddon C, Rene F;

XX DR WPI; 2004-071743/07.

XX DR P-PSDB; ADM36176.

XX PT Diagnosing, prognosing and monitoring neuromuscular disease, particularly  
PT amytrophic lateral sclerosis, comprises detecting modulation of the  
PT reticulon 3 gene.

XX PS Claim 35; SEQ ID NO 58; 116pp; French.

XX CC The present invention relates to a method for diagnosing, or evaluating  
CC progression of, a neuromuscular disease. The method comprises detecting  
CC modulation of the expression of a product (I) of the RTN (reticulon)3  
CC gene. Differential expression of RTN3 is a specific marker of  
CC neuromuscular disease, allowing early diagnosis from readily available  
CC muscle biopsies. The method is also useful for determining the efficacy  
CC of treatment. The method is used to diagnose (also to evaluate  
CC progression or therapy of) neuromuscular disorders, specifically  
CC amytrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies  
CC specific for isoforms of RTN3 or oligonucleotides (antisense sequences or  
CC small interfering RNA) that can block/reduce expression of these isoforms  
CC are useful for treating neuromuscular diseases and (ii) cells that  
CC express RTN3 are useful in screening for therapeutic agents. The present  
CC sequence is a RTN3 DNA sequence used to illustrate the invention.

XX SQ Sequence 3231 BP; 947 A; 717 C; 690 G; 877 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	2.89e-65	Length:	3231
Score:	623.50	Matches:	115
Percent Similarity:	80.95%	Conservative:	38
Best Local Similarity:	60.85%	Mismatches:	35
Query Match:	66.97%	Indels:	1
DB:	12	Gaps:	1

US-09-830-972-29\_copy\_990\_1178 (1-189) x ADM36175 (1-3231)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
1585 GTGCACGATCTGATTTCTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCACCACG 1644

Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaIleAla 41  
1645 CTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTGCATCAGTGGTTCCTTACCTCATC 1704

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
1705 CTGGCTCTTCTCTCTGTCCATCAGCTTCAGATCTACAGTCCGTCATCCAGCTGTA 1764

Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
1765 CAGAAGTCAGAAGAAGGCCATCAATTCAAGGCTTACCTGGAGCTAGACATTACTCTGTCC 1824

Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
1825 TCAGAAGCTTTCCATAATTACATGAATGCTGCATGGTGCAATCAACAGGCGCCCTGAAA 1884

Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
1885 CTCATTATTCGTCCTTCTCTGTGTAGAGATCTGGTTGACTCTTGAAGCTGGCTGCTTC 1944

Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
1945 ATGTGGCTGATGACCTATGTTGGTGTCTGTTTAAACGGAATCACCCCTTCTAATTCTTGT 2004

Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
2005 GAACTGCTCATTTTCAGTGTCCGATGTGTATAGAAGATACAAAGCCAGATTGATCAC 2064

Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
2065 TATGTTGGCATGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAGACCAAACTC 2124

Qy 182 ProGlyLeu---LysArgLysAlaGlu 189

Db 2125 CCTGGAATCGCCAAAAAAGGCGAGAA 2151

## RESULT 97

ADM36169  
ID ADM36169 standard; DNA; 3288 BP.

XX AC ADM36169;

XX DT 03-JUN-2004 (first entry)

XX DE Human RTN3 isoform II coding sequence, SEQ ID 52.

XX KW Neuroprotective; Myotrophic; neuromuscular disease; RTN3; reticulon 3;  
KW amytrophic lateral sclerosis; ALS; myopathy; human; gene; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 124..2211

XX FT /\*tag= a

XX FT /product= "RTN3 isoform II"

XX PN WO2004001069-A2.

XX PD 31-DEC-2003.

XX PF 20-JUN-2003; 2003WO-FR001910.

XX PR 25-JUN-2002; 2002FR-00007846.

XX PA (UYPA-) UNIV PASTEUR LOUIS.

XX PI Dupuis L, Di Scala F, De Tapia M, Larmet Y, Loeffler J;

PI Gonzales De Aguilar J, Boutillier AL, Gaidon C, Rene F;  
XX WPI: 2004-071743/07.  
DR P-PSDB; ADM36170.  
XX  
XX Diagnosing, prognosing and monitoring neuromuscular disease, particularly  
PT amyotrophic lateral sclerosis, comprises detecting modulation of the  
PT reticulon 3 gene.  
XX  
XX Claim 35; SEQ ID NO 52; 116pp; French.  
XX  
XX The present invention relates to a method for diagnosing, or evaluating  
CC progression of, a neuromuscular disease. The method comprises detecting  
CC modulation of the expression of a product (I) of the RTN (reticulon)3  
CC gene. Differential expression of RTN3 is a specific marker of  
CC neuromuscular disease, allowing early diagnosis from readily available  
CC muscle biopsies. The method is also useful for determining the efficacy  
CC of treatment. The method is used to diagnose (also to evaluate  
CC progression or therapy of) neuromuscular disorders, specifically  
CC amyotrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies  
CC specific for isoforms of RTN3 or oligonucleotides (antisense sequences or  
CC small interfering RNA) that can block/reduce expression of these isoforms  
CC are useful for treating neuromuscular diseases and (ii) cells that  
CC express RTN3 are useful in screening for therapeutic agents. The present  
CC sequence is a RTN3 DNA sequence used to illustrate the invention.  
XX  
XX Sequence 3288 BP; 955 A; 736 C; 695 G; 902 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 2,96e-65 Length: 3288  
Score: 623.50 Matches: 115  
Percent Similarity: 80.95% Conservative: 38  
Best Local Similarity: 60.85% Mismatches: 35  
Query Match: 66.97% Indels: 1  
DB: 12 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADM36169 (1-3288)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysValThrGlyValValPheGlyAlaSer 21  
DB 1642 GTGCAGCATCTGATTTCTCGAGAGATGTGAAGAGACTGGTTTGTCTTTGGCCACCAG 1701  
QY 22 LeupheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaIleAla 41  
DB 1702 CTGATCATGCTGCTTTCTCCCTGCAGCTTTCACTGTCATGCTGTTCTTACCTCATC 1761  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 1762 CTGGCTCTTCTCTGTCCACCATCATGCTTCAAGATCTCAAGTCCGTCTCATCAAGCTGA 1821  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 1822 CAGAGTCAGAGAGAGGCCATCCATCAAGGCTTACCTGACGTGACGTAGCATCTCTGTCC 1881  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
DB 1892 TCAGAAGCTTCCATAATTACATGAATGCTGCCATGTCACATCAACAGGCCCTCGAA 1941  
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 1942 CTCATATTATCTGCTCTTTCTGTTAGAGATCTGTTGACTCTCTTGAAGCTGGCTGCTTC 2001  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeuAla 141  
DB 2002 ATGTGGCTGATGACCTATGTGTGCTGTTTAAACGAATCACCTCTTAATCTTCTGCT 2061  
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
DB 2062 GAACGTCTCATTTTTCAGTGTCCGATGCTATGAGAGATGACAGACCCAGATGATCATC 2121  
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 2122 TATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAGATCAAGCAAGCAAACTC 2181

QY 182 ProGlyLeu---LysArgLysAlaGlu 189  
DB 2182 CCTGGATCGCCAAAAAAGGCGAGAA 2208

RESULT 98  
ADM36179  
ID ADM36179 standard; DNA; 4092 BP.

XX AC ADM36179;

XX DT 03-JUN-2004 (first entry)

XX DE Human RTN3 isoform VII coding sequence, SEQ ID 62.

XX KW Neuroprotective; Myotropic; neuromuscular disease; RTN3; reticulon 3;

XX KW amyotrophic lateral sclerosis; ALS; myopathy; human; gene; db.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 163..3015

XX FT /\*tag= a

XX FT /product= "RTN3 isoform VII"

XX PN WO2004001069-A2.

XX PD 31-DEC-2003.

XX PF 20-JUN-2003; 2003WO-FR001910.

XX PR 25-JUN-2002; 2002FR-00007846.

XX PA (UYPA-) UNIV PASTEUR LOUIS.

XX PI Dupuis L, Di Scala F, De Tapia M, Larmet Y, Loeffler J;

XX PI Gonzales De Aguilar J, Boutillier AL, Gaidon C, Rene F;

XX DR WPI: 2004-071743/07.

XX DR P-PSDB; ADM36180.

XX PT Diagnosing, prognosing and monitoring neuromuscular disease, particularly  
PT amyotrophic lateral sclerosis, comprises detecting modulation of the  
PT reticulon 3 gene.

XX PS Claim 35; SEQ ID NO 62; 116pp; French.

XX The present invention relates to a method for diagnosing, or evaluating  
CC progression of, a neuromuscular disease. The method comprises detecting  
CC modulation of the expression of a product (I) of the RTN (reticulon)3  
CC gene. Differential expression of RTN3 is a specific marker of  
CC neuromuscular disease, allowing early diagnosis from readily available  
CC muscle biopsies. The method is also useful for determining the efficacy  
CC of treatment. The method is used to diagnose (also to evaluate  
CC progression or therapy of) neuromuscular disorders, specifically  
CC amyotrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies  
CC specific for isoforms of RTN3 or oligonucleotides (antisense sequences or  
CC small interfering RNA) that can block/reduce expression of these isoforms  
CC are useful for treating neuromuscular diseases and (ii) cells that  
CC express RTN3 are useful in screening for therapeutic agents. The present  
CC sequence is a RTN3 DNA sequence used to illustrate the invention.

XX SQ Sequence 4092 BP; 1286 A; 834 C; 836 G; 1136 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.02e-65 Length: 4092  
Score: 623.50 Matches: 115  
Percent Similarity: 80.95% Conservative: 38  
Best Local Similarity: 60.85% Mismatches: 35  
Query Match: 66.97% Indels: 1  
DB: 12 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADM36179 (1-4092)

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QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 2446 GTGCACGATCTGATTTTTCGAGAGATGTGAAGAGACTGGTGTCTTCTTGGCACCAGC 2505
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValleAla 41
Db 2506 CTGATCATGCTGTTCCCTGGCAGCTTTCAGTGTCTCAGTGTGGTGTCTTACTCATC 2565
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 2566 CTGGCTCTTCTCTGTCCACCATCAGTTTCAGATCTCAAGTCCGTCTCATCAAGCTGTA 2625
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 2626 CAGAAGTCAGAAGAGCCCATTCATTCAAGGCTTACCTGAGCTAGACATTACTCTGTCC 2685
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db 2686 TCAGAAGCTTTCATTAATTACATGAATGCTGCATGTCACATCAACAGGCCCTGAAA 2745
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 2746 CTCAATTATTCGTCCTCTCTGGTAGAAGATCTGTTGACTCCTTGAAGCTGCTCTTC 2805
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
Db 2806 ATGTGGCTGATGACCTATGTTGGTGTGTTTAAACGAATCACCTTCTTAATTTCTGCT 2865
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 2866 GAACCTCTCATTTTCAGTGTCCGATGTCGTATGAGAAGTACAAAGACCAGATTGATCAC 2925
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 2926 TATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAACAACTC 2985
QY 182 ProGlyLeu---LysArgLysAlaGlu 189
Db 2986 CCTGGAATCGCCAAAAGGAGGAGAA 3012
RESULT 99
ADM36173
ID ADM36173 standard; DNA; 4239 BP.
XX
AC ADM36173;
XX
CT 03-JUN-2004 (first entry)
XX
DE Human RTN3 isoform IV coding sequence, SEQ ID 56.
XX
KW Neuroprotective; Myotrophic; neuromuscular disease; RTN3; reticulon 3;
KW amyotrophic lateral sclerosis; ALS; myopathy; human; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 124..3162
FT /tag= a
FT /product= "RTN3 isoform IV"
XX
FN WO2004001069-A2.
XX
PD 31-DEC-2003.
XX
PF 20-JUN-2003; 2003WO-FR001910.
XX
PR 25-JUN-2002; 2002FR-00007846.
XX
(PYPA-) UNIV PASTEUR LOUIS.
XX
PI Dupuis L, Di Scala F, De Tapia M, Larmet Y, Loeffler J,
PI Gonzales De Aguilar J, Boutillier AL, Gaidon C, Rene F;

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XX WPI; 2004-071743/07.
DR P-PSDB; ADM36174.
XX
PT Diagnosing, prognosing and monitoring neuromuscular disease, particularly
PT amyotrophic lateral sclerosis, comprises detecting modulation of the
PT reticulon 3 gene.
XX
PS Claim 35; SEQ ID NO 56; 116pp; French.
XX
CC The present invention relates to a method for diagnosing, or evaluating
CC progression of, a neuromuscular disease. The method comprises detecting
CC modulation of the expression of a product (I) of the RTN (reticulon)3
CC gene. Differential expression of RTN3 is a specific marker of
CC neuromuscular disease, allowing early diagnosis from readily available
CC muscle biopsies. The method is also useful for determining the efficacy
CC of treatment. The method is used to diagnose (also to evaluate
CC progression or therapy of) neuromuscular disorders, specifically
CC amyotrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies
CC specific for isoforms of RTN3 or oligonucleotides (antisense sequences or
CC small interfering RNA) that can block/reduce expression of these isoforms
CC are useful for treating neuromuscular diseases and (ii) cells that
CC express RTN3 are useful in screening for therapeutic agents. The present
CC sequence is a RTN3 DNA sequence used to illustrate the invention.
XX
SQ Sequence 4239 BP; 1282 A; 925 C; 890 G; 1142 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4,23e-65 Length: 4239
Score: 623.50 Matches: 115
Percent Similarity: 80.9% Conservative: 38
Best Local Similarity: 60.8% Mismatches: 35
Query Match: 66.9% Indels: 1
DB: 12 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x ADM36173 (1-4239)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 2593 GTGCACGATCTGATTTTTCGAGAGATGTGAAGAGACTGGGTGTCTTCTTGGCACCAGC 2652
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValleAla 41
Db 2653 CTGATCATGCTGCTTTCCTGGCAGCTTTCAGTGTCTCAGTGTGGTGTCTTACTCATC 2712
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 2713 CTGGCTCTTCTCTGTCCACCATCAGTTTCAGATCTCAAGTCCGTCTCATCAAGCTGTA 2772
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 2773 CAGAAGTCAGAAGAGGCCATCCATTCAAGGCTTACCTGGAGCTAGACATTACTCTGTCC 2832
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db 2833 TCAGAAGCTTTCATTAATTACATGAATGCTGCATGTCATCAAGGCCCTGAAA 2892
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 2893 CTCAATTATTCGTCCTCTTCTGGTAGAAGATCTGTTGACTCCTTGAAGCTGCTGTCTTC 2952
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
Db 2953 ATGTGGCTGATGACCTATGTTGGTGTGTTTTTAAACGAATCACCTTCTTAATTTCTGCT 3012
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 3013 GAACCTCTCATTTTCAGTGTCCGATGTCGTATGAGAAGTACAAAGACCAGATTGATCAC 3072
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 3073 TATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAACAACTC 3132

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Qy 182 ProGlyLeu---LysArgLysAlaGlu 189  
 Db 3133 CCTGGATCGCCAAAAAAGGCAGAA 3159

## RESULT 100

ADM36167  
 ID ADM36167 standard; DNA; 4296 BP.

XX ADM36167;

XX 03-JUN-2004 (first entry)

XX Human RTN3 isoform I coding sequence, SEQ ID 50.

XX Neuroprotective; Myotrophic; neuromuscular disease; RTN3; reticulon 3;  
 XX amyotrophic lateral sclerosis; ALS; myopathy; human; gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 124..3219

XX FT /\*tag= a

XX FT /product= "RTN3 isoform I"

XX WO2004001069-A2.

XX 31-DEC-2003.

XX 20-JUN-2003; 2003WO-FR001910.

XX 25-JUN-2002; 2002FR-00007846.

XX (UYPA-) UNIV PASTEUR LOUIS.

XX Dupuis L, Di Scala F, De Tapia M, Larmet Y, Loeffler J;

XX Gonzales De Aguilar J, Bouillier AL, Gaidon C, Rene F;

XX WPI; 2004-071743/07.

XX P-PSDB; ADM36168.

XX Diagnosing, prognosing and monitoring neuromuscular disease, particularly  
 PT amyotrophic lateral sclerosis, comprises detecting modulation of the  
 PT reticulon 3 gene.

XX Claim 35; SEQ ID NO 50; 116pp; French.

XX The present invention relates to a method for diagnosing, or evaluating  
 CC progression of, a neuromuscular disease. The method comprises detecting  
 CC modulation of the expression of a product (I) of the RTN (reticulon)3  
 CC gene. Differential expression of RTN3 is a specific marker of  
 CC neuromuscular disease, allowing early diagnosis from readily available  
 CC muscle biopsies. The method is also useful for determining the efficacy  
 CC of treatment. The method is used to diagnose (also to evaluate  
 CC progression or therapy of) neuromuscular disorders, specifically  
 CC amyotrophic lateral sclerosis (ALS) and myopathy. Also (i) antibodies  
 CC specific for isoforms of RTN3 or oligonucleotides (antisense sequences or  
 CC small interfering RNA) that can block/reduce expression of these isoforms  
 CC are useful for treating neuromuscular diseases and (ii) cells that  
 CC express RTN3 are useful in screening for therapeutic agents. The present  
 CC sequence is a RTN3 DNA sequence used to illustrate the invention.

XX Sequence 4296 BP; 1290 A; 944 C; 895 G; 1167 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	4.31e-65	Length:	4296
Score:	623.50	Matches:	115
Percent Similarity:	80.95%	Conservative:	38
Best Local Similarity:	60.85%	Mismatches:	35
Query Match:	66.97%	Indels:	1
DB:	12	Gaps:	1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x ADM36167 (1-4296)

Qy 2 ValValAspLeuLeuTyrTyrArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 2650 GTGCACCATCTGATTTCTCGAGAGATGTGAGAAGACTGGGTTTGCTTTGGCCACACG 2709  
 Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 2710 CTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTCTCATGTGTGGTTTCTTACCTATC 2769  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 2770 CTGGCTCTTCTCTCTGTCCACCATCAGCTTCAGGATCTACAGTCCGTCATCAAGCTGTA 2829  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 2830 CAGAAGTCAGAAGAAGGCCATCCATTCAAGGCCCTACCTGGACGTAGACATTACTCTGTCC 2889  
 Qy 82 GluLeuLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 2890 TCAGAAGCTTTCCATATAATTACATGAATGCTGCCATGTGTGCACATCAACAGGCCCTGAAA 2949  
 Qy 102 GluLeuArgGluLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 2950 CTCATTATTCGTCTCTTCTGTGGTAGAAGATCTGGTTGACTCTTGAAGCTGGCTGTCTTC 3009  
 Qy 122 MetTyrValPheThrTyrValGlyValAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 Db 3010 ATGTGGCTGATGACCTATGTGTGGTGTGTTTAAACGGAATCACCTCTTAATTTCTTGTCT 3069  
 Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 3070 GAACGTGCTCATTTTTCAGTGTCCCGATTGCTATGAGAAGTACAAAGACCCAGATTGATCAC 3129  
 Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 3130 TATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAAACTC 3189  
 Qy 182 ProGlyLeu---LysArgLysAlaGlu 189  
 Db 3190 CCTGGAATCGCCAAAAAAGGCAGAA 3216

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Title: US-09-830-972-29\_COPY\_990\_1178

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Delop 6.0, Delext 7.0

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	927	99.6	499	2	Sequence 106, App
3	927	99.6	1669	4	Sequence 2, Appli
4	914	98.2	2610	4	Sequence 3253, Ap
5	682	73.3	3202	4	Sequence 382, App
6	627.5	67.4	4262	4	Sequence 3309, Ap
7	624.5	67.1	1766	3	Sequence 1127, Ap
8	624.5	67.1	1766	3	Sequence 2988, Ap
9	624.5	67.1	2664	3	Sequence 254, App
10	543	58.3	3517	4	Sequence 255, App
11	526.5	56.6	1095	2	Sequence 111, App
12	518	55.6	2014	4	Sequence 4, Appli
					Sequence 13561, A

13	508.5	54.6	794	3	US-09-149-476-102	Sequence 102, App
14	473.5	50.9	2181	4	US-09-949-016-1419	Sequence 1419, Ap
c 15	341	36.6	601	4	US-09-949-016-117588	Sequence 117588, A
c 16	341	36.6	601	4	US-09-949-016-117589	Sequence 117589, A
c 17	341	36.6	42075	4	US-09-949-016-14995	Sequence 14995, A
18	286	30.7	443	4	US-09-513-999C-3784	Sequence 3784, Ap
19	279.5	30.0	135667	4	US-09-949-016-15051	Sequence 15051, A
20	279.5	30.0	152486	4	US-09-949-016-12869	Sequence 12869, A
c 21	276.5	29.7	601	4	US-09-949-016-40169	Sequence 40169, A
c 22	276.5	29.7	601	4	US-09-949-016-119335	Sequence 119335, A
23	276	29.6	261	2	US-08-700-607-9	Sequence 9, Appli
24	271	29.1	13906	4	US-09-949-016-14730	Sequence 14730, A
25	256	27.5	200	4	US-09-513-999C-11198	Sequence 11198, A
26	236.5	25.4	15661	4	US-09-949-016-13161	Sequence 13161, A
27	144	15.5	1125	4	US-09-248-796A-1905	Sequence 1905, Ap
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c 29	141	15.1	601	4	US-09-949-016-119336	Sequence 119336, A
c 30	122	13.1	601	4	US-09-949-016-117609	Sequence 117609, A
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c 32	102	11.0	601	4	US-09-949-016-48087	Sequence 48087, A
c 33	100	10.7	425	3	US-08-905-223-178	Sequence 178, App
c 34	95	10.2	1722	4	US-08-956-171E-407	Sequence 407, App
c 35	95	10.2	1722	4	US-08-781-986A-407	Sequence 407, App
36	89	9.6	1828	3	US-08-487-596-7	Sequence 7, Appli
37	89	9.6	1828	4	US-08-660-451A-7	Sequence 1, Appli
38	88.5	9.5	4550	3	US-09-462-136-1	Sequence 4281, Ap
39	88.5	9.5	4661	4	US-09-949-016-4281	Sequence 100, App
40	88.5	9.5	4673	4	US-09-814-915A-100	Sequence 5725, Ap
41	88	9.5	1273	4	US-09-949-016-5725	Sequence 2072, Ap
42	87.5	9.4	1779	4	US-09-134-000C-2072	Sequence 2168, Ap
43	87.5	9.4	3156	3	US-09-134-001C-2168	Sequence 81, Appli
44	86	9.2	296	4	US-09-313-294A-81	Sequence 322, App
45	85	9.1	1302	4	US-08-956-171E-322	

ALIGNMENTS

RESULT 1

US-09-484-970B-106

Sequence 106, Application US/09484970B

Patent No. 6426186

GENERAL INFORMATION:

APPLICANT: Jones, Karen A.

APPLICANT: Volkmut, Wayne

APPLICANT: Walker, Michael G.

TITLE OF INVENTION: BONE REMODELING GENES

FILE REFERENCE: EP-0014 US

CURRENT APPLICATION NUMBER: US/09/484,970B

CURRENT FILING DATE: 2000-01-18

NUMBER OF SEQ ID NOS: 172

SOFTWARE: PERL Program

SEQ ID NO 106

LENGTH: 4822

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: Incyte ID No. 6426186 44857.15CB1

NAME/KEY: unsure

LOCATION: 33, 51, 79, 211, 369, 483-484, 731, 748, 4803, 4805-4806, 4808-4809,

OTHER INFORMATION: a, t, c, g, or other

US-09-484-970B-106

Alignment Scores:

Pred. No.: 2.36e-119

Score: 931.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 3

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-484-970B-106 (1-4822)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
DB 3265 TCAGTTGTTGACCTCTCTACTGAGAGACATTAAAGAGACTGGAGTGTGTGGTGC 3324  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 3325 AGCCTATTCCTGCTGCTTTCAATGACAGTATTGAGCAATGAGCGTAAACGCTACAT 3384  
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60  
DB 3385 GCCTGGCCCTGCTCTCTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCT 3444  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleGluSerGluValAlaIle 80  
DB 3445 ATCCAGAAATCAGATGAAGGCCACCCATTCAGGCGATATCTGGAATCTGAAGTTGCTATA 3504  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
DB 3505 TCTGAGGAGTGTGTTGAGAGTACAGTAATTCCTCTTGGTCATGTAAGTGCACGATA 3564  
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
DB 3565 AGGAACTCAGGCGCTCTCTTAGTTGATGATTAGTTGATCTCTGAAGTTGCGAGT 3624  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuLeu 140  
DB 3625 TTGATGTGGGTATTTACCTATGTTGTTGCTGTTTAAATGCTGTGACACTACTGATTTG 3684  
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
DB 3685 GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 3744  
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
DB 3745 CATTATCTAGGACTTCGAAATGAAGATGTTAAAGATGCTATGCTAAATCCAAAGCAAA 3804  
QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
DB 3805 ATCCCTGGATTGAAGCGCAAGCTGAA 3831

## RESULT 2

US-08-700-607-2  
; Sequence 2, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/700,607  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0114 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 799 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE: Consensus  
; US-08-700-607-2

Alignment Scores:  
Pred. No.: 4,778-120 Length: 799  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-08-700-607-2 (1-799)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 108 GTTGTTGACCTCTCTGACGAGACATTAAAGAGACTGGAGTGTGTGGTGCACG 167  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 168 CTATTCCTGCTCTCTTCATTCAGCATTTGAGCGGTAAACAGCCTACATTTGCC 227  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 228 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCTATC 287  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 288 CAGAAATCAGATGAAGCGCCACCCATTCAGGCGATATCTGGAATCTGAAGTTGCTATATCT 347  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
DB 348 GAGGAGTGTGTTGAGAGTACAGTAATTCCTCTCTGCTGTCATGTAACCTGCACGATAAAG 407  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 408 GAACTCAGGCGCTCTCTTATGATGATTTAGTTGATTTCTGTAAGTTGAGTGTG 467  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
DB 468 ATGTGGGTATTTACCTATGTTGGTGGCTGTTTAAATGCTCTGACACTACTGATTTGGCT 527  
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
DB 528 CTCAATTCACCTCTCTGATGTTCTGTTATTTATGAACGCGCATCAGGCACAGATAGATCAT 587  
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 588 TATCTAGGACTTGCATAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAATC 647  
QY 182 ProGlyLeuLysArgLysAlaGlu 189  
DB 648 CTGGAATGAAGCGCAAGCTGAA 671

## RESULT 3

US-09-949-016-3253  
; Sequence 3253, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14

;; PRIOR APPLICATION NUMBER: 60/241,755  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/237,768  
;; PRIOR FILING DATE: 2000-10-03  
;; PRIOR APPLICATION NUMBER: 60/231,498  
;; PRIOR FILING DATE: 2000-09-08  
;; NUMBER OF SEQ ID NOS: 207012  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 3253  
;; LENGTH: 1669  
;; TYPE: DNA  
;; ORGANISM: Human  
US-09-949-016-3253

Alignment Scores:  
Pred. No.: 1,56e-119 Length: 1669  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-3253 (1-1669)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 248 GTTGTGACCTCTCTACTGGAGACATTAAGAAGACTGGAGTGTGTGGTGCCAGC 307  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 308 CTATTCTGCTGCTTTCATTGACAGTATTGACGATTTGAGCGTTAAGCGCTTACATTGCC 367  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 368 TTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCAAGCTATC 427  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 428 CAGAAATCAGATGAAGGCCACCCATTACAGGCGATATCTGGAATCTGGAAGTTGCTATATCT 487  
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 488 GAGGAGTTGGTTTTCAGAAAGTACAGTAATTTCTGCTCTTGTGTCATGTGAACTGCACGATAAG 547  
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 548 GAACTCAGCGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTGCAGTGTG 607  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
Db 608 ATGTGGGTATTTACCTATGTTGGTGCTTGTATATGCTGACACTACTGATTTGGCT 667  
Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 668 CTCAATTCACCTCTTCAGTGTCTCTTATTTATGAACGCGCATCAGGCGACAGATGATCAT 727  
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 728 TATCTAGGACTTGCAAATTAAGAATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAATC 787  
Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 788 CTGGATTGAAGCGCAAGCTGAA 811

## RESULT 4

US-09-023-655-382  
; Sequence 382, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

;; TITLE OF INVENTION: EXPRESSION  
;; NUMBER OF SEQUENCES: 1508  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
;; STREET: 3174 PORTER DRIVE  
;; CITY: PALO ALTO  
;; STATE: CALIFORNIA  
;; COUNTRY: USA  
;; ZIP: 94304  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/023,655  
;; FILING DATE: HEREWITH  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; CLASSIFICATION:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Zeller, Karen J.  
;; REGISTRATION NUMBER: 37,071  
;; REFERENCE/DOCKET NUMBER: PA-0001 US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (650) 855-0555  
;; TELEFAX: (650) 845-4166  
;; INFORMATION FOR SEQ ID NO: 382:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 2610 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; IMMEDIATE SOURCE:  
;; LIBRARY: LUNGNOT14  
;; CLONE: 1508778  
US-09-023-655-382

Alignment Scores:  
Pred. No.: 2,14e-117 Length: 2610  
Score: 914.00 Matches: 188  
Percent Similarity: 99.47% Conservative: 0  
Best Local Similarity: 99.47% Mismatches: 0  
Query Match: 98.17% Indels: 1  
DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-023-655-382 (1-2610)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 1311 GTTGTGACCTCTCTGACTGGAGACATTAAGAAGACTGGAGTGTGTGGTGCCAGC 1370  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr-IleAl 41  
Db 1371 CTATTCTGCTGCTTTCATTGACAGTATTGACGATTTGAGCGTTAAGCGCTTACAAATTC 1430  
Qy 41 aLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 1431 CTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTTGTGATCCAGCTAT 1490  
Qy 61 eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 81  
Db 1491 CCAGAAATCAGATGAAGGCCACCCATTTCAGGCGCATATCTGGAATCTGAAGTTGCTATATC 1550  
Qy 81 rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleL 101  
Db 1551 TGAGGAGTTGGTTTCAGAAAGTACAGTAATTTCTGCTCTTGGTCTATGTGAACTGCACGATAA 1610  
Qy 101 sGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 121  
Db 1611 GGAATCTCAGGCGCTCTCTTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGT 1670

QY 121 uMetTTPValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
Db 1671 GATGGGGTATTACCTATGTTGGTCCCTGTTTAAATGGTCTGACACTACTGATTTTGGC 1730  
QY 141 aleuileSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHi 161  
Db 1731 TCTCAITTCACCTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATATCA 1790  
QY 161 sTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysI 181  
Db 1791 TTATCTAGGACTTGCAATAAGAAATGTTAAAGATGCTATGGCTTAAATCCAGCAAAAT 1850  
QY 181 eProGlyLeuLysArgLysAlaGlu 189  
Db 1851 CCCTGGGTTGAAGCGCAAGCTGAA 1875  
RESULT 5  
US-09-949-016-3309  
; Sequence 3309, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3309  
; LENGTH: 2069  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-3309  
Alignment Scores:  
Pred. No.: 5,11e-85 Length: 2069  
Score: 682.00 Matches: 128  
Percent Similarity: 85.03% Conservative: 31  
Best Local Similarity: 68.45% Mismatches: 28  
Query Match: 73.25% Indels: 0  
DB: 4 Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-3309 (1-2069)  
QY 3 ValAspLeuLeuTyrTTPArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22  
Db 757 ATTGACCTGTGTATTTGGGGACATCAAGCAGCGGCATCGTGTGGAGATTTCCTG 816  
QY 23 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
Db 817 CTGCTGCTCTCTCTCCAGCCCATCAGCGTGTGAGCGTCTGTCGCTACCTGGCCCTG 876  
QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
Db 877 GCGGCACTCTCAGCCACCATCAGTTCCGCACTCAAGTCTGTTTACAGCAGTGCAG 936  
QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
Db 937 AAAACCGACGAGGCCACCTTTCAAGGCTACTTGGAGCTTGAGATCACCTTTCTCAG 996  
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102  
Db 997 GAGCAGATTGAGAAGTACAGGAGACTGCTGCTGAGTCTAGCTGAACAGCACACTTAAGGAA 1056  
QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122

Db 1057 CTGAGAGGCTCTTCTGTGTCAGGACCTGGTGGATTCCTTAAATTTGAGTCTCTGATG 1116  
QY 123 TTPValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAlaLeu 142  
Db 1117 TGGCTCTGACCTACGTGGGCTCTCTTCAATGCGCTGACCTGCTGCTCATGGCTGTG 1176  
QY 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162  
Db 1177 GTTTCATGTTTACTTACTCTACCTGATGTATGTTAAAGCACCAGGCACAGATTCACCAATAT 1236  
QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
Db 1237 CTGGGACTTGTGAGGACTCACATAAATGCTGTTGTGGCAAGATTTCAGGCTAAATCCCA 1296  
QY 183 GlyLeuLysArgLysAlaGlu 189  
Db 1297 GCGCTAAGAGGCACGCTGAG 1317  
RESULT 6  
US-09-949-016-1127  
; Sequence 1127, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1127  
; LENGTH: 3202  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-1127  
Alignment Scores:  
Pred. No.: 1.03e-84 Length: 3202  
Score: 682.00 Matches: 128  
Percent Similarity: 85.03% Conservative: 31  
Best Local Similarity: 68.45% Mismatches: 28  
Query Match: 73.25% Indels: 0  
DB: 4 Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-1127 (1-3202)  
QY 3 ValAspLeuLeuTyrTTPArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22  
Db 1890 ATTGACCTGTGTATTTGGGGACATCAAGCAGCGGCATCGTGTGGAGATTTCCTG 1949  
QY 23 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
Db 1950 CTGCTGCTCTCTCTCCAGCCCATCAGCGTGTGAGCGTCTGTCGCTACCTGGCCCTG 2009  
QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
Db 2010 GCGGCACTCTCAGCCACCATCAGTTCCGCACTCAAGTCTGTTTACAGCAGTGCAG 2069  
QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
Db 2070 AAAACCGACGAGGCCACCTTTCAAGGCTACTTGGAGCTTGAGATCACCTTTCTCAG 2129  
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102  
Db 2130 GAGCAGATTGAGAAGTACAGGAGACTGCTGCTGAGTCTAGCTGAACAGCACACTTAAGGAA 2189

QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuValPheAlaValLeuMet 122  
 DB 2190 CTGAGAGGCTCTTCTGTGTGACAGACCTGGTGGATTCCTTAAATTTGCAGTCTGTATG 2249  
 QY 123 TTPValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuLeuAlaLeu 142  
 DB 2250 TGGCTCTGACCTACGTGTTGGCGCTCTCTTCAATGGCTGACCTGCTGCTCATGCTGTG 2309  
 QY 143 lIeSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162  
 DB 2310 GTTTCATGTTTACTCTACCTGTAGTATGTATTAAGCACCAGGCACAGATTCACCAATAT 2369  
 QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
 DB 2370 CTGGGACTGTGAGGACTCACATAATGCTGTGTGGCAAGATTCAGGCTTAAATATCCCA 2429  
 QY 183 GlyLeuLysArgLysAlaGlu 189  
 DB 2430 GCGGCTAAGAGGCACGCTGAG 2450

## RESULT 7

US-09-949-016-2988  
 ; Sequence 2988, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq For Windows Version 4.0  
 ; SEQ ID NO 2988  
 ; LENGTH: 2262  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-09-949-016-2988

## Alignment Scores:

Pred. No.: 2,6e-77 Length: 2262  
 Score: 627.50 Matches: 116  
 Percent Similarity: 81.05% Conservative: 38  
 Best Local Similarity: 61.05% Mismatches: 25  
 Query Match: 67.40% Indels: 1  
 DB: 4 Gaps: 1

US-09-830-972-29\_copy\_990\_1178 (1-189) x US-09-949-016-2988 (1-2262)

QY 1 SerValAlaAspLeuLeuTyrTTPArgAspIleLysThrGlyValValPheGlyAla 20  
 DB 7 TCAGTGCACGATCTGATTTCTGGAGAGATGTGAAGAGACTGGGTGTCTTTGGCACC 66  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 67 AGCTGATCATGCTCTTCTCCCTGCGACGCTTCAGTGTTCATGTCAGTGTGTTCTTACCTC 126  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 127 ATCTGGCTCTTCTCTGTCCACCATCAGTTCAGGATCTCAAGTCGTCATCCAGCT 186  
 QY 61 lIeGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 187 GTACAGAAGTCAGAAGAGGCGCATCCATTCAAGCGCTACCTGGACGTAGACATTACTCTG 246  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100

DB 247 TCCTCAGAGCTTTCATATTAATGCTGCCATGCTGCATCAACAGGSCCCTG 306  
 QY 101 LysGluLeuArgArgLeuPheLeuValAspSerLeuValAspSerLeuLysPheAlaVal 120  
 DB 307 AAATCATATTATTCGTTCTCTTCTGTGAGAGATCTGTTGACTCTCTTGAAGCTGCTGTC 366  
 QY 121 LeuMetTTPValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuLeu 140  
 DB 367 TTCATGTGGCTGATGACCTATGTTGGTCTGTTTTTAACGGAATCACCTTCTTAATTCCT 426  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 DB 427 GCTGAACGCTCATTTTTCAGTGTCCGATTTGCTATGAGAAGTAGTCAACAGCCAGATTGAT 486  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 487 CACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAAGCAAA 546  
 QY 181 lIeProGlyLeu--LysArgLysAlaGlu 189  
 DB 547 CTCCTGGATCGCCAAAAGGACGAA 576

## RESULT 8

US-09-149-476-254  
 ; Sequence 254, Application US/09149476  
 ; Patent No. 6420526  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: 186 Human Secreted proteins  
 ; FILE REFERENCE: P2002P1  
 ; CURRENT APPLICATION NUMBER: US/09/149,476  
 ; CURRENT FILING DATE: 1998-09-08  
 ; EARLIER APPLICATION NUMBER: PCT/US98/04493  
 ; EARLIER FILING DATE: 1998-03-06  
 ; EARLIER APPLICATION NUMBER: 60/040,162  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/040,333  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/038,621  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/040,626  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/040,334  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/040,336  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/040,163  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/047,600  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,615  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,597  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,502  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,633  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,583  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,617  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,618  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,503  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,592  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,581  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,584  
 ; EARLIER FILING DATE: 1997-05-23

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EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

## Alignment Scores:

Pred. No.: 4, 6e-77 Length: 1766  
Score: 624.50 Matches: 115  
Percent Similarity: 81.0% Conservative: 39  
Best Local Similarity: 60.53% Mismatches: 35  
Query Match: 67.08% Indels: 1  
Gaps: 3

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-149-476-254 (1-1766)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspLeuLysThrGlyValValPheGlyAla 20  
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Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db ACGCTGATCATGCTGCTTCCCTGGCAGCTTTTCAGTGTTCATGAGTGTGTTTACCTC 406  
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db ATCTGGCTCTCTCTCTGTCACCATCAGTTTCAGATCTCAAGTCCGTATCCAGCT 466  
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db GTACAGAAGTCAGAAAGAGGCCATCCATTCAAAGCTACCTGGAGCTAGACATTACTCTG 526  
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db TCCTCAGAAGCTTTCATTAATTTACATGAATGCTGCATGTCATCAACAGAGCCCTG 586  
Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db AAATCATATATTCGTCTCTCTCTGTTAGAGATCTGGTGTGACTCTTGAAGCTGCTGTC 646  
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeu 140  
Db TTCTATGTCGTCATGACCTATGTTGCTGCTGTTTAAAGCAATCAACCTTCTAATCTT 706  
Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db GCTGAACCTGCTCATTTTCAGTGTCCCGATTGCTATGAGAAGTACAGACCCAGATTGAT 766  
Qy 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaValIleGlnAlaLys 180  
Db CACTATGTTGGATCGCCGAGATCAGACCAAGTCAATTTGAAAGATCAAGCAAAA 826  
Qy 181 IleProGlyLeu---LysArgLysAlaGlu 189  
Db CTCCTCGAATCGCCAAAAAAGGCAGAA 856

## RESULT 9

US-09-149-476-255  
Sequence 255, Application US/09149476  
Patent No. 6420526  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: P2002P1  
CURRENT APPLICATION NUMBER: US/09/149,476  
CURRENT FILING DATE: 1998-09-08  
EARLIER APPLICATION NUMBER: PCT/US98/04493  
EARLIER FILING DATE: 1998-03-06  
EARLIER APPLICATION NUMBER: 60/040,162  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,333  
EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/038,621  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,626  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,334  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,336  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,163  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/047,600  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,615  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,597  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,502  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,633  
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EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,581  
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EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,492  
EARLIER FILING DATE: 1997-05-23  
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EARLIER APPLICATION NUMBER: 60/047,582  
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EARLIER FILING DATE: 1997-05-23  
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EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,580  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,568  
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EARLIER APPLICATION NUMBER: 60/043,314  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,569  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,311  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,671  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,674  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,669  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,312  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,313

[illegible]





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; LENGTH: 1095 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: THPINOB01
; CLONE: 31870
US-08-700-607-4

Alignment Scores:
Pred. No.: 119e-63 Length: 1095
Score: 526.50 Matches: 104
Percent Similarity: 72.77% Conservative: 35
Best Local Similarity: 54.45% Mismatches: 30
Query Match: 56.55% Indels: 22
DB: 2 Gaps: 2

US-09-830-972-29_COPY_990_1178 (1-189) x US-08-700-607-4 (1-1095)
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Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
329 GCGGTGCACGATCTGATTTMTGGAGAGATGTGAAGAGACTGGGTTTCTTTGGCACC 388
QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
389 ACCTGATCATGCTGCTTCCCTGGCAGCTTTTCAGTGTCTATCAGTGTGGTTTCTTACCTC 448
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
449 ATCTGGCTCTCTCTCTGTCACCATCAGCTTCAGGATCTACAGTCCGCTCATCCAGCT 508
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
509 GTACAGAAGTCAGAGAAGGCCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCTG 568
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
569 TCCTCAGAAGCTTTCATTAATACATGAATGTGCTGATGTCACATCAACAGGGCCCTG 628
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
629 AAATCATTAATTCGCTCTCTCTGTTAGAGATCTGTTGACTCTCTTGAAGCTGGCTGTC 688
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
689 TTCATGTGGCTGATGACCTATGTTGGTGTGTTTAAACGAATCACCCTTCTAATCTT 748
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
749 GCTGAACCTGCTCAATTTTNAAGTGTCGCGATGTTNATNAGAAGTAC----- 793
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
794 -----AAGGTTCCAGCAA 808

QY 180 sileProGlyLeu---LysArgLysAlaGlu 189
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809 ACTCCCTGGAATGCCCAAAAAAAGGAGAA 839

RESULT 12
US-09-270-767-13561
; Sequence 13561, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; EARLIER FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13561

RESULT 13
US-09-149-476-102
; Sequence 102, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; EARLIER FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
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1	EARLIER FILING DATE: 1997-04-11
2	EARLIER APPLICATION NUMBER: 60/043,315
3	EARLIER FILING DATE: 1997-04-11
4	EARLIER APPLICATION NUMBER: 60/048,974
5	EARLIER FILING DATE: 1997-06-06
6	EARLIER APPLICATION NUMBER: 60/056,886
7	EARLIER FILING DATE: 1997-08-22
8	EARLIER APPLICATION NUMBER: 60/056,877
9	EARLIER FILING DATE: 1997-08-22
10	EARLIER APPLICATION NUMBER: 60/056,889
11	EARLIER FILING DATE: 1997-08-22
12	EARLIER APPLICATION NUMBER: 60/056,893
13	EARLIER FILING DATE: 1997-08-22
14	EARLIER APPLICATION NUMBER: 60/056,630
15	EARLIER FILING DATE: 1997-08-22
16	EARLIER APPLICATION NUMBER: 60/056,878
17	EARLIER FILING DATE: 1997-08-22
18	EARLIER APPLICATION NUMBER: 60/056,662
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22	EARLIER APPLICATION NUMBER: 60/056,882
23	EARLIER FILING DATE: 1997-08-22
24	EARLIER APPLICATION NUMBER: 60/056,837
25	EARLIER FILING DATE: 1997-08-22
26	EARLIER APPLICATION NUMBER: 60/056,903
27	EARLIER FILING DATE: 1997-08-22
28	EARLIER APPLICATION NUMBER: 60/056,888
29	EARLIER FILING DATE: 1997-08-22
30	EARLIER APPLICATION NUMBER: 60/056,894
31	EARLIER FILING DATE: 1997-08-22
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33	EARLIER FILING DATE: 1997-08-22
34	EARLIER APPLICATION NUMBER: 60/056,636
35	EARLIER FILING DATE: 1997-08-22
36	EARLIER APPLICATION NUMBER: 60/056,874
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43	EARLIER FILING DATE: 1997-08-22
44	EARLIER APPLICATION NUMBER: 60/057,761
45	EARLIER FILING DATE: 1997-08-22
46	EARLIER APPLICATION NUMBER: 60/047,595
47	EARLIER FILING DATE: 1997-05-23
48	EARLIER APPLICATION NUMBER: 60/047,599
49	EARLIER FILING DATE: 1997-05-23
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55	EARLIER FILING DATE: 1997-05-23
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57	EARLIER FILING DATE: 1997-05-23
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59	EARLIER FILING DATE: 1997-05-23
60	EARLIER APPLICATION NUMBER: 60/047,589
61	EARLIER FILING DATE: 1997-05-23
62	EARLIER APPLICATION NUMBER: 60/047,593
63	EARLIER FILING DATE: 1997-05-23
64	EARLIER APPLICATION NUMBER: 60/047,614
65	EARLIER FILING DATE: 1997-05-23

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EARLIER APPLICATION NUMBER: 60/043,670  
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EARLIER APPLICATION NUMBER: 60/056,632  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,664  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,876  
EARLIER FILING DATE: 1997-08-22  
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EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,875  
EARLIER FILING DATE: 1997-08-22  
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EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

## Alignment Scores:

Pred. No.: 2,37e-61 Length: 794  
Score: 508.50 Matches: 102  
Percent Similarity: 76.37% Conservative: 37  
Best Local Similarity: 56.04% Mismatches: 41  
Query Match: 54.62% Indels: 3  
DB: 3 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-149-476-102 (1-794)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
Db 254 GCGGTGACGATCTGATTTCTGGAGAGATGTGAAGAGACTGGGTTTCTTTGGAC-- 311  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerVal-ThrAlaTyrIle 40  
Db 312 AGCGTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTCATCARTGTGGGTTCTTAMCT 371  
QY 40 eAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAl 60  
Db 372 CATCTCGGCTCTCTCTGTCCACCATCARTTCAGGATCTACAGTCGTCATCCAGC 431  
QY 60 alleGlnLysSerAspGluGlyHisProPhe-ArgAlaTyrLeuGluSerGluValAlaI 80  
Db 432 TGTWAGARTCAGAAAGGCCATCCAWTCCAAAGCCCTACCTGGAGCTAGACATTACTC 491  
QY 80 leSerGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrI 100  
Db 492 TGTCTCTCAGAAAGCTTCCATTAATCATGAATGCTGCCAATGTGTCATCAACAGGCC 551  
QY 100 leLysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaV 120  
Db 552 TGAACATCATTTATTCCTCTCTTCTGTGTAAGAGATCTGTTGACTCTCTTGAAGCTGGCTG 611

QY 120 alLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleL 140  
Db 612 TCTTCATGTGGCTGATGACCTATGTGTGTGTTTAAACGAATCACCTTCTAATTC 671  
QY 140 eAlaLeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleA 160  
Db 672 TTGCTGAACCTGCTCAITTTTCAGTGCCCGATTTGCTATGAGAGATGACAGCCAGATTG 731  
QY 160 sPHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAla 180  
Db 732 ATCACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAGATCCCAAGCA 791  
QY 180 ys 180  
Db 792 AA 793

## RESULT 14

US-09-949-016-1419  
Sequence 1419, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1419  
LENGTH: 2181  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-1419

Alignment Scores:  
Pred. No.: 9,77e-56 Length: 2181  
Score: 473.50 Matches: 95  
Percent Similarity: 65.67% Conservative: 37  
Best Local Similarity: 47.26% Mismatches: 56  
Query Match: 50.86% Indels: 13  
DB: 4 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-1419 (1-2181)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 1162 GTGGCGGACCTGCTGCTACTGGAAGGACACGAGGAGTCTTTCACAGGCTG 1221  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 1222 ATGGTCTCCCTCTGCTCTGCTGTCATCTTAGCATCTGTCGTCGCGCGCACTTGGCT 1281  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 1282 CTGTGTGCTCTGCGGCACCATCTCTCTCAGGGTTTACCGCAAGTGTCTGAGCGCTG 1341  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 1342 CACCGGGGGATGGAGCCCAACCCCTTTCAGGCTTACCTGATGTGGACCTCACCTGACT 1401  
QY 82 GluGlnLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 1402 CGGGAGCAGACGGAACGTTGTGTCACCATGATCACTCCCGCTGGTCTTCGCGGCCACG 1461  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121

Db 1462 CAGCTGGCGCATTCTTCTGGTAGAGACCTCGTGGATTCCCTCAAGTCGCCCTCCTC 1521  
Qy 122 MetTpvAlpheThrTyxValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
Db 1522 TTCTACATCTGACCTTCTGGTGCCATCTTCAATGGTTTGACTCTCTCATCTGGGA 1581  
Qy 142 LeuLeuSerLeuPheSerValProValletyGluArgHisGlnAlaGlnleAspHis 161  
Db 1582 GTGATTGGCTTATTCACCATCCCTGCTGTACCGCGCAGCACCAGGCTCAGATCGACCA 1641  
Qy 162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 1642 TATGGGGTGGTGGTACCAATCAGTTGAGCCACATCAAAAGCTTAAGATCCGAGCTAAAATC 1701  
Qy 182 ProGlyLeu-----LysArgLysAla 188  
Db 1702 CAGGACCGGAGCCCTGCTCTGCAGCGCGCAGTCTCGGATCCAAAGCCAAAGCC 1761  
Qy 189 Glu 189  
Db 1762 GAA 1764  
RESULT 15  
US-09-949-016-117588/c  
; Sequence 117588, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 117588  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-117588  
Alignment Scores:  
Pred. No.: 4,72e-38 Length: 601  
Score: 341.00 Matches: 70  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 36.63% Indels: 0  
Gaps: 0  
DB: 4  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-117588 (1-601)  
Qy 2 ValValAspLeuLeuTyxTyrArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 224 GTTGTGACCTCTGCTACTGGAGACATTAAGAAGACTGGAGTGGTGTGGTGGCCAGC 165  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValAlaTyrlleAla 41  
Db 164 CTATTCCTGCTGCTTTCATTCAGATATTCAGCTTTGAGCGTAAACAGCTTACATTC 105  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyLysGlyValIleGlnAlaIle 61  
Db 104 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 45  
Qy 62 GlnLysSerAspGluGlyHisProPheArg 71  
Db 44 CAGAAATCAGATGAAGGCCACCCATTCAGG 15  
Alignment Scores:  
Pred. No.: 4,72e-38 Length: 601  
Score: 341.00 Matches: 70  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 36.63% Indels: 0  
Gaps: 0  
DB: 4  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-117588 (1-601)  
Qy 2 ValValAspLeuLeuTyxTyrArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 224 GTTGTGACCTCTGCTACTGGAGACATTAAGAAGACTGGAGTGGTGTGGTGGCCAGC 165  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValAlaTyrlleAla 41  
Db 164 CTATTCCTGCTGCTTTCATTCAGATATTCAGCTTTGAGCGTAAACAGCTTACATTC 105  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyLysGlyValIleGlnAlaIle 61  
Db 104 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 45  
Qy 62 GlnLysSerAspGluGlyHisProPheArg 71  
Db 44 CAGAAATCAGATGAAGGCCACCCATTCAGG 15

RESULT 16  
US-09-949-016-117589/c  
; Sequence 117589, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 117589  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-117589  
Alignment Scores:  
Pred. No.: 4,72e-38 Length: 601  
Score: 341.00 Matches: 70  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 36.63% Indels: 0  
Gaps: 0  
DB: 4  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-117589 (1-601)  
Qy 2 ValValAspLeuLeuTyxTyrArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 518 GTTGTGACCTCTGCTACTGGAGACATTAAGAAGACTGGAGTGGTGTGGTGGCCAGC 459  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValAlaTyrlleAla 41  
Db 458 CTATTCCTGCTGCTTTCATTCAGATATTCAGCTTTGAGCGTAAACAGCTTACATTC 399  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyLysGlyValIleGlnAlaIle 61  
Db 398 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 339  
Qy 62 GlnLysSerAspGluGlyHisProPheArg 71  
Db 338 CAGAAATCAGATGAAGGCCACCCATTCAGG 309  
RESULT 17  
US-09-949-016-14995  
; Sequence 14995, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14995  
; LENGTH: 42075  
; TYPE: DNA

ORGANISM: Human  
US-09-949-016-14995

## Alignment Scores:

Pred. No.: 4,39e-35 Length: 42075  
Score: 341.00 Matches: 70  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 36.63% Indels: 0  
DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-14995 (1-42075)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 24648 GTTGTGACCTCTGCTACTGGAGACATTAAGAGACTGGAGTGTGTTGGTCCAGC 24707  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 24708 CTATTCCTGCTGCTTTCATTTGACAGTATTGAGCATTTGAGCGTAACAGCCTACATTGCC 24767  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 24768 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 24827  
QY 62 GlnLysSerAspGluGlyHisPropheArg 71  
Db 24828 CAGAAATCAGATGAGAGGCCACCCATTTCAGG 24857

## RESULT 18

US-09-513-999C-3784  
; Sequence 3784, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 3784  
; LENGTH: 443  
; TYPE: DNA  
; ORGANISM: Homo sapiens

FEATURE:  
NAME/KEY: CDS  
LOCATION: 96..437  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 96..239  
OTHER INFORMATION: score 4.6  
OTHER INFORMATION: seq VFGSFLLLFLSLT/QF  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 305

OTHER INFORMATION: n=a, g, c or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 323  
OTHER INFORMATION: n=a, g, c or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 335  
OTHER INFORMATION: s=g or c  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 360

OTHER INFORMATION: n=a, g, c or t

FEATURE:  
NAME/KEY: UNSURE  
LOCATION: 22  
OTHER INFORMATION: Xaa=Phe or Leu

FEATURE:  
NAME/KEY: UNSURE  
LOCATION: 41  
OTHER INFORMATION: Xaa= \* or Gly or Arg

US-09-513-999C-3784  
Alignment Scores:  
Pred. No.: 1.5e-30 Length: 443  
Score: 286.00 Matches: 59  
Percent Similarity: 80.00% Conservative: 17  
Best Local Similarity: 62.11% Mismatches: 19  
Query Match: 30.72% Indels: 1  
DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-513-999C-3784 (1-443)

QY 3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22  
Db 159 ATTGACCTGTTGTTATTTGGCGGACATCAAGCAGCGGCATCGTGTGTTGGAGATTTCCTG 218  
QY 23 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
Db 219 CTGCTGCTCTTCTCCCTGACCCAGTTTCAGCGTGTGAGCGTGTGGCCCTTACCTGGCCCTG 278  
QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
Db 279 GCGGCACTCTCAGCCACCACCATCAGTTTNCGCATCTACAGTCTGTNTTACAGCAGTSCAG 338  
QY 63 LysSerAspGluGlyHisPropheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
Db 339 ATAACCGACGAGGCCACCG-TNGAAGGCTTACTTGGAGCTTGAGATCACCTTTCTCAG 397  
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsn 97  
Db 398 GAGCAGATTACAGAGTACACGAGCTGCCTGCAGTTCCTACGTGAAC 442

## RESULT 19

US-09-949-016-15051  
; Sequence 15051, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15051  
; LENGTH: 135667  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-15051

## Alignment Scores:

Pred. No.: 1.22e-25 Length: 135667  
Score: 279.50 Matches: 73  
Percent Similarity: 50.00% Conservative: 23  
Best Local Similarity: 38.02% Mismatches: 52  
Query Match: 30.02% Indels: 44  
DB: 4 Gaps: 4

```
US-09-830-972-29_COPY_990_1178 (1-189) x US-09-949-016-15051 (1-135667)
QY 1 SerValValAspLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 122176 GCAGCTATTGACCTGTTGATGGCGGACATCAAGCAGACGGGCATCGTGTGGGAGT 122235
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 122236 TTCCTGCTGCTCTCTCTCCCTGACCCAGTTACGGGTGGTGGAGCGTGTGGCTACCTG 122295
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 122296 GCCCTGGCGGCACTCTCAGCCACCATCAGTTTCCGCACTACAACTCTGTTTACAGCA 122355
QY 61 IleGlnLysSerAspGluGlyHisProPheArg 71
Db 122356 GTGCAGAAACCGACGAGGCCACCTTTCAAGTGAGTGCTCTCAGCTGAGGAGCCCTCAC 122415
QY 72 -----AlaTyrLeuGluSerGluValAlaIleSerGlu 82
Db 122416 CCACGTACACGGGCTTTTACCTCAGCTGATTTTTCAGCTCAGATGCATCTGATCAT 122475
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCyThr 99
Db 122476 -----GTTTCTCTGAGACCCAAACAGACCTCTTAGAGTCTCCCTTAACACCCCTGCTTTG 122529
QY 100 -----IleLysGluLeuArgLeuPheLeuValAspAspLeu 112
Db 122530 AATATCTAACATTTCTGTGTAATTTCTGAAACAACTCGATTATTTTATTCATATCTT 122589
QY 113 ValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPhe 132
Db 122590 ATTGCTTTGTGAGTTTTCATATGAT 122616
QY 133 AsnGlyLeuThrLeuLeuLeuAlaLeuLeuSerLeuPheSer-ValProValIleTyr 152
Db 122617 -----TTACTATTAACTAGTAATATAATCCAACTTACTTAATCTCTCAGCAATATC 122670
QY 152 rGluArgHisGlnAlaGlnIleAspHisTyrLeu 163
Db 122671 AGAAAGGCACAGCAGGCATTTTGTCCCTATTATA 122704

RESULT 20
US-09-949-016-12869
; Sequence 12869, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12869
; LENGTH: 152486
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12869

Alignment Scores: 1.47e-25 Length: 152486
Pred. No.: 279.50 Matches: 73
Percent Similarity: 50.00% Conservativeness: 23
Best Local Similarity: 38.02% Mismatches: 52

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-949-016-12869 (1-152486)
QY 1 SerValValAspLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 90995 GCAGCTATTGACCTGTTGATGGCGGACATCAAGCAGACGGGCATCGTGTGGGAGT 91054
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 91055 TTCCTGCTGCTCTCTCTCCCTGACCCAGTTACGGGTGGTGGAGCGTGTGGCTACCTG 91114
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 91115 GCCCTGGCGGCACTCTCAGCCACCATCAGTTTCCGCACTACAACTCTGTTTACAGCA 91174
QY 61 IleGlnLysSerAspGluGlyHisProPheArg 71
Db 91175 GTGCAGAAACCGACGAGGCCACCTTTCAAGTGAGTGCTCTCAGCTGAGGAGCCCTCAC 91234
QY 72 -----AlaTyrLeuGluSerGluValAlaIleSerGlu 82
Db 91235 CCACGTACACGGGCTTTTACCTCAGCTGATTTTTCAGCTCAGATGCATCTGATCAT 91294
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCyThr 99
Db 91295 -----GTTTCTCTGAGACCCAAACAGACCTCTTAGAGTCTCCCTTAACACCCCTGCTTTG 91348
QY 100 -----IleLysGluLeuArgLeuPheLeuValAspAspLeu 112
Db 91349 AATATCTAACATTTCTGTGTAATTTCTGAAACAACTCGATTATTTTATTCATATCTT 91408
QY 113 ValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPhe 132
Db 91409 ATTGCTTTGTGAGTTTTCATATGAT 91435
QY 133 AsnGlyLeuThrLeuLeuLeuAlaLeuLeuSerLeuPheSer-ValProValIleTyr 152
Db 91436 -----TTACTATTAACTAGTAATATAATCCAACTTACTTAATCTCTCAGCAATATC 91489
QY 152 rGluArgHisGlnAlaGlnIleAspHisTyrLeu 163
Db 91490 AGAAAGGCACAGCAGGCATTTTGTCCCTATTATA 91523

RESULT 21
US-09-949-016-40169/c
; Sequence 40169, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40169
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-40169

Alignment Scores: 5.26e-29 Length: 601
Pred. No.: 276.50 Matches: 72
Score: 72
```

```
Percent Similarity: 50.00% Conservative: 23
Best Local Similarity: 37.89% Mismatches: 55
Query Match: 29.70% Indels: 40
DB: 4 Gaps: 4

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-949-016-40169 (1-601)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
   :::::
Db 580 GCAGCTATTGACCTGTTGTTGGCGGACATCAAGCAGACGGGCATCGTTTGGGAGT 521
QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
   :::::
Db 520 TTCCTGCTGCTCTCTCCCTGACCCAGTTTCAGCGTGTGAGCGTCTGGCGCTACCTG 461
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
   :::::
Db 460 GCCTGGCGGCACCTCTCAGCCACCATCAGTTTCCGCACTTACAAGTCTGTTTACAAGCA 401
QY 61 IleGlnLysSerAspGluGlyHisProPheArg-----AlaTyrLeuGluSerGluVal 78
   :::::
Db 400 GTGCAGAAAACCGACGAGGCCACCTTTCAAGTGAGTGCCTCAGCTGAGGAGCCCTCAC 341
QY 79 AlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAla-----LeuGlyHis 95
   :::::
Db 340 CCAGTACAGGAGGGCTTTTACCTCAGCTGATTTTTCAGTCACAGATGACCTTGAGTCA 281
QY 96 ValAsnCysThr----- 99
   :::::
Db 280 GTTTCCTGAGACCCCAACAGACCTCTTAGAGTCTCCCTAAACACCTGCTTTGAAATATC 221
QY 100 -----IleLysGluLeuArgLeuPheLeuValAspLeuValAsp 114
   :::::
Db 220 TAACATTTCTGGTGAATTTCTGAAACAACTCGAATTTCTTATTTCCAACTACTTATTGCT 161
QY 115 SerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGly 134
   :::::
Db 160 TTGTTGAGTTTTCATATGAT----- 140
QY 135 LeuThrLeuLeuLeuAlaLeuIleSerLeuPheSer-ValProValIleTyrGluAr 154
   :::::
Db 139 TTACTATTAACTAATCAATCAACAACTACTTAATCTCTCAGCAATATCAGAAAG 80
QY 154 gHisGlnAlaGlnIleAspHisTyrLeu 163
   :::::
Db 79 GCACAGCAGGCATTTTGTGCTCTATTATTA 52

RESULT 23
US-09-949-016-119335/C
; Sequence 119335, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119335
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-119335
Alignment Scores:
```

```
Pred. No.: 5,26e-29 Length: 601
Score: 276.50 Matches: 72
Percent Similarity: 50.00% Conservative: 23
Best Local Similarity: 37.89% Mismatches: 55
Query Match: 29.70% Indels: 40
DB: 4 Gaps: 4

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-949-016-119335 (1-601)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
   :::::
Db 580 GCAGCTATTGACCTGTTGTTGGCGGACATCAAGCAGACGGGCATCGTTTGGGAGT 521
QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
   :::::
Db 520 TTCCTGCTGCTCTCTCCCTGACCCAGTTTCAGCGTGTGAGCGTCTGGCGCTACCTG 461
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
   :::::
Db 460 GCCTGGCGGCACCTCTCAGCCACCATCAGTTTCCGCACTTACAAGTCTGTTTACAAGCA 401
QY 61 IleGlnLysSerAspGluGlyHisProPheArg-----AlaTyrLeuGluSerGluVal 78
   :::::
Db 400 GTGCAGAAAACCGACGAGGCCACCTTTCAAGTGAGTGCCTCAGCTGAGGAGCCCTCAC 341
QY 79 AlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAla-----LeuGlyHis 95
   :::::
Db 340 CCAGTACAGGAGGGCTTTTACCTCAGCTGATTTTTCAGTCACAGATGACCTTGAGTCA 281
QY 96 ValAsnCysThr----- 99
   :::::
Db 280 GTTTCCTGAGACCCCAACAGACCTCTTAGAGTCTCCCTAAACACCTGCTTTGAAATATC 221
QY 100 -----IleLysGluLeuArgLeuPheLeuValAspLeuValAsp 114
   :::::
Db 220 TAACATTTCTGGTGAATTTCTGAAACAACTCGAATTTCTTATTTCCAACTACTTATTGCT 161
QY 115 SerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGly 134
   :::::
Db 160 TTGTTGAGTTTTCATATGAT----- 140
QY 135 LeuThrLeuLeuLeuAlaLeuIleSerLeuPheSer-ValProValIleTyrGluAr 154
   :::::
Db 139 TTACTATTAACTAATCAATCAACAACTACTTAATCTCTCAGCAATATCAGAAAG 80
QY 154 gHisGlnAlaGlnIleAspHisTyrLeu 163
   :::::
Db 79 GCACAGCAGGCATTTTGTGCTCTATTATTA 52

RESULT 23
US-08-700-607-9
; Sequence 9, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
```



APPLICATION NUMBER: US/08/700,607  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0114 US  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY: SPINJET01  
CLONE: 28742  
US-08-700-607-9

Alignment Scores:  
Pred. No.: 1,628-29 Length: 261  
Score: 276.00 Matches: 59  
Percent Similarity: 89.71% Conservativeness: 2  
Best Local Similarity: 86.76% Mismatches: 7  
Query Match: 29.65% Indels: 0  
DB: Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-08-700-607-9 (1-261)

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrlleAla 41  
DB 2 CTATNCNGCTGCTTCATTGACATATTACCATTTGAGGTGAGGCTACATTGCC 61  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrlleValIleGlnAlaIle 61  
DB 62 TTNGCCCTGCNCCTCTGTGACCATCAGTNTAGGCTATACAGGGTGTGATCCAGCTATC 121  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrlleLeuGluSerGluValAlaIleSer 81  
DB 122 CAGAAATCAGATGAAGGNCACCATTCAGGGCATATCTGGANTCTGAAGTTGCTATATCT 181  
QY 82 GluGluLeuValGlnLysTyrlleSer 89  
DB 182 GAGGAGTTGNTTCAGAGTACAG 205

RESULT 24  
US-09-949-016-14730  
Sequence 14730, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14730  
LENGTH: 13906  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-14730  
Alignment Scores:  
Pred. No.: 1,628-29 Length: 200  
Score: 256.00 Matches: 52  
Percent Similarity: 100.00% Conservativeness: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 27.50% Indels: 0  
DB: Gaps: 0

Pred. No.: 4,87e-26 Length: 13906  
Score: 271.00 Matches: 50  
Percent Similarity: 87.32% Conservativeness: 12  
Best Local Similarity: 70.42% Mismatches: 9  
Query Match: 29.11% Indels: 0  
DB: Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-14730 (1-13906)  
QY 1 SerValValAspLeuLeuTyrlleArgAspIleLysValThrGlyValValPheGlyAla 20  
DB 2007 TCAGTGCACGATCTGATTTCTGGAGAGATGGAAGAAGACTGGGTTGTCTTTGGCACC 2066  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrlle 40  
DB 2067 AGCTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTGCATCAGTGTGGTTCTTACCTC 2126  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrlleGlyValIleGlnAla 60  
DB 2127 ATCTGGGCTCTCTCTGTCCATCAGTTCAGGATCTACAAGTCCGTCAATCAAGCT 2186  
QY 61 IleGlnLysSerAspGluGlyHisProPheArg 71  
DB 2187 GTACAGAAGTCAGAAGAAGGCCATCCATTCACG 2219  
RESULT 25  
US-09-513-999C-11198  
Sequence 11198, Application US/09513999C  
Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclert, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
FILE REFERENCE: 59.US2.REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 11198  
LENGTH: 200  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-513-999C-11198  
Alignment Scores:  
Pred. No.: 6,72e-27 Length: 200  
Score: 256.00 Matches: 52  
Percent Similarity: 100.00% Conservativeness: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 27.50% Indels: 0  
DB: Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-513-999C-11198 (1-200)  
QY 138 LeuLeuAlaLeuLeuSerLeuPheSerValProValIleTyrlleGluArgHisGlnAla 157  
DB 2 CTGATTTGGCTCTCAATTCATCTTCACTTCTGTTCTGTTATTTATGAACGGCATCAGGCA 61  
QY 158 GlnIleAspHisTyrlleLeuGlyLeuAlaAsnLysValIleAspAlaMetAlaLysIle 177  
DB 62 CAGATAGATCATATTATCTAGGACTTGCATAAATGAAGATGTTAAAGATGCTATGGCTAAATC 121  
QY 178 GlnAlaLysIleProGlyLeuLysArgLysAlaGlu 189  
DB 122 CAGCAAAATCCCTCGGATTGAAGCGCAAGCTGNA 157  
RESULT 26  
US-09-949-016-13161  
Sequence 13161, Application US/09949016



Db 247 CTGTTTGGTTGATGCTCTGAAACCTGCAATTTATTCATATCTTTTCCATTTA 306  
Qy 38 AlaTyrIleAlaLeu-----Ala-LeuLeuSerValThrIleSerPheArgIleTy 54  
Db 307 GCTTACATTGGTTTATGATCTCTGCTGCTGCTGAATATTCGGTAAATTTGATTCTGT 366  
Qy 54 rIysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrIle 74  
Db 367 AAAGGCT----- 373  
Qy 74 uGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGl 94  
Db 374 -----TCCTTGCTAATTTCAAACCACTG----- 397  
Qy 94 yHisValAsnCysThrIleLysGlu----- 102  
Db 398 -----GTAATTTGCTTAAGATTCAATGATGAAGTATTCGCCAATTTGCCAACTTT 453  
Qy 103 -----LeuArgLeuPheLeuValAspLeuValAspLe 115  
Db 454 AATGTGCATTTCGAAGAAAGTTTAAATAAATTTGCTATTCA-CATGACATTGAAACCCAC 512  
Qy 115 rLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLe 135  
Db 513 TTGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 572  
Qy 135 uThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHi 155  
Db 573 CACTTGAATTTTCATTTTCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 632  
Qy 155 sGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAl 175  
Db 633 CAAGAAGAAATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 692  
Qy 175 aLysIleGlnAlaLys 180  
Db 693 TGAATTTACTGAAAG 708

RESULT 28  
US-09-949-016-40170/c  
; Sequence 40170, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 40170  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-40170  
Alignment Scores:  
Pred. No.: 5,33e-10 Length: 601  
Score: 141.00 Matches: 28  
Percent Similarity: 80.00% Conservative: 8  
Best Local Similarity: 62.22% Mismatches: 9  
Query Match: 15.15% Indels: 0  
Gaps: 4  
US-09-830-972-29\_copy\_990\_1178 (1-189) x US-09-949-016-40170 (1-601)

Qy 71 ArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsn 90  
Db 136 AGGGCTACTTGGAGCTTGAGATCACCTTTCTCAGGAGCAGATTACAGAGTACACGGAC 77  
Qy 91 SerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgLeuPheLeuValAsp 110  
Db 76 TGCCTGCAGTTCTACGTGAACAGCACACTTAAGGAAGCTCCTTCTCTGTGTCAG 17  
Qy 111 AspLeuValAspSer 115  
Db 16 GACCTGGTGGATTCC 2  
RESULT 29  
US-09-949-016-119336/c  
; Sequence 119336, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 119336  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-119336  
Alignment Scores:  
Pred. No.: 5,33e-10 Length: 601  
Score: 141.00 Matches: 28  
Percent Similarity: 80.00% Conservative: 8  
Best Local Similarity: 62.22% Mismatches: 9  
Query Match: 15.15% Indels: 0  
Gaps: 4  
US-09-830-972-29\_copy\_990\_1178 (1-189) x US-09-949-016-119336 (1-601)

Qy 71 ArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsn 90  
Db 136 AGGGCTACTTGGAGCTTGAGATCACCTTTCTCAGGAGCAGATTACAGAGTACACGGAC 77  
Qy 91 SerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgLeuPheLeuValAsp 110  
Db 76 TGCCTGCAGTTCTACGTGAACAGCACACTTAAGGAAGCTCCTTCTCTGTGTCAG 17  
Qy 111 AspLeuValAspSer 115  
Db 16 GACCTGGTGGATTCC 2  
RESULT 30  
US-09-949-016-117609/c  
; Sequence 117609, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768

```
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 117609
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-117609

Alignment Scores:
Pred. No.: 2,46e-07 Length: 601
Score: 122.00 Matches: 38
Percent Similarity: 35.19% Conservative: 0
Best Local Similarity: 35.19% Mismatches: 3
Query Match: 13.10% Indels: 67
DB: 4 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-949-016-117609 (1-601)
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHis-----155
DB 505 GCCTCATTTCACTCTCTAGTGTCTCTGTATTATGACGGCATCAGGTAATTTCTTAA 446
QY 155 -----155
DB 445 CTAAGTCTGCTACTTCAGAAATAGACACTCACTATTACATGGGATTACGGATGTATTA 386
QY 155 -----155
DB 385 GTGCCCATTTTCAATGCTCTTACAAAATGAGAAGTGTGATGGTTCTTAAAGCTTTAGCT 326
QY 155 -----155
DB 325 TGACACATAGTAGTGTGTTAATAAGMTCTTTAGCAACGGTAAATAATCTTTTATACCTCT 266
QY 156 ----GlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMe 174
DB 265 CTTTCAGGCACAGATAGATCATTTATCTAGACTTGCAAAATAGAAATGTTAAAGATGCTAT 206
QY 174 tAlaLysIleGlnAlaLysIle 181
DB 205 GGCTAAGTAGTATTAAATATC 184

RESULT 31
US-09-313-294A-703
; Sequence 703, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 703
; LENGTH: 266
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700549677H1
US-09-313-294A-703

Alignment Scores:
Pred. No.: 2.32e-06 Length: 266
Score: 111.00 Matches: 22
Percent Similarity: 65.08% Conservative: 19
Best Local Similarity: 34.92% Mismatches: 20

Query Match: 11.92% Indels: 2
DB: 4 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-313-294A-703 (1-266)
QY 106 LeuPheLeuValAspAspLeuValAspSerLeu-----LysPheAlaValLeuMetTyr 123
DB 71 CTTCTAATTATATGCTCTTATCCCTGTTCTTGTCGCAAAAGGTGATGATGTTTGCG 130
QY 124 ValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAlaLeuLeu 143
DB 131 GTGGTTTCATTCATTGGAATGCTCTTCAATTTCTTACGCTTATTACATTCGTGTAATG 190
QY 144 SerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeu 163
DB 191 CTTTCTCTGTTGTTCCACCACTCTATGAGAAGTACCAGGACCAGGTTGATGAGAAGGTT 250
QY 164 GlyLeuAla 166
DB 251 GGTGTAGCG 259

RESULT 32
US-09-949-016-48087/c
; Sequence 48087, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48087
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-48087

Alignment Scores:
Pred. No.: 0.000157 Length: 601
Score: 102.00 Matches: 21
Percent Similarity: 70.00% Conservative: 7
Best Local Similarity: 52.50% Mismatches: 12
Query Match: 10.96% Indels: 0
DB: 4 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-949-016-48087 (1-601)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
DB 120 ACAGTGGCGGACCTGCTGTACTGGAAGGACACAGGACGTCAGGAGTGGTCTTCACAGGC 61
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 60 CTGATGGTCTCCCTCTCTGCTCTGCTGCACTTAGCATGCTGTCCTGCGCGGCGCACTTG 1

RESULT 33
US-08-905-223-178
; Sequence 178, Application US/08905223
; Patent No. 622029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duclert, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
```

NUMBER OF SEQUENCES: 503  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 501 West Broadway  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-3505  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Win95  
SOFTWARE: Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/905,223  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Israel, Ned A.  
REGISTRATION NUMBER: 29,655  
REFERENCE/DOCKET NUMBER:  
TELEPHONE: (619) 235-8550  
TELEFAX: (619) 235-0176  
INFORMATION FOR SEQ ID NO: 178:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 425 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: DOUBLE  
TOPOLOGY: LINEAR  
MOLECULE TYPE: CDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo Sapiens  
TISSUE TYPE: Brain  
FEATURE:  
NAME/KEY: other  
LOCATION: 73..317  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 97  
OTHER INFORMATION: region 1..245  
OTHER INFORMATION: id HUM506F10B  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 314..376  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 98  
OTHER INFORMATION: region 243..305  
OTHER INFORMATION: id HUM506F10B  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 63..193  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 99  
OTHER INFORMATION: region 1..131  
OTHER INFORMATION: id AA056148  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 314..401  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 95  
OTHER INFORMATION: region 254..341  
OTHER INFORMATION: id AA056148  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 277..317  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 97  
OTHER INFORMATION: region 216..256  
OTHER INFORMATION: id AA056148

OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 397..426  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 96  
OTHER INFORMATION: region 338..367  
OTHER INFORMATION: id AA056148  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 88..189  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 98  
OTHER INFORMATION: region 1..102  
OTHER INFORMATION: id HSC1FF051  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 314..401  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 96  
OTHER INFORMATION: region 230..317  
OTHER INFORMATION: id HSC1FF051  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 187..271  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 95  
OTHER INFORMATION: region 101..185  
OTHER INFORMATION: id HSC1FF051  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 269..317  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 93  
OTHER INFORMATION: region 184..232  
OTHER INFORMATION: id HSC1FF051  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 397..426  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 96  
OTHER INFORMATION: region 314..343  
OTHER INFORMATION: id HSC1FF051  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 87..200  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 92  
OTHER INFORMATION: region 1..114  
OTHER INFORMATION: id HSC16E081  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 314..401  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 96  
OTHER INFORMATION: region 231..318  
OTHER INFORMATION: id HSC16E081  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 199..275  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 94  
OTHER INFORMATION: region 114..190  
OTHER INFORMATION: id HSC16E081  
OTHER INFORMATION: est

```
FEATURE:
NAME/KEY: other
LOCATION: 269..317
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: identity 91
OTHER INFORMATION: region 185..233
OTHER INFORMATION: id HSC16E081
FEATURE:
NAME/KEY: other
LOCATION: 397..426
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: identity 96
OTHER INFORMATION: region 315..344
OTHER INFORMATION: id HSC16E081
FEATURE:
NAME/KEY: other
LOCATION: 85..186
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: identity 99
OTHER INFORMATION: region 24..125
OTHER INFORMATION: id AAL57365
OTHER INFORMATION: est
FEATURE:
NAME/KEY: other
LOCATION: 183..263
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: identity 90
OTHER INFORMATION: region 123..203
OTHER INFORMATION: id AAL57365
OTHER INFORMATION: est
FEATURE:
NAME/KEY: other
LOCATION: 337..401
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: identity 95
OTHER INFORMATION: region 278..342
OTHER INFORMATION: id AAL57365
OTHER INFORMATION: est
FEATURE:
NAME/KEY: other
LOCATION: 273..326
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: identity 90
OTHER INFORMATION: region 213..266
OTHER INFORMATION: id AAL57365
```

```
Alignment Scores:
Pred. No.: 0.000172 Length: 425
Score: 100.00 Matches: 20
Percent Similarity: 80.00% Conservative: 8
Best Local Similarity: 57.14% Mismatches: 7
Query Match: 10.74% Indels: 1
DB: 3 Gaps: 0
```

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-08-905-223-178 (1-425)

```
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
DB 321 GCGTGCAGCACTGATTTCTCGAGAGATGTGAGAGACTGGGTTTGTCTTTGGCACC 380
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSer 35
DB 381 ACGCTGATCATGCTGCTTTC-CTGGCAGCTTTCAGTGTGCATCAGT 424
```

## RESULT 34

```
US-08-956-171E-407/c
Sequence 407, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
```

```
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannion
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 407:
SEQUENCE CHARACTERISTICS:
LENGTH: 1722 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 407:
US-08-956-171E-407
```

```
Alignment Scores:
Pred. No.: 0.00821 Length: 1722
Score: 95.00 Matches: 36
Percent Similarity: 48.87% Conservative: 29
Best Local Similarity: 27.07% Mismatches: 42
Query Match: 10.20% Indels: 26
DB: 4 Gaps: 6
```

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-08-956-171E-407 (1-1722)

```
QY 26 LeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle----- 40
DB 1067 TTGAGTTTAATTGATATATAATCTTAATCTTAATGTAATGTCACGGGTTTGTCTTT 1008
QY 41 -----AlaLeuAlaLeuLeuSerValThr-----IleSerPhe 51
DB 1007 AACTCTGCAGCTGTAAAGCCGATGCATTAAACAATATGACAGATATTATCGTTTCTTTA 948
QY 52 ArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArg 71
DB 947 GCTGTTATTATTGGATTGAAATTTCAATTAAACCTGCCGATCGAAATCATCCTTAT--- 891
QY 72 AlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSer 91
DB 890 GCCCATTTGAAGTCTGAAATATTCTTCA-----TTATTGCTGTCATTGTCATTATG 837
QY 92 AlaLeuGlyHisValAsnCysThrIleLysGluLeuArgArgLeuValAspAsp 111
DB 836 TTTGTAGGT---ATCCAAGTAGTTATTCAAAATGCACCTCGTTTGTTCAAAGAAGATGAC 780
```

QY 112 LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyValGlyAlaLeu 131  
Db 779 GTTGACCTAAC-----GCAATAACAATATTCTGTCAGCTTA 744  
QY 132 PheAsnGlyLeuThrLeuLeuLeuLeuLeuLeuSer 144  
Db 743 ATCAGTGGTCTTGTAAATGTTGATTGTTATTTGTCAGTCAAT 705

RESULT 35  
US-08-781-986A-407/c  
; Sequence 407, Application US/08781986A  
; Patent No. 6737248  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 5255  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/781.986A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Benson, Bob  
; REGISTRATION NUMBER: 30,446  
; REFERENCE/DOCKET NUMBER: PB248PP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 407:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1722 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
US-08-781-986A-407

Alignment Scores:  
Pred. No.: 0.00821 Length: 1722  
Score: 95.00 Matches: 36  
Percent Similarity: 48.87% Conservative: 29  
Best Local Similarity: 27.07% Mismatches: 42  
Query Match: 10.20% Indels: 26  
DB: 4 Gaps: 6

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-08-781-986A-407 (1-1722)

QY 26 LeuSerLeuThrValPheSerIleValSerValThrAlaTyIle----- 40  
Db 1067 TTGAGTTAATGTATATATATATCTTCTATTGTTAGTAGTACGGGTTTGTCTTT 1008  
QY 41 -----AlaLeuAlaLeuSerValThr-----IleSerPhe 51  
Db 1007 AACTCTGACGCTGTAAAGCCGATGCTATTAAACAATATGACAGATATTATCTTCTTTA 948  
QY 52 ArgIleTyLysGlyValIleGlnAlaLeuGlnLysSerAspGluGlyHisPropPheArg 71  
Db 947 GCTGTTATTATTTGATTGAAATTTCAATTAAACCTGCCGATCGAAATCATCCTTAT--- 891  
QY 72 AlaTyLysGluSerGluValAlaIleSerGluGluValGlnLysTySerAsnSer 91

Db 890 GGCCATTGGAAGTCTGAAATATTCTTCA-----TTATTGGTGTCAATTTGTCATTATG 837  
QY 92 AlaLeuGlyHisValAsnCyThrIleLysGluLeuArgArgLeuPheLeuValAspAsp 111  
Db 836 TTTGTAGGT---ATCCAAGTAGTTATTCAAATGCACCTCGTTTGTTCACAAAGAGATGAC 780  
QY 112 LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyValGlyAlaLeu 131  
Db 779 GTTGACCTAAC-----GCAATAACAATATTCTGTCAGCTTA 744  
QY 132 PheAsnGlyLeuThrLeuLeuLeuLeuLeuLeuSer 144  
Db 743 ATCAGTGGTCTTGTAAATGTTGATTGTTATTTGTCAGTCAAT 705

RESULT 36  
US-08-487-596-7  
; Sequence 7, Application US/08487596  
; Patent No. 6440681  
; GENERAL INFORMATION:  
; APPLICANT: Elliot, Kathryn J.  
; APPLICANT: Ellis, Steven B.  
; APPLICANT: Harpold, Michael M.  
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND  
; TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL  
; TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,596  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO US94/02447  
; FILING DATE: 08-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/149,503  
; FILING DATE: 08-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/028,031  
; FILING DATE: 08-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/938,154  
; FILING DATE: 30-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/504,455  
; FILING DATE: 03-APR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L.  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 6362-9951  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-238-0999  
; TELEFAX: 619-238-0062  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1828 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cdna  
; FEATURE:

```
; NAME/KEY: CDS
; LOCATION: 155...1561
; OTHER INFORMATION: /product= "ALPHA-5 SUBUNIT"
; US-08-487-596-7

Alignment Scores:
Pred. No.: 0.0627 Length: 1828
Score: 89.00 Matches: 42
Percent Similarity: 38.54% Conservatve: 32
Best Local Similarity: 21.88% Mismatches: 61
Query Match: 9.56% Indels: 58
DB: 3 Gaps: 5

US-09-830-972-29_COPY_990_1178 (1-189) x US-08-487-596-7 (1-1828)

QY 24 LeuLeuLeuSerLeuThrValPheSerIleVal----- 34
Db 1016 GTACTTGTCTCTTGAAGAGATATTTCTTCTGTTATTGAAGAGATCATCATCTTCA 1075

QY 35 -----SerValThrAlaTyrlleAlaLeuAlaLeuSerValThrIleSer 50
Db 1076 AAAGTCATACCTTAATTCGAGAGATCTCGTATTATTCATCATGATTTTGTGACACTGTCA 1135

QY 51 PheArgIleTyrlsGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPhe 70
Db 1136 ATTATGTTAACCGTCTTCGTCATCAACATTCATCATCTCGTTCCTCAACACATAATGCC 1195

QY 71 ArgAlaTyrlLeu----- 74
Db 1196 ATGGCGCCTTTGGTCCGCAAGATATTTCTTCACAGCTTCCCAAACTGTTTGCATGAGA 1255

QY 75 -----GluSerGlu-ValAlaIleSerGluGl 83
Db 1256 AGTCATGTAGACAGGTAATTCATCAGAAAGAGAACTGAGAGTGTGTGACCAAAA 1315

QY 83 uLeuValGlnLysTyrlSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLe 103
Db 1316 TCTTCAGAAACACATG-GAAGTCGCTCAATTCCTATTCGTCATCATTACAGACACAT 1374

QY 103 uArgArgLeuPheLeuValAspLeuValAspSerLeuLysPhe----- 118
Db 1375 CATGAAGAAATGATGTCGTCGAGGTGTGTAAGATTGGAATTCATGACCCAGGTCT 1434

QY 119 ----AlaValLeuMetTrpValPheThrTyrlValGlyAlaLeuPheAsnGlyLeuThrIle 137
Db 1435 TCATCGGATGTTTCTGTCGACTTTTCTTTTCGTTCA----- 1471

QY 137 uLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrlGluArgHisGlnAl 157
Db 1472 ----ATGTTGGATCTCTGGGCTTTT---GTTCCTGTTATTATTAATGGCAATAT 1524

QY 157 aGlnIleAspHisTyrlLeuGlyLeuAlaAsnLys 168
Db 1525 ATTAATACCAAGTTTCATATTGGAATGCAATTAAG 1558

RESULT 37
US-08-660-451A-7
; Sequence 7, Application US/08660451A
; Patent No. 6524789
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
```





QY 147 SerValProValIleTyrGluArgHisGln-----AlaGlnIleAspHisTyr 162  
Db 2231 ATTCTGGTGCAGCCCTACAGAGAGATGAACGCTTTCAAGGGGAACCCCTGGATCAGCAG 2290  
QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMet 174  
Db 2291 CTGGCAGGGTCTTAGGAGAAGTGGCTCCAGATG 2326

## RESULT 40

US-09-814-915A-100  
; Sequence 100, Application US/09814915A  
; Patent No. 6750015  
; GENERAL INFORMATION:  
; APPLICANT: Horwitz, Kathryn  
; APPLICANT: Richer, Jennifer  
; TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Relat  
; TITLE OF INVENTION: Theteto  
; FILE REFERENCE: 2848-39  
; CURRENT APPLICATION NUMBER: US/09/814,915A  
; CURRENT FILING DATE: 2002-03-21  
; PRIOR APPLICATION NUMBER: 60/214,870  
; PRIOR FILING DATE: 2000-06-28  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 100  
; LENGTH: 4673  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-814-915A-100

Alignment Scores:  
Pred. No.: 0.334 Length: 4673  
Score: 88.50 Matches: 39  
Percent Similarity: 42.11% Conservative: 25  
Best Local Similarity: 25.66% Mismatches: 51  
Query Match: 9.51% Indels: 37  
DB: 4 Gaps: 7

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-814-915A-100 (1-4673)

QY 46 SerValIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAsp 65  
Db 1915 AATCTGACCATTTCTCTCACTGCTGAACGAGTATTGAAGTAACTAATCGTGAAGT 1974  
QY 66 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuVal 85  
Db 1975 GACAGTGATGCTCTC-----ACCGTTGTAATTAGCTATGCAATCATG 2016  
QY 86 GlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgArg 105  
Db 2017 TTTCATATATTTCCCTAGCCCTTGGGGCAC-----ATCAAAAGCTGTCGAGG 2064  
QY 106 LeuPheLeuValAspAsp-----LeuValAspSerLeu 116  
Db 2065 CTT---CTGGTGATTCGAGGTCTCACTAGGCATCGGGGCATCTTGATCGTGCAGC 2121  
QY 117 LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr 136  
Db 2122 TCGGTGGCTGCTCCCTTGGGTGCTTCAGCTACATTGGGTG-----CCCTTGACC 2172  
QY 137 LeuLeuIleLeuAlaLeuIle-----SerLeuPhe 146  
Db 2173 CTCATTGTGATTGAAGTCATCCCGTTCCTGGTCTGGTGTGGAGTGGACAACATCTTC 2232  
QY 147 SerValProValIleTyrGluArgHisGln-----AlaGlnIleAspHisTyr 162  
Db 2233 ATTCTGGTGCAGCCCTACAGAGAGATGAACGCTTTCAAGGGGAACCCCTGGATCAGCAG 2292  
QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMet 174  
Db 2293 CTGGCAGGGTCTTAGGAGAAGTGGCTCCAGATG 2328

## RESULT 41

US-09-949-016-5725  
; Sequence 5725, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5725  
; LENGTH: 1273  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-5725

Alignment Scores:  
Pred. No.: 0.0484 Length: 1273  
Score: 88.00 Matches: 42  
Percent Similarity: 38.54% Conservative: 32  
Best Local Similarity: 21.88% Mismatches: 61  
Query Match: 9.45% Indels: 58  
DB: 4 Gaps: 5

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-5725 (1-1273)

QY 24 LeuLeuLeuSerLeuThrValPheSerIleVal----- 34  
Db 605 GTACTGTGCTCTTGACTGCTCTTCTCTGTTATTGAAGAGATCATCATCTTCA 664  
QY 35 -----SerValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSer 50  
Db 665 AAGTCATACCTCTAATTGGAGATATCTGTATTACCATGATTTTGTGACACTGTCA 724  
QY 51 PheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPhe 70  
Db 725 ATTATGGTAACCGTCTTCCTATCAACATTCATCATCGTCTCTCTCAACACATATGCC 784  
QY 71 ArgAlaTyrLeu----- 74  
Db 785 ATGGCGCCTTTGGTCGCAAGATATTCTTCAACGCTTCCCAAACTGCTTTGCATGAGA 844  
QY 75 -----GluSerGlu-ValAlaIleSerGlu 83  
Db 845 AGTCATGTAGACAGGTACTTCTCAGAAAGAGAACTGAGAGTGGTAGGCCAAAA 904  
QY 83 uLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLe 103  
Db 905 TCTTCTAGAAACACATG-GAAGCTCGCTCGATTCATTCTATTCGTACATTACAGACACAT 963  
QY 103 uArgArgLeuPheLeuValAspLeuValAspSerLeuLysPhe----- 118  
Db 964 CATGAAGGAAATGATGTCGAGGTGTTGAAGATTGGAAATTCATAGCCAGGTCT 1023  
QY 119 ---AlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLe 137  
Db 1024 TGATCGGATGTTTCTGTGGACTTTCTTTCTGTTCA----- 1060  
QY 137 uLeuLeuLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAl 157  
Db 1061 ----ATTGTTGATCTCTGGGCTTTT---GTTCTGTTATTATAATGGCAATAT 1113  
QY 157 aGlnIleAspHisTyrLeuGlyLeuAlaAsnLys 168  
Db 1114 ATTAATACCAGTTTCATATTGGAAATGCAAAATAG 1147

RESULT 42  
US-09-134-000C-2072  
; Sequence 2072, Application US/09134000C  
; Patent No. 6617156  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; FILE REFERENCE: 032796-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; PRIOR FILING DATE: 1997-08-15  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2072  
; LENGTH: 1779  
; TYPE: DNA  
; ORGANISM: Enterococcus faecalis  
US-09-134-000C-2072

Alignment Scores:  
Pred. No.: 0.0975 Length: 1779  
Score: 87.50 Matches: 48  
Percent Similarity: 38.53% Conservative: 41  
Best Local Similarity: 20.78% Mismatches: 65  
Query Match: 9.40% Indels: 77  
DB: 4 Gaps: 10

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-134-000C-2072 (1-1779)

Qy 7 TyrTrpArgAspIleLysValThrGlyValValPheGlyAlaSerLeuPheLeuLeu 26  
Db 133 TTCTGGAAAACAGTGAACGT-----TTATTTCGATACATG 168

Qy 27 SerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuLeuSer 46  
Db 169 TCTAACCAATGCTGCTCAATTATTGCTGTC-----TTAGTATTAGCAATTCGACGC 219

Qy 47 ValThrIleSerPheArg-----IleTyrLys 55  
Db 220 GTCTGTTTCCAAATTCAAACACCAAAAGTATTAGCACAGGCAACCAACTGAAATTTTAA 279

Qy 56 GlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAla----- 72  
Db 280 GCGGTCATGAAGAGCGCTGCTGAAATGAAGAAACAAGGCTTAAATAACATCTTTTCCAAAT 339

Qy 73 -----TyrLeuGluSerGlu 77  
Db 340 GATTTTGACAAATTTGGTCAATTTTATTAATTTGTTATTGTCATGCTATTCTTCTGCT 399

Qy 78 Val-----Ala 79  
Db 400 GTCTTTAATTTCTTGACGAAGTAAATTATGACAGCTGTTTCACAGCGAAGTATTATGAA 459

Qy 80 IleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGly-----His 95  
Db 460 TTACGTCGAAGAATTAGAACGCAAAATGAACAAAGTTCCCAATTTCTATTATGATATTCT 519

Qy 96 ValAsnCysThrIleLysGluLeuArgLeuPheLeuValAspLeuValAspSer 115  
Db 520 AGTAATGGGACATTATGTCAC---CGGCAATTAAACGACATGGATTAATTTCCGAGTACT 576

Qy 116 LeuLys-----PheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPhe 132  
Db 577 TTACAGCAAACTTAAACCAATTAATACCAAGTATCGTGACATTTGTGGGTGACTTTGG 636

Qy 133 AsnGlyLeuThrLeu---LeuIleLeuAlaIleSerLeuPheSerValproValle 151  
Db 637 ATGATGTCGACCATTAGCTGGCAGTTAACTAATTTGCTTTAGCAACAGTCCCAATTAGT 696

Qy 152 Tyr-----GluArgHisGlnAlaGlnIleAspHis 161

Db 697 TTAATTGTTGTGATGTTGTGCGCTCGCTCGCAAAACATTTTGGCGCTCAACAAAA 756  
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAsp 172  
Db 757 AGCTTAGGATTATTGAATAACCAAGTCGAAGAA 789

RESULT 43  
US-09-134-001C-2168  
; Sequence 2168, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 2168  
; LENGTH: 3156  
; TYPE: DNA  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-2168

Alignment Scores:  
Pred. No.: 0.245 Length: 3156  
Score: 87.50 Matches: 44  
Percent Similarity: 41.15% Conservative: 35  
Best Local Similarity: 22.92% Mismatches: 68  
Query Match: 9.40% Indels: 45  
DB: 3 Gaps: 8

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-134-001C-2168 (1-3156)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 1138 ATCGTTATTCCTCTGTTTTTAAAGAAATATAAGAACTACAGCTATT----- 1182

Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerVal----- 36  
Db 1183 -----TCATTTGTATCTATACCAATGTCATATTA 1212

Qy 37 ThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGly 56  
Db 1213 ATTCGCTCATAGCATTTAAATAATTAAAGCAACGATATCATTAATAATTCTTACTTTAGTGCA 1272

Qy 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76  
Db 1273 TTAACGGTTGCAATCGGCGCA-----GTTATAGATGAT 1305

Qy 77 GluValAlaIleSerGluGluLeuValGlnLysTyrSer-----AsnSerAlaLeuGly 94  
Db 1306 TCTATAGTTGCTGTTGAGATATATTTAGAGATATCTGATCCGAATGCAAGCTCAAA 1365

Qy 95 HisValAsnCysThrIleLysGluLeuArgArgLeuPhe-----LeuValAspAsp 111  
Db 1366 GGTCAAAATTTAATTATAAGCGCTACTAGAGAACTATTAAACCTATTATGTCATCGACC 1425

Qy 112 LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeu 131  
Db 1426 CTTGTTACTATAGTAGTGTGTTTTTACCACCTAGTGTGTCAGGTTCTAGTAGGTAATG 1485

Qy 132 PheAsn-----GlyLeuThrLeuLeuIleLeuAla-----LeuIleSerLeu 145  
Db 1486 TTTAGACCAATTCGCTAGCAATTTAGTTTATTTAGTTTACTTACTTCTTCTGATTT 1545

Qy 146 PheSerValproValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeu 165  
Db -----





```
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-149

Alignment Scores:
Pred. No.: 5,96 Length: 12566
Score: 84,50 Matches: 40
Percent Similarity: 46,39% Conservative: 37
Best Local Similarity: 24,10% Mismatches: 58
Query Match: 3,08% Indels: 31
DB: Gaps: 8

US-09-830-972-29_COPY_990_1178 (1-189) x US-08-961-527-149 (1-12566)
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 344 TCGATAGTCTTACTATTGACGGCCACCTGATGGTCTACTGAGTTTAGCTATTTTCG 403
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIlyGlyValIleGlnAla 60
Db 404 ---CTGACCTTTATGAGTCTGACCTGATTTATCGGATC---AAATCCCTTCGTCAGGCA 457
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 458 GGGATTCGGCTTAATAGCTGGT-----GAGAGCTTGTTCGAGTT 496
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 497 GCT-----CTCAGACGACGGTGA 514
QY 101 LysGluLeuArgGluPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 515 GAAGATGTGAGAGCTT---ATCTGCTCAGTCTGCTGTATCCAGTCTTTTGGGATTCGGG 571
QY 121 LeuMetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db 572 ATTCCTCG-----TATCAAGGTGCTTGTATTATGCAACGGTGCACCTGGTCATC 622
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 623 ATTCCTCTTCTACTTTATGATGATGACCTTGGCAGGAGTTTCTACCTTACTTAAGTGTGCTC 682
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 683 TATCTACTTGGTTTACAGAAATAGTCTGGTGGATCTA-----TTGAAAGGGAAA 733
QY 181 IleProGlyLeuLysArg 186
Db 734 CTCCT---CTCAACGT 748

RESULT 48
US-08-961-527-104
; Sequence 104, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:

; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6735 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-104

Alignment Scores:
Pred. No.: 2,57 Length: 6735
Score: 84,00 Matches: 54
Percent Similarity: 46,49% Conservative: 32
Best Local Similarity: 29,19% Mismatches: 66
Query Match: 9,02% Indels: 33
DB: Gaps: 11

US-09-830-972-29_COPY_990_1178 (1-189) x US-08-961-527-104 (1-6735)
QY 11 IleLysLysThrGlyValValPhe-----GlyAlaSerLeuPheLeuLeu 25
Db 2885 ATTCATCTACAGGAGTACTTCCCTTCCTTATCCAGGGTGGAAATAGTCTTCTAGTC 2944
QY 26 LeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLeu 45
Db 2945 TTATCAGTGGCAGTAGCTTCTCTAAATATTGATGCAGTGAACGCGCTAAATTCG 3004
QY 46 -----SerValThrIle-SerPheArgIleTyrIlyGcl 56
Db 3005 TACCAGAGATTGGAAATCAACCAATGACCTTCTGTGAAGT---AGGATAAGAAAGG 3061
QY 56 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSe 76
Db 3062 ATAGTTTATGCTCTCTCAAAAATTA---GAAAATATAGTATAAAGTGTGCAAGA 3118
QY 76 rGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVa 96
Db 3119 AGAAGTCTTGATTTCTAACAGAAATTACTGGAAGATATTACTAAAAATATGCTTGC 3178
QY 96 lAsnCys---ThrIleLysGluLeuArgArgLeuPheLeuValAspAsp----- 111
Db 3179 GACCTTTGAAAAAATAATACAGTTGAAAGAAATTATCAACGAGGAGAGATTATCAAGG 3238
QY 112 -----LeuValAspSerLeuLysPheAlaValLeuMetTyrValPheThrTyrValG 129
Db 3239 AAACCGTCTAGTACTAGTCTTATCAATGATCAATGGTCTATATTTCACGCTAT----- 3293
QY 129 yAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValPr 149
Db 3294 -----TTCTCTATCTCTGCTCTTTTGATT-----AATATTTCa---GAGGATG 3337
QY 149 oValIleTyrGlu---ArgHisGlnAlaGlnIleAspHis---TyrLeuGlyLeuAla 167
Db 3338 TTAGCTTATGAATCAATCATCAAAATAATATTGATCAGGACTATTTAGTAAATATTC 3397
QY 167 nLysAsnValLys 171
Db 3398 TACAACGATTAA 3410

RESULT 49
US-09-557-884-1
; Sequence 1, Application US/09557884
; Patent No. 6506581
```

GENERAL INFORMATION:  
APPLICANT: Fleischmann et al.  
TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments Thereof, and Uses Thereof  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3 1/2 inch diskette  
COMPUTER: Dell Pentium  
OPERATING SYSTEM: MS DOS v6.22  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/557,884  
FILING DATE: 25-Apr-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/476,102  
FILING DATE: JUN-5-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Michelle S. Marks  
REGISTRATION NUMBER: 41,971  
REFERENCE/DOCKET NUMBER: PB186P3  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1830121 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-557-884-1  
Alignment Scores:  
Pred. No.: 2.12e+04 Length: 1830121  
Score: 84.00 Matches: 62  
Percent Similarity: 33.71% Conservative: 28  
Best Local Similarity: 23.22% Mismatches: 80  
Query Match: 9.02% Indels: 97  
DB: 4 Gaps: 13  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-557-884-1 (1-1830121)  
Qy 6 LeuTyrTrp-----ArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPhe 23  
Db 37676 CTTATTGGATTTTACAAACGCTAGCCATCCCTCAGTCGTCTTTAGTTTGGCATTTT 37735  
Qy 24 LeuLeuLeuSerLeuThr----- 29  
Db 37736 CTTTGGTGGCTTTTACCAATGGGAAACAAATTTTGAGTTTGCAGCGGTATCTT 37795  
Qy 30 -----ValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu 44  
Db 37796 TCACCTAAAGTAGCATTAACCTATCTTCTCTCTTCTGCTTATTGTTGCAATGACATTA 37855  
Qy 45 LeuSerValThrIleSerPhe-----ArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 37856 CTTAGCGTACGTATCAGCGCTTGTAATTTCTGAGTGTATATAAAATATGTATACCTCATTT 37915  
Qy 62 GlnLysSerAspGluGlyHisProPhe----- 70  
Db 37916 CAAGAATTTATGAA---CATGTATTTTGGCAACAAATGGGCTTATTCTGGTCAATGCCA 37972  
Qy 71 -----ArgAlaTyrLeuGluSerGluValAlaIle--- 80  
Db 37973 GCAAAGTTCTGTTTCAGCAGCATTTAGTAAGCTATTATTTAGAGCAACGTTTCGTCAATCAAC 38032  
Qy 81 -----SerGluGluLeuValGlnLys-----Tyr 88  
Db 38033 TGGATTGAATGGCTTACGAGCAGCTTGTTAATAATGATGGCACATCGCGCCTATTATAC 38092  
Qy 89 SerAsnSerAlaLeuGlyHis-----Val 96  
Db 38093 AAAACACAGTATTATCAGAAAAATCTTGATAACCCCGATCAACGATTATTCACAAGATGTG 38152  
Qy 97 AsnCysThrIleLysGluLeuArgArgLeuPhe-----LeuValAspAspLeuValAsp 114  
Db 38153 CAATCTTATGTAAACACACGCTTTCTTTAAGCACTGGCGTCATTGATGCGGTACACCTCG 38212  
Qy 115 SerLeuLysPheAlaValLeuMetTrp----- 123  
Db 38213 ATGATCTCTTACACGATTTTGTATGGGATTAGCCGGTCCAAATGATAGTCTTGGTGTGA 38272  
Qy 124 -----ValPheThrTyrValGlyAlaLeuPheAsnGly 134  
Db 38273 GAAATTCGCATATGATGTTATTTTGTATGTTTGTATGTC-----ATTTTCAACAACC 38326  
Qy 135 LeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArg 154  
Db 38327 CTCATCGCATTTCTGGCTCGGTGCGC---CCATTAATCTCATTTTATTAATGAACGC 38383  
Qy 155 HisGlnAlaGlnIleAspHisTyr-LeuGlyLeuAlaAsnLysAsnValLysAspAlaMe 174  
Db 38384 CTAACGCAAACTAT---CGTTATCTTAAATTCGCATTAAGAATATGCTGAAGACATT 38440  
Qy 174 tAlaLysIleGlnAlaLys 180  
Db 38441 GCTTTTATGCGCGGAAA 38459  
RESULT 50  
US-09-643-990A-1  
; Sequence 1, Application US/09643990A  
; Patent No. 6528289  
; GENERAL INFORMATION:  
; APPLICANT: Robert D. Fleischmann  
; Mark D. Adams  
; Owen White  
; Hamilton O. Smith  
; J. Craig Venter  
TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments Thereof, and Uses Thereof  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville,  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3 1/2 inch diskette  
COMPUTER: Dell Pentium  
OPERATING SYSTEM: MS DOS v6.22  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/643,990A  
FILING DATE: 23-Aug-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/487,429  
FILING DATE: 1995-06-07  
APPLICATION NUMBER: 08/426,787  
FILING DATE: 1995-04-21  
ATTORNEY/AGENT INFORMATION:  
NAME: Kenley K. Hoover  
REGISTRATION NUMBER: 40,302  
REFERENCE/DOCKET NUMBER: PB186P1C1

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-610-5790  
TELEFAX: 310-309-8439  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1830121 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-643-990A-1

## Alignment Scores:

Pred. No.: 2,12e+04 Length: 1830121  
Score: 84.00 Matches: 62  
Percent Similarity: 33.71% Conservative: 28  
Best Local Similarity: 23.22% Mismatches: 80  
Query Match: 9.02% Indels: 97  
DB: 4 Gaps: 13

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-643-990A-1 (1-1830121)

QY 6 LeuTyrTrp-----ArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPhe 23  
DB 37676 CTTATTGGATTTCACAGCGTAGCCATCAGTCAGTCGCTTAGTTGGCATTTT 37735  
QY 24 LeuLeuSerLeuThr----- 29  
DB 37736 CTTTGGTGGTTTACCCAAAGTGGGAAACAAATTTTGGATGTTTGCAGCGGTTATCTT 37795  
QY 30 -----ValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu 44  
DB 37796 TCACCTAAACGTAGCATTAACCTATCTTATCTTCTGCTTATGTTGCAATGACATTA 37855  
QY 45 LeuSerValThrIleSerPhe-----ArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 37856 CTTAGCGTAGTATCAGCTTGTAAATTCGTAGTGTATATAAATATGATATACCTCATG 37915  
QY 62 GlnLysSerAspGluGlyHisProPhe----- 70  
DB 37916 CAAGATTTTAATGAA---CATGTATTTTGGCAAAATGGCTTATTCTCGTCATCGCA 37972  
QY 71 -----ArgAlaTyrLeuGluSerGluValAlaIle----- 80  
DB 37973 GCAAGTTCTGTTTACGACGATTTAGTAAGCTATTTATTAGAGCAACGTTTCGTCAAC 38032  
QY 81 -----SerGluGluLeuValGlnLys-----Tyr 88  
DB 38033 TGGATTGAATGGCTTAACGAGCAGCTTGTATTAATATGATGGCACATCGCGCTATTAC 38092  
QY 89 SerAsnSerAlaLeuGlyHis-----Val 96  
DB 38093 AAAACACAGATTATTATCAGAAATCTTGTAAACCCGATCAAGTATTCAACAGATGTG 38152  
QY 97 AsnCysThrIleLysGluLeuArgLeuPhe-----LeuValAspAspLeuValAsp 114  
DB 38153 CAATCTTATGTAAAAACACGCTTTCTTTAAGCAGCTGGCGCTCATGTCGCTCACCTCG 38212  
QY 115 SerLeuLysPheAlaValLeuMetTrp----- 123  
DB 38213 ATGATCTCTACAGATTGTTGATGGGATAGCCGCTCCATGATGATGTTGGTGTGTA 38272  
QY 124 -----ValPheThrTyrValGlyAlaLeuPheAsnGly 134  
DB 38273 GAAATTCGCATATGATGTTATTTTGTGTTGTTATGTC-----ATTTCACAACC 38326  
QY 135 LeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArg 154  
DB 38327 CTCATCGCATTCGCTCGCTGCGC---CCATTAACTCTCAATTAATTTTATTAATGAACGC 38383  
QY 155 HisGlnAlaGlnIleAspHisTyr-LeuGlyLeuAlaAsnLysAsnValLysAspAlaMe 174  
DB 38384 CTAAACGCAAACTAT---CGTTATTTTAAATTCGCATTAAAGAAATATGCTGAACGATT 38440

QY 174 tAlaLysIleGlnAlaLys 180  
DB 38441 GCTTTTATGACGGCGAAA 38459

## RESULT 51

US-09-543-681A-2003  
Sequence 2003, Application US/09543681A  
Patent No. 6605709  
GENERAL INFORMATION:

APPLICANT: GARY BRETON  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
FILE REFERENCE: 2709.1002-001  
CURRENT APPLICATION NUMBER: US/09/543,681A  
CURRENT FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: US 60/128,706  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 8344  
SEQ ID NO 2003  
LENGTH: 843  
TYPE: DNA  
ORGANISM: Proteus mirabilis  
US-09-543-681A-2003

## Alignment Scores:

Pred. No.: 0.107 Length: 843  
Score: 83.50 Matches: 38  
Percent Similarity: 38.71% Conservative: 34  
Best Local Similarity: 20.43% Mismatches: 68  
Query Match: 8.97% Indels: 46  
DB: 4 Gaps: 6

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-543-681A-2003 (1-843)

QY 2 ValValAspLeuLeuTyr---TrpArgAspIleLysLysThr----- 14  
DB 58 GTGGTAGGATCATTTTATGATGG-----ATPAAACGCTCTCTACCCCTAAACAGT 111  
QY 15 -----GlyValValPheGlyAlaSerLeuPheLeuLeuSerLeu 28  
DB 112 ATGAAATATCTCTGGGAGGAGTAAATAGTAGGAATACTACTCTCTATTCTTTTAGCTCT 171  
QY 29 ThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuSerValThr 48  
DB 172 AGCATTTATGGGTATTTAGTCTCTTAGAAGATATCTGCAATCTCTGTTATGTTATG 231  
QY 49 IleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln---LysSerAspGluGly 67  
DB 232 ATGGAATCATTCCTGCTGCTTAAATTTTTCAGATGGTCTATTGGATGAACAACAGT 291  
QY 68 HisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLys 87  
DB 292 AATCCTAAAGCAATATCGAAAC-----GAATTGACACAAAA 333  
QY 88 TyrSerAsnSerAlaLeu----- 93  
DB 334 ACGCAACAAAGTGTCTGGGGGATTTTACTGATCATCGCCATTCGCCATTCGGAGAA 393  
QY 94 -----GlyHisValAsnCysThrIleLysGluLeuArg 104  
DB 394 GCGCAGGAGTGGTGTGTTTCTCATCAAGCCATATTATGGCTCTCACAGCAAAACCGG 453  
QY 105 ArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpVal 124  
DB 454 TTGCTCTTCTTGAAGTATTCATTCGCTTATTCGCTTATTCAGTGGGACTAATCTATGTTA 513  
QY 125 PheThrTyrValGlyAlaLeu-PheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIle 144  
DB 514 TTTTGTCTAACATAAAATGATTTCTGGCGTAAATTTCTTTGTTATTACCGGATTTT 573  
QY 144 rLeuPheSerValPro 149  
|||||



```
Db 574 CTGCTTTTCTCGCG 589
RESULT 52
US-09-785-381-4
; Sequence 4, Application US/09785381
; Patent No. 6602992
; GENERAL INFORMATION:
; APPLICANT: DALLOS, Peter
; APPLICANT: ZHENG, Jing
; APPLICANT: MADISON, Laird
; TITLE OF INVENTION: A MAMMALIAN PRESTIN
; FILE REFERENCE: 0290-3701
; CURRENT APPLICATION NUMBER: US/09/785,381
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 60/183,461
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 2441
; TYPE: DNA
; ORGANISM: Mus sp.
US-09-785-381-4
Alignment Scores:
Pred. No.: 0.694 Length: 2441
Score: 83.00 Matches: 63
Percent Similarity: 39.08% Conservative: 39
Best Local Similarity: 24.14% Mismatches: 67
Query Match: 8.92% Indels: 92
DB: 4 Gaps: 14
US-09-830-972-29_COPY_990_1178 (1-189) x US-09-785-381-4 (1-2441)
Qy 3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22
Db 1074 ATTCTCTAGAGTTCTTTGCTGTGTGAGTGGGACTGGCAITTTCTGCAGGATTTAAACCTA 1133
Qy 23 PheLeuLeuSerLeuThrVal----- 30
Db 1134 CATGAGTCTCAGTGTTGGATGCTTGGAACTTCTCTGGGGCTACTTCTCCCGGCC 1193
Qy 31 -----PheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu 44
Db 1194 AACCCAGACACAGCGCTTCCACTGTGTGTGTGGACGCC---ATTGCCATGCCATC 1250
Qy 45 Leu-----SerValThrIleSerPheArg----- 52
Db 1251 GTTGGATTTTCAGTGACGATCTCCATGGCCAAACCTTGGCAAAATAGCATGGCTACCAG 1310
Qy 53 -----IleTyrLysGlyValIleGlnAlaIleGlnLysSerAsp 65
Db 1311 GTTGATGCCAATCAGAGCTCATTTGCCCTTGGGATATGCAACTCCATT----- 1358
Qy 66 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluLeuVal 85
Db 1359 ---GGATCTCTCTCCAAACCTTCTCGATTCC---TGCTCTGTGTCTGAGGCTTGT 1412
Qy 86 GlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCys-----ThrIleLysGluLeu 103
Db 1413 CAGGAAGGAATGGAGGGAACACAGCTTGCAGGTTGTTGGCTCGTTCGTTGATCTG 1472
Qy 104 ArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu----- 121
Db 1473 TTGTCATATTAGCCACCGGATTCCTCTTTCAGTCGTTTACCCAGGCTGCTCTTCCGCC 1532
Qy 121 ----- 121
Db 1533 ATTGTATCGTCAACCTGAAAGGATGTTTCATGAGTTCTCAGACCTGCCCTTTTGTGG 1592
Qy 122 -----MetTrpValPheThrTyrValGlyAlaLeuPheAsn 133
Db 1593 AGAACCAAAATAGAGCTGACCATCTGGCTGACCACTTTTGTGCTCTCCCTCTGTTCTC 1652
Qy 134 GlyLeu-----ThrLeuLeuIleAlaLeuIleSerLeuPheSerVal 148
Db 1653 GGCTTGAGCTACGAGCTGATTACCGCGTGAITGCTCTGCTCACA----- 1700
Qy 149 ProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGly---LeuAlaAsn 167
Db 1701 ---GTGATTTAT---AGAACACAGAGTCCAAGCTACAAAGTCTCTGGGGCAGCTCCCTGAC 1754
Qy 168 LysAsnValLys-----AspAlaMetAlaLysIleGlnAlaLysIleProGlyLeu 184
Db 1755 ACGGATGTGATCATTTGACATAGATGATATGAGGAGGTGAAA---GAAATTCCTGGAATA 1811
Qy 185 Lys 185
Db 1812 AAA 1814
RESULT 53
US-09-785-381-2
; Sequence 2, Application US/09785381
; Patent No. 6602992
; GENERAL INFORMATION:
; APPLICANT: DALLOS, Peter
; APPLICANT: ZHENG, Jing
; APPLICANT: MADISON, Laird
; TITLE OF INVENTION: A MAMMALIAN PRESTIN
; FILE REFERENCE: 0290-3701
; CURRENT APPLICATION NUMBER: US/09/785,381
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 60/183,461
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 4113
; TYPE: DNA
; ORGANISM: Meriones unguiculatus
US-09-785-381-2
Alignment Scores:
Pred. No.: 1.61 Length: 4113
Score: 83.00 Matches: 63
Percent Similarity: 39.08% Conservative: 39
Best Local Similarity: 24.14% Mismatches: 67
Query Match: 8.92% Indels: 92
DB: 4 Gaps: 14
US-09-830-972-29_COPY_990_1178 (1-189) x US-09-785-381-2 (1-4113)
Qy 3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22
Db 1091 ATTCTCTAGAGTTCTTTGCTGTGTGAGTGGGAACTTCTCTGGGGCTACTTCTCCCTGCC 1150
Qy 23 PheLeuLeuSerLeuThrVal----- 30
Db 1151 CACGAGTCTCAGTGTTGGATGCTTGGAACTTCTCTCTGGGGCTACTTCTCCCTGCC 1210
Qy 31 -----PheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu 44
Db 1211 AACCCGACACAGCGCTTCTCCACTCGTGTGTGTGATGCC---ATTGCCATGCCATC 1267
Qy 45 Leu-----SerValThrIleSerPheArg----- 52
Db 1268 GTTGGATTTTCAGTGACAAATTTCCATGGCCAAACCTTGGCAATAGCATGGCTACGAG 1327
Qy 53 -----IleTyrLysGlyValIleGlnAlaIleGlnLysSerAsp 65
Db 1328 GTTGATGCCAATCAGGAGCTCATCGCTTGGGATATGCAACTCCATC----- 1375
Qy 66 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluLeuVal 85
Db 1376 ---GGATCTCTCTCCAGACCTTCTCCATTTC---TGCTCTTGTCTCGCAGCGCTTGT 1429
```



RESULT 56  
US-09-252-991A-11439/c  
; Sequence 11439, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 11439  
; LENGTH: 1500  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-11439

Alignment Scores:  
Pred. No.: 0.372 Length: 1500  
Score: 82.50 Matches: 39  
Percent Similarity: 42.58% Conservative: 27  
Best Local Similarity: 25.16% Mismatches: 56  
Query Match: 8.86% Indels: 33  
DB: 4 Gaps: 7  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-252-991A-11439 (1-1500)  
Qy 15 GlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIleVal 34  
Db 1200 GCGCGGGTTCGGCAAG-----CTGATCGAGCTGGCGGCTTCTCCGCTCC 1153  
Qy 35 SerValThrAlaTyrIleAlaLeu-----AlaLeuLeuSerValThrIle 49  
Db 1152 ATGTCGCGGGCGGATCGCTGTCGCGACCCGCGGAGATGTCGCGATGCTACTG 1093  
Qy 50 -----SerPheArgIleTyrLysGly-----ValIleGlnAlaIleGln 62  
Db 1092 GTCTGCGCGCTGCTCACCTACGCGGCTCTCGCTGTTGTTGGTGGTTCGCGTC 1036  
Qy 63 LysSerAspGluGlyHisPropheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
Db 1035 -----TACCCGTTCCGCGGAGATGTTCCGCGAGCGATCCCGACGATCCCGCAAG 991  
Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCyThrIleLysGlu 102  
Db 990 CGATTGATTCG-----GCGACCATCGCTTCGCGCGGTTTCCTTCACCATGAGCGCG 937  
Qy 103 LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
Db 936 CTGCCCGGACCCCGCAGATCAGAACATCATCCCTCGACCTTCTTCGGCACCCACGCC 877  
Qy 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeu 142  
Db 876 TGGCGCGCGCTGCTGCTCGGAC-----CTCGGCGCG 844  
Qy 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAla 157  
Db 843 CTGTTGCTTCGCGGCTGCTGCTTACTTGGACGCCAGCGCG 799

RESULT 57  
US-09-252-991A-11397  
; Sequence 11397, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 11397  
; LENGTH: 1665  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-11397

FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 11397  
LENGTH: 1665  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-11397

Alignment Scores:  
Pred. No.: 0.44 Length: 1665  
Score: 82.50 Matches: 39  
Percent Similarity: 42.58% Conservative: 27  
Best Local Similarity: 25.16% Mismatches: 56  
Query Match: 8.86% Indels: 33  
DB: 4 Gaps: 7

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-252-991A-11397 (1-1665)  
Qy 15 GlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIleVal 34  
Db 478 GCGCGGGTTCGGCAAG-----CTGATCGAGCTGGCGGCTTCTCCGCTCC 525  
Qy 35 SerValThrAlaTyrIleAlaLeu-----AlaLeuLeuSerValThrIle 49  
Db 526 ATGTCGCGGGCGGATCGCTGTCGCGACCCGCGGAGATGTCGCGATGCTACTG 585  
Qy 50 -----SerPheArgIleTyrLysGly-----ValIleGlnAlaIleGln 62  
Db 586 GTCTGCGCGCTGCTCACCTACGCGGCTCTCGCTGTTGTTGGTGGTTCGCGTC 642  
Qy 63 LysSerAspGluGlyHisPropheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
Db 643 -----TACCCGTTCCGCGGAGATGTTCCGCGAGCGATCCCGACGATCCCGCAAG 687  
Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCyThrIleLysGlu 102  
Db 688 CGATTGATTCG-----GCGACCATCGCTTCGCGCGGTTTCCTTCACCATGAGCGCG 741  
Qy 103 LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
Db 742 CTGCCCGGACCCCGCAGATCAGAACATCATCCCTCGACCTTCTTCGGCACCCACGCC 801  
Qy 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeu 142  
Db 802 TGGCGCGCGCTGCTGCTCGGAC-----CTCGGCGCG 834  
Qy 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAla 157  
Db 835 CTGTTGCTTCGCGGCTGCTGCTTACTTGGACGCCAGCGCG 879

RESULT 58  
US-08-853-659A-28  
; Sequence 28, Application US/08853659A  
; Patent No. 5925522  
; GENERAL INFORMATION:  
; APPLICANT: Wong, K.K.; Saffer, J.D.  
; TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection  
; TITLE OF INVENTION: Of A  
; TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella  
; NUMBER OF SEQUENCES: 67  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Paul W. Zimmerman  
; ADDRESSEE: Intellectual Property Services  
; ADDRESSEE: Battelle Memorial Institute  
; ADDRESSEE: PNNL P.O. Box 999  
; STREET: Washington Way  
; CITY: Richland

```

; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 99352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (WordPerfect 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/853,659A
; FILING DATE: Unknown
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
; FILING DATE: n/a
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1797 bases
; TYPE: nucleotide
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: the coding nucleotides of SEQ ID
; NO:28 correspond to nucleotides 22630 through
; OTHER INFORMATION: 24426 of SEQ ID NO:2
;
US-08-853-659A-28

Alignment Scores:
Pred. No.: 0.688 Length: 1797
Score: 81.50 Matches: 36
Percent Similarity: 41.24% Conservative: 37
Best Local Similarity: 20.34% Mismatches: 71
Query Match: 8.75% Indels: 33
DB: 2 Gaps: 6

US-09-830-972-29_COPY_990_1178 (1-189) x US-08-853-659A-28 (1-1797)

QY 8 TrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu 26
DB 487 TGGAAATGAGTTTCAGAAAAATAAACCCGTTTTTATTAAACTCGATCTTTCAACGTATAGCC 546
QY 27 SerLeuThrValPheSerIleValSerValThrAlaTyrlleAlaLeuAlaLeu----- 44
DB 547 GATATTCGAATATTATTATATTTCTCATTTGTTATATATATGTAATTTAGTCTGGTTGTT 606
QY 45 -----LeuSerValThrIleSerPheArgIleTyrlsGly 56
DB 607 ATTGTACCTATTACCATGTTTATCGTCTCTATTATTATTTCCCTCGTTAACCAACCATTTAT 666
QY 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrlsGluSer 76
DB 667 ACTAATGAGTTTAATGAACAAACAAAGAGGACAGACAGAAAGGACAGGAAATTTTATCTCA 726
QY 77 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeu----- 93
DB 727 GAAGTTTCTTATCTATTAAATGATCCATACCTTAATAATCAAGTTTACTTTTGTAT 786
QY 94 -----GlyHisValAsnCysThrIleLysGluLeuArg 105
DB 787 TGGGTTAATACATCAAAATGAACAGTCGTATCTTAACCTGAAGATAAGGAATAATTAATCTT 846
QY 106 LeuPhe-----LeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 123
DB 847 ATCTATCAATCTATATTTGGGAGTATGTCATCTATTACCCTAAATTAACCTATTTATGTAATA 906
QY 124 ValPheThrTyrlsVal-----GlyAlaLeuPheAsnGlyLeuThr 136
DB 907 GCCTTTTATGTTATCAAGGGTGTATGTTACTACTGGCGCAATTTGTTTCATCTGTCATT 966
QY 137 Leu-----LeuIleLeuAlaIleSerLeuPheSerValProValIle 151
DB 967 GTCTCTGGCGGATTTCCGGGATCATTTCCGAATTTTCTTCTACATAATC 1017
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RESULT 59
US-08-853-659A-6
; Sequence 6, Application US/08853659A
; Patent No. 592522
; GENERAL INFORMATION:
; APPLICANT: Wong, K.K.; Saffer, J.D.
; TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
; TITLE OF INVENTION: Of A
; TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Paul W. Zimmerman
; ADDRESSEE: Intellectual Property Services
; ADDRESSEE: Battelle Memorial Institute
; ADDRESSEE: PNNL P.O. Box 999
; STREET: Washington Way
; CITY: Richland
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 99352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (WordPerfect 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/853,659A
; FILING DATE: Unknown
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
; FILING DATE: n/a
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8967 bases
; TYPE: nucleotide
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: SEQ ID NO:6 corresponds to
; OTHER INFORMATION: nucleotides 15735 through 24701 of SEQ ID NO:2
;
US-08-853-659A-6

Alignment Scores:
Pred. No.: 9.13 Length: 8967
Score: 81.50 Matches: 36
Percent Similarity: 41.24% Conservative: 37
Best Local Similarity: 20.34% Mismatches: 71
Query Match: 8.75% Indels: 33
DB: 2 Gaps: 6

US-09-830-972-29_COPY_990_1178 (1-189) x US-08-853-659A-6 (1-8967)

QY 8 TrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu 26
DB 7382 TGGAAATGAGTTTCAGAAAAATAAACCCGTTTTTATTAAACTCGATCTTTCAACGTATAGCC 7441
QY 27 SerLeuThrValPheSerIleValSerValThrAlaTyrlleAlaLeuAlaLeu----- 44
DB 7442 GATATTCGAATATTATTATATTTCTCATTTGTTATATATGTAATTTAGTCTGGTTGTT 7501
QY 45 -----LeuSerValThrIleSerPheArgIleTyrlsGly 56
DB 7502 ATTGTACCTATTACCATGTTTATCGTCTCTATTATTATTTCCCTCGTTAACCAACCATTTAT 7561
QY 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrlsGluSer 76
DB 7562 ACTAATGAGTTTAATGAACAAACAAAGAGGACAGACAGAAAGGACAGGAAATTTTATCTCA 7621
QY 77 GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeu----- 93
DB 7622 GAAGTTTCTTATCTATTAAATGATCCATACCTTAATAATGATCCATACCTTAATAATGATCCAT 7681
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QY 94 -----GlyHisValAsnCysThrIleLysGluLeuArg 105
Db 7682 TGGGTTAATACAAATCAACAGCTGTTATCTTAACCTGAAGTAAGGAATAATCTT 7741
QY 106 LeuPhe-----LeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 123
Db 7742 ATCTATCAATCTATATTTGGGAGTATGTCATCTATTACCCAAATAACTATTATGGTAATA 7801
QY 124 ValPheThrTyrVal-----GlyAlaLeuPheAsnGlyLeuThr 136
Db 7802 GCCTTTTATGTAATCAAGGGTATGTTACTACTGGCGCAATGTTTCATCTGTCATT 7861
QY 137 Leu-----LeuIleLeuAlaLeuSerLeuPheSerValProValIle 151
Db 7862 GTCTCTGGCGGATTTCCGGGATCAATTCGAATTTTCTTCTACATTATC 7912

RESULT 60
US-08-853-659A-9/c
; Sequence 9, Application US/08853659A
; Patent No. 5925522
; GENERAL INFORMATION:
; APPLICANT: Wong, K.K.; Saffer, J.D.
; TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
; TITLE OF INVENTION: Of A
; TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Paul W. Zimmerman
; ADDRESSEE: Intellectual Property Services
; ADDRESSEE: Battelle Memorial Institute
; ADDRESSEE: PNNL P.O. Box 999
; STREET: Washington Way
; CITY: Richland
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 99352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (WordPerfect 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/853,659A
; FILING DATE: Unknown
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
; FILING DATE: n/a
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8967 bases
; TYPE: nucleotide
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
US-08-853-659A-9

Alignment Scores:
Pred. No.: 9.13 Length: 8967
Score: 81.50 Matches: 36
Percent Similarity: 41.24% Conservative: 37
Best Local Similarity: 20.34% Mismatches: 71
Query Match: 8.75% Indels: 33
DB: 2 Gaps: 6

US-09-830-972-29_COPY_990_1178 (1-189) x US-08-853-659A-9 (1-8967)

QY 8 TrpArgAspIleLysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu 26
Db 1586 TGGATGAGTTTCAGAAATTAACCCGTTTATTAACTCGATCTTCAACGATATGCC 1527
QY 27 SerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu----- 44
Db 1526 GATATTCCAATATTATTATATATTCTCATTTGTTATATATGTAATAATTAGGTCGTGTTGTT 1467

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QY 45 -----LeuSerValThrIleSerPheArgIleTyrLysGly 56
Db 1466 ATTGTACCTATTACCATGTTTATCTCTATTATTATTTCCCTGTTAACCAACCATTTAT 1407
QY 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76
Db 1406 ACTAATGAGTTAATGAACAAACAAAGAGGACAGAGAAATATTTTATCTCTCA 1347
QY 77 GluValAlaIleSerGluLeuValGlnLysTyrSerAsnSerAlaLeu----- 93
Db 1346 GAAGTTTCTTATCTATTAAATGATCCATACCTTTAAATAATAACAAGGTTTACTTTTGTAT 1287
QY 94 -----GlyHisValAsnCysThrIleLysGluLeuArg 105
Db 1286 TGGGTTAATACATCAATGAACAGCTGTTATCTTAACCTGAAGTAAGGAATAATCTT 1227
QY 106 LeuPhe-----LeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 123
Db 1226 ATCTATCAATCTATATTTGGGAGTATGTCATCTATTACCCAAATAACTATTATGGTAATA 1167
QY 124 ValPheThrTyrVal-----GlyAlaLeuPheAsnGlyLeuThr 136
Db 1166 GCCTTTTATGTAATCAAGGGTATGTTACTACTGGCGCAATGTTTTCATCTGTCATT 1107
QY 137 Leu-----LeuIleLeuAlaLeuSerLeuPheSerValProValIle 151
Db 1106 GTCTCTGGCGGATTTCCGGGATCAATTCGAATTTTCTTCTACATTATC 1056

RESULT 61
US-08-853-659A-64
; Sequence 64, Application US/08853659A
; Patent No. 5925522
; GENERAL INFORMATION:
; APPLICANT: Wong, K.K.; Saffer, J.D.
; TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
; TITLE OF INVENTION: Of A
; TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Paul W. Zimmerman
; ADDRESSEE: Intellectual Property Services
; ADDRESSEE: Battelle Memorial Institute
; ADDRESSEE: PNNL P.O. Box 999
; STREET: Washington Way
; CITY: Richland
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 99352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (WordPerfect 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/853,659A
; FILING DATE: Unknown
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
; FILING DATE: n/a
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8967 bases
; TYPE: nucleotide
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
US-08-853-659A-64

Alignment Scores:
Pred. No.: 9.13 Length: 8967
Score: 81.50 Matches: 36
Percent Similarity: 41.24% Conservative: 37

```

```
; FILING DATE: n/a
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8967 bases
; TYPE: nucleotide
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
US-08-853-659A-67

Alignment Scores:
Pred. No.: 9.13 Length: 8967
Score: 81.50 Matches: 36
Percent Similarity: 41.24% Conservatives: 37
Best Local Similarity: 20.34% Mismatches: 71
Query Match: 8.75% Indels: 33
DB: 2 Gaps: 6

US-09-830-972-29_COPY_990_1178 (1-189) x US-08-853-659A-67 (1-8967)

QY 8 TtpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu 26
   ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
1586 TCGAATGAGTTTCAGAAAAATTAAACCCGTTTATTATTAACCTCGATCTTTCAACGTATAGCC 1527

QY 27 SerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu----- 44
   ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
1526 GATATTCCAATATTATTATATTTCTCATTTGTTATATATGTAATTTAGTCTGGTTGTT 1467

QY 45 -----LeuSerValThrIleSerPheArgIleTyrIysGly 56
   ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
1466 ATTGTACCTATTACCATGTTTATCGTCCTATTATTATTATTTCCCTCGTTAACCCACCATTTAT 1407

QY 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76
   ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
1406 ACTAATGAGTTAATGAACAAACAAAGAGGACAGACAGGAAATATTTTATCTCTCA 1347

QY 77 GluValAlaIleSerGluLeuValGlnLysTyrSerAsnSerAlaLeu----- 93
   ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
1346 GAAGTTTCTTATCTATTAAATGATCCATACCTTAATTAATCAAGTTTACTTTTGAT 1287

QY 94 -----GlyHisValAsnCysThrIleLysGluLeuArgArg 105
   ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
1286 TGGGTTAATACATCAAAATGAACAGTCGTATCTTAACCTGAAGATAAGGAAATTAATCTT 1227

QY 106 LeuPhe-----LeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTTP 123
   ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
1226 ATCTATCAATCTATATTGGGAGTATGTCATCTATTACCATAACTATTATGGTAATA 1167

QY 124 ValPheThrTyrVal-----GlyAlaLeuPheAsnGlyLeuThr 136
   ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
1166 GCCTTTTATGTTATCAAGGGTATGTTACTACTGGCGCAATGTTTCACTGTCATT 1107

QY 137 Leu-----LeuIleLeuAlaLeuLeuSerLeuPheSerValProValIle 151
   ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
1106 GTCTCTGGCGGTATTTCCGGGATCATTCGAATTTTCTTCTACATAATC 1056

RESULT 63
US-08-853-659A-2
; Sequence 2, Application US/08853659A
; Patent No. 5925522
; GENERAL INFORMATION:
; APPLICANT: Wong, K.K.; Saffer, J.D.
; TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
; TITLE OF INVENTION: Of A
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Paul W. Zimmerman
; ADDRESSEE: Intellectual Property Services
; ADDRESSEE: Battelle Memorial Institute
; STREET: Washington Way
; CITY: Richland
; STATE: Washington
; ZIP: 99352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (WordPerfect 5.1)
; CURRENT APPLICATION DATA:
; FILING DATE: Unknown
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
```

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Best Local Similarity: 20.34% Mismatches: 71
Query Match: 8.75% Indels: 33
DB: 2 Gaps: 6

US-09-830-972-29_COPY_990_1178 (1-189) x US-08-853-659A-64 (1-8967)

QY 8 TtpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu 26
   ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
7382 UGGAUGAGUUUCAGAAAAUAAACCCGUUUUAUAAACCGAUGUUUUAACCAUGUAGCC 7441

QY 27 SerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu----- 44
   ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
7442 GAUUAUCCAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 7501

QY 45 -----LeuSerValThrIleSerPheArgIleTyrIysGly 56
   ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
7502 AUUGUACCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 7561

QY 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 76
   ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
7562 ACUAAUGAGUUAUGAACAAACAAAGAGGACAGACAGGAAUUAUUAUUAUUAUUAU 7621

QY 77 GluValAlaIleSerGluLeuValGlnLysTyrSerAsnSerAlaLeu----- 93
   ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
7622 GAAGUUUUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 7681

QY 94 -----GlyHisValAsnCysThrIleLysGluLeuArgArg 105
   ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
7682 UGGGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 7741

QY 106 LeuPhe-----LeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTTP 123
   ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
7742 AUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 7801

QY 124 ValPheThrTyrVal-----GlyAlaLeuPheAsnGlyLeuThr 136
   ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
7802 GCCUUUUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 7861

QY 137 Leu-----LeuIleLeuAlaLeuLeuSerLeuPheSerValProValIle 151
   ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
7862 GUCUCUGCGGAUUUUUCCGGGAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 7912
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RESULT 62
US-08-853-659A-67/c
; Sequence 67, Application US/08853659A
; Patent No. 5925522
; GENERAL INFORMATION:
; APPLICANT: Wong, K.K.; Saffer, J.D.
; TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
; TITLE OF INVENTION: Of A
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Paul W. Zimmerman
; ADDRESSEE: Intellectual Property Services
; ADDRESSEE: Battelle Memorial Institute
; STREET: Washington Way
; CITY: Richland
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 99352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (WordPerfect 5.1)
; CURRENT APPLICATION DATA:
; FILING DATE: Unknown
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
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Sequence 67, Application US/08853659A, And Methods Of Detection Of Salmonella

COUNTRY: U.S.A.  
ZIP: 99352  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage  
COMPUTER: IBM PC/XT/AT  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Word Processor (WordPerfect 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/853,659A  
FILING DATE: Unknown  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: none  
FILING DATE: n/a  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24701 bases  
TYPE: nucleotide  
STRANDEDNESS: double stranded  
TOPOLOGY: linear  
US-08-853-659A-2

Alignment Scores:  
Pred. No.: 46.6 Length: 24701  
Score: 81.50 Matches: 36  
Percent Similarity: 41.24% Conservative: 37  
Best Local Similarity: 20.34% Mismatches: 71  
Query Match: 8.75% Indels: 33  
DB: 2 Gaps: 6

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-08-853-659A-2 (1-24701)

QY 8 TrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu 26  
DB 23116 TGGAAATGAGTTTCAGAAATTAACCCGTTTATTAAATCGATCTTTCAACGATATAGCC 23175  
QY 27 SerLeuThrValPheSerIleValSerValThrAlaTyrlleAlaLeuAlaLeu----- 44  
DB 23176 GATATTCGAATTTATTATATTTCTCATTTGTTATATATGTAATTTAGGCTGGTGT 23235  
QY 45 -----LeuSerValThrIleSerPheArgIleTyrlsGly 56  
DB 23236 ATTGACCTATTACCAGTTTATCGTCTCTATTATTATTTTCCCTCGTTAAACCCATTAT 23295  
QY 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrlleuGluSer 76  
DB 23296 ACTAATGAGTTTATGAACAAACAAAGAGGACAGAGACAGAGAAATTTTATCTCA 23355  
QY 77 GluValAlaIleSerGluLeuValGlnLysTyrlSerAsnSerAlaLeu----- 93  
DB 23356 GAAGTTTCTTATCTATTAAATGATCCATCTTAAATATCAAGTTTACTTTTTCAT 23415  
QY 94 -----GlyHisValAsnCysThrIleLysGluLeuArg 105  
DB 23416 TGGGTTAATACATCAATGAACAGTCGTATCTTAACTGAAGATAAGAAATTAATCTT 23475  
QY 106 LeuPhe-----LeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 123  
DB 23476 ATCTATCAATCTATATGGGAGTATGTCATCTATTATCCAAATTAATATTATGGTAATA 23535  
QY 124 ValPheThrTyrlVal-----GlyAlaLeuPheAsnGlyLeuThr 136  
DB 23536 GCCTTTATGTTAATCAAGGTCATGTTACTACTGGCGCAATGTTTCTCATCTGTCATT 23595  
QY 137 Leu-----LeuIleAlaLeuIleSerLeuPheSerValProValIle 151  
DB 23596 GTCCTGGCCGATTTCCGGGATCATCTCGAATTTTCTTCTCATTAATTAATC 23646

## RESULT 64

US-08-853-659A-3/c  
Sequence 3, Application US/08853659A  
Patent No. 5925522  
GENERAL INFORMATION:

APPLICANT: Wong, K.K.; Saffer, J.D.  
TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection  
TITLE OF INVENTION: Of A  
TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Paul W. Zimmerman  
ADDRESSEE: Intellectual Property Services  
ADDRESSEE: Battelle Memorial Institute  
ADDRESSEE: PNNL P.O. Box 999  
STREET: Washington Way  
CITY: Richland  
STATE: Washington  
COUNTRY: U.S.A.  
ZIP: 99152

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage  
COMPUTER: IBM PC/XT/AT  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Word Processor (WordPerfect 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/853,659A  
FILING DATE: Unknown  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: none  
FILING DATE: n/a  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24701 bases  
TYPE: nucleotide  
STRANDEDNESS: double stranded  
TOPOLOGY: linear  
US-08-853-659A-3

Alignment Scores:  
Pred. No.: 46.6 Length: 24701  
Score: 81.50 Matches: 36  
Percent Similarity: 41.24% Conservative: 37  
Best Local Similarity: 20.34% Mismatches: 71  
Query Match: 8.75% Indels: 33  
DB: 2 Gaps: 6

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-08-853-659A-3 (1-24701)

QY 8 TrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPhe---LeuLeuLeu 26  
DB 1586 TGGAAATGAGTTTCAGAAATTAACCCGTTTATTAAATCGATCTTTCAACGATATAGCC 1527  
QY 27 SerLeuThrValPheSerIleValSerValThrAlaTyrlleAlaLeuAlaLeu----- 44  
DB 1526 GATATTCGAATTTATTATATTTCTCATTTGTTATATATGTAATTTAGGCTGGTGT 1467  
QY 45 -----LeuSerValThrIleSerPheArgIleTyrlsGly 56  
DB 1466 ATTGACCTATTACCAGTTTATCGTCTCTATTATTATTTTCCCTCGTTAAACCCATTAT 1407  
QY 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrlleuGluSer 76  
DB 1406 ACTAATGAGTTTATGAACAAACAAAGAGGACAGAGACAGAGAAATTTTATCTCA 1347  
QY 77 GluValAlaIleSerGluLeuValGlnLysTyrlSerAsnSerAlaLeu----- 93  
DB 1346 GAAGTTTCTTATCTATTAAATGATCCATCTTAAATTAATCAAGTTTACTTTTTCAT 1287  
QY 94 -----GlyHisValAsnCysThrIleLysGluLeuArg 105  
DB 1286 TGGGTTAATACATCAATGAACAGTCGTATCTTAACTGAAGATAAGAAATTAATCTT 1227  
QY 106 LeuPhe-----LeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 123  
DB 1226 ATCTATCAATCTATATGGGAGTATGTCATCTATTATCCAAATTAATATTATGGTAATA 1167







```
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLeuLysLysThrGlyVal-----16
Db 2864 GTCGTGGAGGTGCTGTATGGTGTGACGCTTTTGTGACCCACGCTGCTGTGTGAGTGA 2805
QY 17 -----ValPheGlyAlaSerLeuPheLeuLeuSer 27
Db 2804 GATTGTCATTCTCTCCGCTCTCTACTGTTTCTCTGCTCTCT-----TTGACTGTTCT 2751
QY 28 LeuThrValPheSerIleValSerValThrAlaTyrIleAla-LeuAlaLeuLeuSerVa 47
Db 2750 GTGACGTGTTGATGTGTTGTTCCGTTACTGTTTATTTTATTCATGCGCTTTACTTTCAGT 2691
QY 47 lThrIleSerPheArgIleTyr 54
Db 2690 GGTTCCTATTATTTAAACATATTT 2669

RESULT 69
US-09-795-927-8
; Sequence 8, Application US/09795927
; Patent No. 6531309
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James A.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Revelli, Jean-Pierre
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6531309el Human Transporter Proteins and Polynucleotides Enc
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0141-USA
; CURRENT APPLICATION NUMBER: US/09/795,927
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/185,956
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 3749
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-795-927-8

Alignment Scores:
Pred. No.: 2.64 Length: 3749
Score: 81.00 Matches: 48
Percent Similarity: 42.93% Conservative: 37
Best Local Similarity: 24.24% Mismatches: 69
Query Match: 8.70% Indels: 44
DB: 4 Gaps: 10

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-795-927-8 (1-3749)

QY 21 SerLeuPheLeuLeuLeu-----SerLeuThrValPheSerIle 33
Db 1577 AGCTCTCTTTCTGTCATATTTCTGGCAAGAGATTGCCAGTCTTCACAAATTACAGTGTG 1636
QY 34 ValSerValThrAlaTyrIleAlaLeuLeuSerValThrIleSerPhe-----51
Db 1637 AATTCCACAGGATTATAGCCATCGGCTTTGCAATGTGTCAGTTCATTTTTCAGA 1696
QY 52 -----ArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAsp 65
Db 1697 TCTTGTGTGTTTACTGCTGTTATTTAGTACGACTATTATCCAG-----GATAAATCTGGA 1750
QY 66 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuVal 85
Db 1751 GGAAGACAAACAGTTTGCATCTCTGTTAGGCGCAGGTGTGATGCTGCTC-----CTGATG 1804
QY 86 GlnLysTyr-Ser-----AsnSerAlaLeuGlyHisValAsnCys 98
Db 1805 GTGACATGGGACACTTTTCTACACACTGCCAAATGCTGCTGCTGGTATTATTTCTG 1864
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QY 99 -----ThrIleLysGluLeuLeuArgLeuPheLeuValAsp 110
Db 1865 AGCAACGTCATTCCCTACCTTGAACACCATTTCTAACCTTACCAGCTGTGGAGGAGGAC 1924
QY 111 AspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAla 130
Db 1925 -----CAATATGACTGTGCTCTTTGGATGATGACATTTCTCATCTTCA 1966
QY 131 LeuPheAsnGlyLeuThrLeu-----LeuIleLeuAlaLeuIleSerLeuPheSerValPro 149
Db 1967 ATTTCTCGGACGTGACATTTGACTATATCTCAGTAGTTCCTGCTTCTTCTCATCACC 2026
QY 150 ValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaLeuLysAsn 169
Db 2027 ACTGTT--CGTTACACAGAGCTAAGATTCTCTCTGGGTCAAAATCCCTAACCAAC 2083
QY 170 ValLysAspAlaMetAlaLysIleGln-----AlaLysIleProGlyLeuLys 185
Db 2084 ATTTATGAAGCATCAATGATTATCGGAGATCATCACCATTTCTGGGGTGAA 2137

RESULT 70
US-09-328-352-740
; Sequence 740, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 740
; LENGTH: 1782
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-740

Alignment Scores:
Pred. No.: 0.937 Length: 1782
Score: 80.50 Matches: 35
Percent Similarity: 43.84% Conservative: 29
Best Local Similarity: 23.97% Mismatches: 44
Query Match: 8.65% Indels: 39
DB: 4 Gaps: 7

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-328-352-740 (1-1782)

QY 8 TrpArgAspIleLeuLysThr-----GlyValValPheGlyAlaSerLeuPheLeuLeu 25
Db 772 TGCGGTGGTGTGTTAAGGAACTTGGCTCGGTATTGTCGGTGGTGGTGGTGGTGGTGGT 831
QY 26 LeuSerLeuThrValPheSerIleVal-----SerValThrAlaTyrIle 40
Db 832 GCCCAGTATCTCACTTCTAATTTATGGCCCTGAGTATCCACAGATACCCAGCAATT 891
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 892 GCT---TCATTGGTCAGCTGAGTGTGTTATTCCGCTGTTGGAAA-----933
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 934 -----CCAAACATATTTTCCGTTTTTGAACTTGAACCTGGAACGGGTGAGCTTTG 978
QY 81 SerGluGlu-----LeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsn--- 97
Db 979 GCTCAGCACCTACACAGTTTCACGTTATAGC-----ATTGGGAAATTTGCAAG 1029
QY 98 -----CysThrIleLysGluLeu 103
Db 1030 GCATGCTCTCCATTTGCTATTATTTAAACGGTAATGGTCACGATTGGAGCGCTTAAGCACTTT 1089
```

QY 104 ArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 123  
Db 1090 AAAGCATTTATTGCCAAGATGGTCTCTTGAACACTGGATTTTAAACTTGAAGTGCC- 1148  
QY 124 ValPheThrTyrValGly 129  
Db 1149 GTATTTCACACAAATGGT 1166

RESULT 71  
US-08-916-421B-1  
; Sequence 1, Application US/08916421B  
; Patent No. 6503729  
; GENERAL INFORMATION:  
; APPLICANT: Bult et al.  
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus  
; Patent No. 6503729  
; FILE REFERENCE: jannaschii  
; CURRENT APPLICATION NUMBER: US/08/916,421B  
; CURRENT FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: US 60/024,428  
; PRIOR FILING DATE: 1996-08-22  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1664976  
; TYPE: DNA  
; ORGANISM: Methanococcus jannaschii  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (28222)..(28222)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (28257)..(28258)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (84773)..(84773)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (84808)..(84808)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (84812)..(84812)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (98120)..(98120)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (98159)..(98159)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (98239)..(98239)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (98266)..(98266)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (98343)..(98343)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (103398)..(103398)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (148948)..(148948)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (163385)..(163385)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (191989)..(191989)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (191995)..(191995)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (231980)..(231980)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (234187)..(234187)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (234220)..(234220)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (234814)..(234814)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (309398)..(309398)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (309418)..(309418)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (312837)..(312837)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (312993)..(312993)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (319226)..(319226)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (559167)..(559167)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (559241)..(559241)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (600992)..(600992)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (622708)..(622708)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (657081)..(657081)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (657203)..(657203)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (674435)..(674435)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (682442)..(682442)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (713652)..(713652)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (741684)..(741684)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (779455)..(779455)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (779676)..(779676)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (855539)..(855539)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (871619)..(871619)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (1084830)..(1084830)  
; OTHER INFORMATION: n equals a, t, c, or g

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; NAME/KEY: misc feature
; LOCATION: (1096846)..(1096846)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1119881)..(1119881)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
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; LOCATION: (1603734)..(1603734)
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; LOCATION: (1637998)..(1637998)
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; NAME/KEY: misc feature
; LOCATION: (1664854)..(1664855)
; OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1
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Pred. No.: 5.57e+04 Length: 1664976
Score: 80.50 Matches: 48
Percent Similarity: 41.24% Conservative: 32
Best Local Similarity: 24.74% Mismatches: 69
Query Match: 8.65% Indels: 45
DB: 4 Gaps: 9
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US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-08-916-421B-1 (1-1664976)

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Qy 19 GlyAlaSerLeuPheLeuLeuSerLeuThrValPheSerIle---ValSerValThr 37
Db 771933 GACGAAAAAAGTTTATTTATTTTAAATAAATATAGCTCGCATACCTCTCTTAATATCA 771992
Qy 38 AlaTyrIleAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyVal 57
Db 771993 TATTTATTACACTTAACCTTAAAGATGATGATTTATTTAGTTATATACGTGGGAGCT 772052
Qy 58 Ile-----GlnAlaIleGlnLysSerAspGluGlyHis 68
Db 772053 GCATTGTTCCATCTATTTTATATGAAAAATAAATAGAACTCTTCGAGATAACATT 772112
Qy 69 ProPheArgAlaTyr-----LeuGluSerGluValAlaIleSerGluGlu 83
Db 772113 CCACAAGCTCTTTATATATGATATTTAGCCCTCGAATCTGGAAGGTCCTAAACGAAGCA 772172
Qy 84 LeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeu 103
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Qy 119 AlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeu 138
Db 772263 GAAGAGTCTATG-----ACAATTGTATCCATTTTATATGATTTCTAAAGTATTAAAG 772313
Qy 139 IleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGln 158
Db 772314 ATGTTAGCAAGATTTATGATTCGAAAC-----AGGAATACGAGGAGAT 772358
Qy 159 IleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAsp 172
Db 772359 TTGTCAGATCTCTTAAAAATATTAGCTAAACCTCTTGAAGAC 772400

RESULT 72
US-09-692-570-1
; Sequence 1, Application US/09692570
; Patent No. 6797466
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275C1
; CURRENT APPLICATION NUMBER: US/09/692,570
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; PRIOR APPLICATION NUMBER: US 08/916,421
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
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## Alignment Scores:

Pred. No.: 1.32 Length: 1990  
 Score: 80.00 Matches: 50  
 Percent Similarity: 37.89% Conservative: 36  
 Best Local Similarity: 22.03% Mismatches: 64  
 Query Match: 8.59% Indels: 77  
 DB: 6 Gaps: 11

US-09-830-972-29\_COPY\_990\_1178 (1-189) x 5518916-5 (1-1990)

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Qy 11 lLeLysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrVal 30
Db 769 GTTGAAGAACTTGGCGTT-----CATATGTTTACTGTCAAAATAAGTCTTGTAGTT 719
Qy 31 PheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSer 50
Db 718 CATGGT-----AGCCATATAGATGACCTTTGTGACAGATATTCACATCGGTAGTTCC 665
Qy 51 PheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAsp----- 65
Db 664 TTCCTCGTGACACAACTTGTGTTCAA-----CAGACCAGTGACGAAGTAGTGGTAATC 611
Qy 66 -----GluGlyHisProPheArgAlaTyrLeuGluSerGluVal 78
Db 610 ACCATGGTTCGCTCCATTCTGAAACGCAACCAATTCGCGTTTAC----- 566
Qy 79 AlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCy8 98
Db 565 -----GCTGTCTTGGCAGGGTTCGATGC 542
Qy 99 ThrIleLysGlu----- 102
Db 541 ACTCTCTTTGAACAATCTGAACGAGCATCCAACTGGTAAGGTTTGGAGAGATAGAGG 482
Qy 103 -----LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPhe 118
Db 481 TTGGTACTCTTGATACAAACGATATTTGACATTTGTCATCGTAAAGCATCGGTACATTTTC 422
Qy 119 AlaValLeuMetTyrPheThrTyr-----ValGlyAlaLeu----- 131
Db 421 ACAACGGTCAGCATTAATTTGTTAACTCTACGACAGTTGGAGTCTCTCAGGAGCATTTAGA 362
Qy 132 -----PheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSer 147
Db 361 GCACACATCATTTACATCTGCTCAGACCATTTGCTCAAAACATGTTTCATATCCTTAGT 302
Qy 148 -----ValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeu-GlyLe 165
Db 301 AATGTTGTGCATGTGTCGTCAGGAGAGTCAATCAAGT-----ATCAGCTGT 257
Qy 165 uAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIleProGly----- 183
Db 256 TTCCAATGTGAGGTTAAATCACTTACCACCTTACCTGAGCGAGAGACTTCTACTCTCTG 197
Qy 184 -LeuLysArgLysAlaGlu 189
Db 196 ATTGTGGCGAAAGACGAC 178

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## RESULT 75

5518916-5/c  
 ;Patent No. 5171685  
 ;APPLICANT: MCELWAIN, TERRY F.;HINES, STEPHEN A.;MCGUIRE,  
 ;TRAVIS C.;PALMER, GUY H.; JASMER, DOUGLAS P.;REDUKER, DAVID W.  
 ;GOFF, WILL L.;PERRYMAN, LANCE E.;DAVIS, WILLIAM C.  
 ;TITLE OF INVENTION: CLONING OF THE BABESIA BOVIS 60 KD ANTIGEN  
 ;NUMBER OF SEQUENCES: 7  
 ;CURRENT APPLICATION DATA:  
 ;APPLICATION NUMBER: US/07/504,461  
 ;FILING DATE: 04-APR-1990  
 ;SEQ ID NO: 5  
 ;LENGTH: 1990  
 5171685-5

## Alignment Scores:

Pred. No.: 1.32 Length: 1990  
 Score: 80.00 Matches: 50  
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 Query Match: 8.59% Indels: 77  
 DB: 6 Gaps: 11

US-09-830-972-29\_COPY\_990\_1178 (1-189) x 5171685-5 (1-1990)

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Db 718 CATGGT-----AGCCATATAGATGACCTTTGTGACAGATATTCACATCGGTAGTTCC 665
Qy 51 PheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAsp----- 65
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Qy 66 -----GluGlyHisProPheArgAlaTyrLeuGluSerGluVal 78
Db 610 ACCATGGTTCGCTCCATTCTGAAACGCAACCAATTCGCGTTTAC----- 566
Qy 79 AlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCy8 98
Db 565 -----GCTGTCTTGGCAGGGTTCGATGC 542
Qy 99 ThrIleLysGlu----- 102
Db 541 ACTCTCTTTGAACAATCTGAACGAGCATCCAACTGGTAAGGTTTGGAGAGATAGAGG 482
Qy 103 -----LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPhe 118
Db 481 TTGGTACTCTTGATACAAACGATATTTGACATTTGTCATCGTAAAGCATCGGTACATTTTC 422
Qy 119 AlaValLeuMetTyrPheThrTyr-----ValGlyAlaLeu----- 131
Db 421 ACAACGGTCAGCATTAATTTGTTAACTCTACGACAGTTGGAGTCTCTCAGGAGCATTTAGA 362
Qy 132 -----PheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSer 147
Db 361 GCACACATCATTTACATCTGCTCAGACCATTTGCTCAAAACATGTTTCATATCCTTAGT 302
Qy 148 -----ValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeu-GlyLe 165
Db 301 AATGTTGTGCATGTGTCGTCAGGAGAGTCAATCAAGT-----ATCAGCTGT 257
Qy 165 uAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIleProGly----- 183
Db 256 TTCCAATGTGAGGTTAAATCACTTACCACCTTACCTGAGCGAGAGACTTCTACTCTCTG 197
Qy 184 -LeuLysArgLysAlaGlu 189
Db 196 ATTGTGGCGAAAGACGAC 178

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## RESULT 76

5518916-5/c  
 ;Patent No. 5518916  
 ;APPLICANT: MCELWAIN, TERRY F.;MCGUIRE, TRAVIS C.;JASMER,  
 ;DOUGLAS P.;REDUKER, DAVID W.;GOFF, WILL L.;STILLNER, DAVID  
 ;TITLE OF INVENTION: CLONED BABESIA DNA  
 ;NUMBER OF SEQUENCES: 7  
 ;CURRENT APPLICATION DATA:  
 ;APPLICATION NUMBER: US/08/342,480  
 ;FILING DATE: 21-NOV-1994  
 ;PRIOR APPLICATION DATA:  
 ;APPLICATION NUMBER: 989,616  
 ;FILING DATE: 14-DEC-1992  
 ;APPLICATION NUMBER: 504,461  
 ;FILING DATE: 04-APR-1990





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; LOCATION: (309418)..(309418)
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; US-08-916-4218-1

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Pred. No.: 6.53e+04 Length: 1664976
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Query Match: 8.59% Indels: 21
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US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-08-916-4218-1 (1-1664976)

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RESULT 78
US-09-692-570-1/c
; Sequence 1, Application US/09692570
; Patent No. 6797466
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275C1
; CURRENT APPLICATION NUMBER: US 09/692,570
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; PRIOR APPLICATION NUMBER: US 08/916,421

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FEATURE:	
NAME/KEY: misc feature	
LOCATION: (622708)..(622708)	OTHER INFORMATION: n equals a, t, c, or g
FEATURE:	
NAME/KEY: misc feature	
LOCATION: (657081)..(657081)	OTHER INFORMATION: n equals a, t, c, or g
FEATURE:	
NAME/KEY: misc feature	
LOCATION: (657203)..(657203)	OTHER INFORMATION: n equals a, t, c, or g
FEATURE:	
NAME/KEY: misc feature	
LOCATION: (674435)..(674435)	OTHER INFORMATION: n equals a, t, c, or g
FEATURE:	
NAME/KEY: misc feature	
LOCATION: (682442)..(682442)	OTHER INFORMATION: n equals a, t, c, or g
FEATURE:	
NAME/KEY: misc feature	
LOCATION: (713652)..(713652)	OTHER INFORMATION: n equals a, t, c, or g
FEATURE:	
NAME/KEY: misc feature	
LOCATION: (741684)..(741684)	OTHER INFORMATION: n equals a, t, c, or g
FEATURE:	
NAME/KEY: misc feature	
LOCATION: (779455)..(779455)	





```

, PRIOR APPLICATION NUMBER: DE 199332128.0
, PRIOR FILING DATE: 1999-07-09
, PRIOR APPLICATION NUMBER: DE 199332180.9
, PRIOR FILING DATE: 1999-07-09
, PRIOR APPLICATION NUMBER: DE 199332182.5
, PRIOR FILING DATE: 1999-07-09
, PRIOR APPLICATION NUMBER: DE 199332190.6
, PRIOR FILING DATE: 1999-07-09
, PRIOR APPLICATION NUMBER: DE 199332191.4
, PRIOR FILING DATE: 1999-07-09
, PRIOR APPLICATION NUMBER: DE 199332209.0
, PRIOR FILING DATE: 1999-07-09
, PRIOR APPLICATION NUMBER: DE 199332212.0
, PRIOR FILING DATE: 1999-07-09
, PRIOR APPLICATION NUMBER: DE 199332227.9
, PRIOR FILING DATE: 1999-07-09
, PRIOR APPLICATION NUMBER: DE 199332228.7
, PRIOR FILING DATE: 1999-07-09
, PRIOR APPLICATION NUMBER: DE 199332229.5
, PRIOR FILING DATE: 1999-07-09
, PRIOR APPLICATION NUMBER: DE 199332230.9
, PRIOR FILING DATE: 1999-07-09
, PRIOR APPLICATION NUMBER: DE 199332927.3
, PRIOR FILING DATE: 1999-07-14
, PRIOR APPLICATION NUMBER: DE 199333005.0
, PRIOR FILING DATE: 1999-07-14
, PRIOR APPLICATION NUMBER: DE 199333006.9
, PRIOR FILING DATE: 1999-07-14
, PRIOR APPLICATION NUMBER: DE 19940764.9
, PRIOR FILING DATE: 1999-08-27
, PRIOR APPLICATION NUMBER: DE 19940765.7
, PRIOR FILING DATE: 1999-08-27
, PRIOR APPLICATION NUMBER: DE 19940766.5
, PRIOR FILING DATE: 1999-08-27
, PRIOR APPLICATION NUMBER: DE 19940830.0
, PRIOR FILING DATE: 1999-08-27
, PRIOR APPLICATION NUMBER: DE 19940831.9
, PRIOR FILING DATE: 1999-08-27
, PRIOR APPLICATION NUMBER: DE 19940832.7
, PRIOR FILING DATE: 1999-08-27
, PRIOR APPLICATION NUMBER: DE 19940833.5
, PRIOR FILING DATE: 1999-08-27
, PRIOR APPLICATION NUMBER: DE 19941378.9
, PRIOR FILING DATE: 1999-08-31
, PRIOR APPLICATION NUMBER: DE 19941379.7
, PRIOR FILING DATE: 1999-08-31
, PRIOR APPLICATION NUMBER: DE 19941395.9
, PRIOR FILING DATE: 1999-08-31
, PRIOR APPLICATION NUMBER: DE 19942077.7
, PRIOR FILING DATE: 1999-09-03
, PRIOR APPLICATION NUMBER: DE 19942078.5
, PRIOR FILING DATE: 1999-09-03
, PRIOR APPLICATION NUMBER: DE 19942079.3
, PRIOR FILING DATE: 1999-09-03
, PRIOR APPLICATION NUMBER: DE 19942088.2
, PRIOR FILING DATE: 1999-09-03
, NUMBER OF SEQ ID NOS: 678
, SEQ ID NO 301
, LENGTH: 1500
, TYPE: DNA
, ORGANISM: Corynebacterium glutamicum
, FEATURE:
, NAME/KEY: CDS
, LOCATION: (101)..(1477)
, OTHER INFORMATION: RXN00456
US-09-602-787A-301

```

Alignment Scores:		
Pred. No.:	0.981	1500
Score:	79.50	Length:
Percent Similarity:	40.38%	Matches:
Best Local Similarity:	26.28%	Conservative:
Query Match:	8.54%	Mismatches:
		Indels:

[illegible]

## RESULT 82

```

RESULTS 82
US-09-949-016-15236
; Sequence 15236, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 15236
; LENGTH: 147840
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15236

```

**Alignment Scores:**

Alignment Scores:			
Pred. No.:	1.58e+03	Length:	147840
Score:	79.50	Matches:	45
Percent Similarity:	39.66%	Conservative:	24
Best Local Similarity:	25.86%	Mismatches:	58
Query Match:	8.54%	Indels:	47
DB:	4	Gaps:	7

US-09-830-972-29 COPY 990 1178 (1-189) x US-09-949-016-15236 (1-147840)

Qy 18 PheGlyAlaSerLeuPheLeuLeuSerLeu-----Thr 29



Db 476 AGACACTTATCAAAATGTTT- ||||| : : : : : GAATCATGTTT 444  
Qy 87 LysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgLeu 106  
Db 443 AAATACAGTAATTTATCATTAATGAATTAAGTTTACAAATAAGTAAGTATCCAGTAC 384  
Qy 107 PheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTyrValPheThr 126  
Db 383 TTGTGATA-----ATTAAATATCAATAAGTTTATCAATCTTTTAAATGACACTTACA 333

RESULT 85  
US-09-949-016-3567  
; Sequence 3567, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3567  
; LENGTH: 3811  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-3567

Alignment Scores:  
Pred. No.: 5,17 Length: 3811  
Score: 79.00 Matches: 44  
Percent Similarity: 41.32% Conservative: 25  
Best Local Similarity: 26.35% Mismatches: 52  
Query Match: 8.49% Indels: 46  
DB: 4 Gaps: 8

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-3567 (1-3811)

Qy 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerIleu 22  
Db 723 ATTCAAGTAATTTATTTGCACAGACTGGGGTCTTACATCAAAATGCCCTACTCAATCTC 782  
Qy 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
Db 783 TCTTTAGACCTGTCCTCAACCTATGAACCTTTATCCAAACGAGTGCAATTTAAAGAAATT 842  
Qy 43 AlaLeuLeuSerValThrIle-----SerPheArgIleTyrLysGlyVal 57  
Db 843 AGGCTTCATAGCTGACCTTTAAGAAATAATTTGTAGTATTTAATGTAATGAATACTGT 902  
Qy 58 IleGlnAlaIleGlnLysSerAspGluGlyHisPropheArgAlaTyrLeuGluSerGlu 77  
Db 903 ATTCAAGGCTGTG-----GCTGGTTTAGAAGTCCAT 932  
Qy 78 ValAlaIle-----SerGluGluLeuValGlnLysTyrSerAsnSerAla 92  
Db 933 CGTTTGGTTCTGGGAGAAATTTAGAAATGAAGGAAACTTGGAAAGATTGCAAAATCTGCT 992  
Qy 93 Leu---GlyHisValAsnCysThrIleLysGluLeuArgLeuPheLeu----- 108  
Db 993 CTAGAGGCGCTGTGCAATTTGACCAATGAAGATTCGATTAAGCATCTTAGACTACTACTAC 1052  
Qy 109 ValAspLeuValAspSerLeuLysPheAlaValLeuMetTyrValPheThrTyrVal 128  
Db 1053 CTCGATGATATTATTGAC----- 1070

Qy 129 GlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuSerLeuPheSer--- 147  
Db 1071 -----TTATTTAATGTTTGACA-----AATGTTTCTTCATTTCCCTG 1109  
Qy 148 ValProValIleTyrGluArg 154  
Db 1110 GTGAGTGTGACTATTGAAAGG 1130

RESULT 86  
US-08-836-687B-29  
; Sequence 29, Application US/08836687B  
; Patent No. 6448034  
; GENERAL INFORMATION:  
; APPLICANT: Gasson, Michael John  
; APPLICANT: Dodd, Helen Mair  
; TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN  
; FILE REFERENCE: 20747/70  
; CURRENT APPLICATION NUMBER: US/08/836,687B  
; CURRENT FILING DATE: 1995-11-20  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 29  
; LENGTH: 7454  
; TYPE: DNA  
; ORGANISM: Lactococcus sp.  
US-08-836-687B-29

Alignment Scores:  
Pred. No.: 15,2 Length: 7454  
Score: 79.00 Matches: 35  
Percent Similarity: 39.44% Conservative: 36  
Best Local Similarity: 19.44% Mismatches: 77  
Query Match: 8.49% Indels: 32  
DB: 3 Gaps: 5

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-08-836-687B-29 (1-7454)

Qy 5 LeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeuPheLeu 24  
Db 2746 CTGTCGTATCTTCAGATATTCAGAAATAGTACAAACCTGGGTGGAAATCTATCTTC 2805  
Qy 25 LeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeu 44  
Db 2806 CTA-----AGATATACTGATCTTAACCCACATATTAGATTGGGTATA 2847  
Qy 45 LeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSer 64  
Db 2848 AAATGTTTCAGATTTA-----TTTTAGCTTACGGATCTATCTTGAATCTTAAAGGAGT 2904  
Qy 65 AspGluGlyHisPropheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeu 84  
Db 2905 CGGAAATAATAGTAATAATGTCAACTTTT-----GATATTTCTATTATGATCAAGAA 2955  
Qy 85 ValGlnLysTyr-----Ser 89  
Db 2956 GTAGAAAGATATGTTGGATTGATCTTTAGAGTTATCCGAAGCAATATTTTGTGCCGAT 3015  
Qy 90 AsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgLeuPheLeuVal 109  
Db 3016 TCTAAATATTATCCAAATTTGCTTACATTTGATAAAGATACATAATAATGATTGGAAGTC 3075  
Qy 110 AspAspLeuValAspSerLeuLysPheAlaValLeuMetTyrValPheThrTyrValGly 129  
Db 3076 GATGATGTA-----TCAATCTTGGTGAATATTATTATATCTGAAA 3114  
Qy 130 AlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuSerLeuPheSerValPro 149  
Db 3115 TGCTTCTTTAGATGATGATACAAAAGATCTTAAATTTTGAATTTAGTTAGTCTCTAAA 3174  
Qy 150 ValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsn 169  
Db 3175 AAGGTTAAAGAAATATGTCATGAAAGATTTGAACATTATCTTAAAGCTTCTGAAAGTTAAT 3234

## RESULT 87

```
US-09-949-016-15309
; Sequence 15309, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15309
; LENGTH: 15346
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15309

Alignment Scores:
Pred. No.: 48.6 Length: 15346
Score: 79.00 Matches: 44
Percent Similarity: 41.32% Conservative: 25
Best Local Similarity: 26.35% Mismatches: 52
Query Match: 8.49% Indels: 46
DB: 4 Gaps: 8

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-949-016-15309 (1-15346)

QY 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22
Db 10258 ATTCAAAGTATTATTGTCACAGACTTTCGGGGTTCTACATCAAAATGCCCTTACTCAATCTC 10317
QY 23 PheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
Db 10318 TCTTTAGACTGTCCTTCAACCCATGACCTTATCCACCGGTGCATTTAAGAAAT 10377
QY 43 AlaLeuLeuSerValThrIle-----SerPheArgIleTyrLysGlyVal 57
Db 10378 AGGCTTCATAAGCTGACTTTAAGAAATAATTTTGATAGTTTAAATGTAATGAAACTTCT 10437
QY 58 IleGlnAlaIleGlnLysSerAspGluGlyHisPropheArgAlaTyrLeuGluSerGlu 77
Db 10438 ATTCAGAGTCTG-----GCTCGTTTAGAAGTCCAT 10467
QY 78 ValAlaIle-----SerGluGluLeuValGlnLysTyrSerAsnSerAla 92
Db 10468 CGTTTCGTTCTGGAGAAATTAGAAATGAGGAACTTGGAAGTTTGCAAAATCTGCT 10527
QY 93 Leu---GlyHisValAsnCysThrIleLysGluLeuArgLeuPheLeu-----108
Db 10528 CTAGAGGCGCTGCAATTGACCAATTGAAGAAATCCGATTAGCACTTAGACTACTAC 10587
QY 109 ValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrVal 128
Db 10588 CTCGATGATATTATTATGAC-----10605
QY 129 GlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeuIleSerLeuPheSer-----147
Db 10606 -----TTATTAAATGTTTGACA-----AATGTTCTTCAITTTCCCTG 10644
QY 148 ValProValIleTyrGluArg 154
Db 10645 GTGAGTGTGACTATTGAAAGG 10665
```

## RESULT 88

```
US-09-949-016-13877
; Sequence 13877, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13877
; LENGTH: 202111
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc feature
; LOCATION: (1).....(202111)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13877

Alignment Scores:
Pred. No.: 3.07e+03 Length: 202111
Score: 79.00 Matches: 35
Percent Similarity: 42.64% Conservative: 20
Best Local Similarity: 27.13% Mismatches: 32
Query Match: 8.49% Indels: 42
DB: 4 Gaps: 9

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-949-016-13877 (1-202111)

QY 68 HisProPheArg---AlaTyrLeuGlu-----SerGluValAlaIleSer--- 81
Db 169976 TATCCTTTTAGATAATCTTATCTGGAACATGTTTAATTTCTCTAGTGTGTTCTTTT 170035
QY 82 -----GluGluLeuValGlnLysTyr-----SerAsnSerAlaLeuGlyHis 95
Db 170036 TAAAGTGACACTTCAAGATAACTCAAAAGCCATTTGAATGAGGAATCCTTCTGACAT 170095
QY 96 ValAsnCysThrIleLysGluLeuArgLeuPheLeuValAspAspLeuValAspSer 115
Db 170096 TTACAATGCTTCCCGACACTTTGACAAAATTTGATTTTATTGATAGTGTGTTTCATTCA 170155
QY 116 LeuLysPheAlaValLeuMetTrpValPhe-----ThrTyrValGly 129
Db 170156 ---AGATTGCTATCTC---TGGTTTTTCCAACTAAATTCAACTTAGTGTATTATAGGA 170209
QY 130 AlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerVal--- 148
Db 170210 GCCAAATTT-----GTTTATATTTTGTCTTTATGTAACATTTATTTAAGTTGA 170257
QY 149 -----ProValIle 151
Db 170258 TGAATTTAAACATTTTAAAGCAAGTCAGTGGAATAAATAAGTTTAAACAAAGTGATT 170317
QY 152 TyrGluArgHisGlnAlaGlnIleAsp 160
Db 170318 TTTGATAACCATATAATTCACAAGAT 170344

RESULT 89
US-09-949-016-14543/C
; Sequence 14543, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
```



; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14543  
; LENGTH: 387902  
; TYPE: DNA  
; ORGANISM: Human  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(387902)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14543

Alignment Scores:  
Pred. No.: 8.78e+03 Length: 387902  
Score: 79.00 Matches: 43  
Percent Similarity: 38.46% Conservative: 22  
Best Local Similarity: 25.44% Mismatches: 57  
Query Match: 8.49% Indels: 47  
DB: 4 Gaps: 7

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-14543 (1-387902)

Qy 8 TrpArgAspIle-----LysLysThrGlyValValPhe-----Gly 19  
Db 105633 TGGCATGAATTTTAAATTTGAAATTTGCAATGCAATGCTACATTCACCATGTAATGGG 105574  
Qy 20 AlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr 39  
Db 105573 GAGGCTTTAAATTTGCTATTTAGATAATATTTTATTTAGAGGTAGGGTGTGTCATAT 105514  
Qy 40 IleAlaLeu---AlaLeuLeuSerValThrIleSerPhe----- 51  
Db 105513 GTGTGTATATATACATGTATGCTTCCACAGATACCACTGACCATTCAAAAGAAATAAG 105454  
Qy 52 -----ArgIleTyrLysGlyValIleGlnAlaIleGlnLys 63  
Db 105453 AAGGATTTCTGGAGCTCACGGGAGAAATAAGCTGGGTAGACTCTTCCATAGAATCC 105394  
Qy 64 SerAspGluGlyHis-----ProPheArgAlaTyrLeuGluSerGluVal 78  
Db 105393 AGTCTGAAGGCCATCTTGCTGAAATAATCCTGTGCAGAGCC----- 105352  
Qy 79 AlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHis----- 95  
Db 105351 -----TCCCTACTTAACCTAGATTTTGCAGAAAAGACTGGA 105316  
Qy 96 ValAsnCys-ThrIleLysGluLeuArgLeuPheLeuValAspAspLeuValAspSe 115  
Db 105315 CAGAGTTGTGTGGTGTGGGACTAGAAAGACGGTCTCTGTGATCATAGTAGGGTTTC 105256  
Qy 115 rLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLe 135  
Db 105255 CTGCAAGGTAGGTGTAGTTTGCACATCAGAAAACAGATGAAGAGTACTAGCAGGAGC 105196  
Qy 135 uThrLeuLeuLeuAlaLeuLeu 143  
Db 105195 TACCTTGCTCTTCTAGTCTTTGTG 105171

RESULT 90

US-09-949-016-12557/c  
; Sequence 12557, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12557  
; LENGTH: 421883  
; TYPE: DNA  
; ORGANISM: Human  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(421883)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-12557

Alignment Scores:  
Pred. No.: 1e+04 Length: 421883  
Score: 79.00 Matches: 43  
Percent Similarity: 38.46% Conservative: 22  
Best Local Similarity: 25.44% Mismatches: 57  
Query Match: 8.49% Indels: 47  
DB: 4 Gaps: 7

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-12557 (1-421883)

Qy 8 TrpArgAspIle-----LysLysThrGlyValValPhe-----Gly 19  
Db 105633 TGGCATGAATTTTAAATTTGAAATTTGCAATGCAATGCTACATTCACCATGTAATGGG 105574  
Qy 20 AlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr 39  
Db 105573 GAGGCTTTAAATTTGCTATTTAGATAATATTTTATTTAGAGGTAGGGTGTGTCATAT 105514  
Qy 40 IleAlaLeu---AlaLeuLeuSerValThrIleSerPhe----- 51  
Db 105513 GTGTGTATATATACATGTATGCTTCCACAGATACCACTGACCATTCAAAAGAAATAAG 105454  
Qy 52 -----ArgIleTyrLysGlyValIleGlnAlaIleGlnLys 63  
Db 105453 AAGGATTTCTGGAGCTCACGGGAGAAATAAGCTGGGTAGACTCTTCCATAGAATCC 105394  
Qy 64 SerAspGluGlyHis-----ProPheArgAlaTyrLeuGluSerGluVal 78  
Db 105393 AGTCTGAAGGCCATCTTGCTGAAATAATCCTGTGCAGAGCC----- 105352  
Qy 79 AlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHis----- 95  
Db 105351 -----TCCCTACTTAACCTAGATTTTGCAGAAAAGACTGGA 105316  
Qy 96 ValAsnCys-ThrIleLysGluLeuArgLeuPheLeuValAspAspLeuValAspSe 115  
Db 105315 CAGAGTTGTGTGGTGTGGGACTAGAAAGACGGTCTCTGTGATCATAGTAGGGTTTC 105256  
Qy 115 rLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLe 135  
Db 105255 CTGCAAGGTAGGTGTAGTTTGCACATCAGAAAACAGATGAAGAGTACTAGCAGGAGC 105196  
Qy 135 uThrLeuLeuLeuAlaLeuLeu 143  
Db 105195 TACCTTGCTCTTCTAGTCTTTGTG 105171

RESULT 91

US-09-543-681A-2407  
; Sequence 2407, Application US/09543681A

```
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 2407
; LENGTH: 1341
; TYPE: DNA
; ORGANISM: Proteus mirabilis
; US-09-543-681A-2407

Alignment Scores:
Pred. No.: 1.13 Length: 1341
Score: 78.50 Matches: 34
Percent Similarity: 37.00% Conservative: 40
Best Local Similarity: 17.00% Mismatches: 55
Query Match: 8.43% Indels: 71
DB: 4 Gaps: 8

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-543-681A-2407 (1-1341)

QY 15 GlyValValPheGlyAlaSerLeuPhe----- 23
Db 199 GGGCTTTTATTGGTACCTCATTGTTGGCTATATTGGACAAAGTAGGCGCCGTAA 258
QY 24 ---LeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42
Db 259 ATGTTCTCGTGTGATATTGGCTATTGGCGGTGATTCT-----ATTGGCACC 306
QY 43 AlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62
Db 307 ATGTTTGTTCACACCAATAGGTTGTAGTATCGCTTCCTTATTGGGATTGG--- 363
QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
Db 364 -----ATTGGCGCTGACTATCTTATGCAACT 390
QY 83 GluLeuValGlnLysTyrSerAsn-----Ser 91
Db 391 TCGATGATCACCAGAAATTTCCAAATAAAAGCAACGTGCTTTTGGCGTGGATTATTGCT 450
QY 92 AlaLeuGlyHisValAsnCysThrIleLysGluLeuArgAlaGluPheLeuValAspAsp 111
Db 451 GCTATGTGGTATATCGGTGGACATGTGCCAATTAGTGGT---TATCTTTTATATGAT 507
QY 112 LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeu 131
Db 508 GTTCAAGATGGCTGGCGT-----TGGATG-----TTAGCAGTGTCT 543
QY 132 PheAsnGlyLeuThrLeuLeuLeuAla----- 141
Db 544 TTATTCTTGGCTTATTATCTTAATTGGTGGCTTTGATCTCCCTGAATCAGCGCTTTGG 603
QY 142 -----LeuIleSerLeuPheSerVal 148
Db 604 TTAATACCGCAGGACGTATTAAAGAGTGAATAAATGATGATCAACTCTTTGGCGAG 663
QY 149 ProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaSerLys 168
Db 664 CCTGTGCTCTTTGAACGACAGAGTGTAAACACGCCGTTTATTCGAATTAATAAAA 723

RESULT 92
US-09-489-039A-5041
; Sequence 5041, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
```

```
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 5041
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-5041

Alignment Scores:
Pred. No.: 0.674 Length: 879
Score: 78.00 Matches: 38
Percent Similarity: 39.87% Conservative: 25
Best Local Similarity: 24.05% Mismatches: 65
Query Match: 8.38% Indels: 30
DB: 4 Gaps: 6

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-489-039A-5041 (1-879)

QY 6 LeuTyrTrpArgAspIleLysLys-----ThrGlyValValPheGly 19
Db 82 CTGCTGTGGCGCGCATTTGATGAAGACCATATGACACCTCGCGGGAACTCGGCTAT 141
QY 20 AlaSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr 39
Db 142 GTGTCACTACTCTCTCGTGGCGGTGATTGCGGTGCTGCTGCTGCTGCTGCTGCTT 201
QY 40 IleAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGln 59
Db 202 CCTATGTTCTCCGAAGTCAGCGTCAGATCCGCTCATTTTATCTGCCAATTTATTCG 261
QY 60 AlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAla 79
Db 262 GCG-----ACCGGGATGTAATCCAGGATATATCGAGCATGTTGCGGCC 306
QY 80 IleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThr 99
Db 307 AACTCCAGCGCATG-----ACCGGTAGGCGCTTTGCGCTGATC 348
QY 100 IleLysGluLeuArgAlaGluPheLeuValAspAspLeuValAspSerLeu----- 116
Db 349 GTCACTCGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 408
QY 117 -----LysPheAlaValLeuMetTrpValPheThrTyrVal 128
Db 409 ACGCGCAGCGCGCCCAAGTTTATCTTTGCGGT-----TACTGGATGATCTTGACCCCTC 465
QY 129 GlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla---LeuIleSerLeu 145
Db 466 GGCCCGCTGCTGCGGGCGCCAGCTGCGGATCAGTTCCTCTATCTGTGTGCTG 519

RESULT 93
US-09-949-016-12900
; Sequence 12900, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
```

; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12900  
; LENGTH: 462589  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-12900

Alignment Scores:  
Pred. No.: 1.61e+04 Length: 462589  
Score: 78.00 Matches: 45  
Percent Similarity: 38.17% Conservativeness: 26  
Best Local Similarity: 24.19% Mismatches: 49  
Query Match: 8.38% Indels: 66  
DB: 4 Gaps: 8

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-12900 (1-462589)

Qy 24 LeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyriLeAlaLeuAla 43  
Db 110616 CTACTTTTGTCTAGTATCTAC-----ATTACACCGATTAACTTAATCAGT 110663  
Qy 44 LeuLeu-----SerValThrIleSerPheArgIleTyriysGly 56  
Db 110664 GTCATGTGCTCTGCTAACTGCAATTAATTTGTCTGTATTTTCATTCGGCATCTACAAAATG 110723  
Qy 57 VallileGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyriLeuGluSer 76  
Db 110724 GTAATAAACATA-----GGACATATTTTATAGGGCTATATATTTGAAT 110765  
Qy 77 GluValAlaIleSerGluGluLeuValGlnLysTyriSerAsnSerAlaLeuGlyHisVal 96  
Db 110766 -----GTATTAAATGAGAAATCCTTCAGTATTCCTTAGCACTGTGCTAGAACATGAA 110819  
Qy 97 Asn-----CysThrIleLysGluLeuArgLeuPheLeuValAsp 110  
Db 110820 AACTCTTAATAAGCTTGGCTATTAGTCTGTGTAACCGTAAGACTGTTCTGTCTTAT 110879  
Qy 111 AspLeuValAspSerLeuLysPheAlaValLeuMetTrp-----123  
Db 110880 CCCTTGTGTTATCCCACTTCTTTGCACAGAACTTGTGGCAGCAGATTAATCATAGAAA 110939  
Qy 124 -----ValPheThr-----126  
Db 110940 TTATTGAATAAATTAATGGTCCCATTTTTCCTAGTCCACTGTGGTGAAGTCTCAGAT 110999  
Qy 127 -----TyrValGlyAlaLeuPheAsnGlyLeu-----135  
Db 111000 TCCCAAGGATGTGGTGTGTGCAGATAGTTCCATGTGGCCAGGGCTCTTGTTCAGTTTA 111059  
Qy 136 -----ThrLeuLeuLeuLeuAlaLeuLeuSerLeuPheSerValPro 149  
Db 111060 GTGTATTATTCTGCCACACTTGTCTTAATCCAGATTGAATTTGCTTTTATGAAGATA 111119  
Qy 150 VallileTyriGluArgHis 155  
Db 111120 GTAATATATGGAGGCAT 111137

## RESULT 94

US-09-949-016-12412  
; Sequence 12412, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12412  
; LENGTH: 476044  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-12412

Alignment Scores:  
Pred. No.: 1.68e+04 Length: 476044  
Score: 78.00 Matches: 45  
Percent Similarity: 38.17% Conservativeness: 26  
Best Local Similarity: 24.19% Mismatches: 49  
Query Match: 8.38% Indels: 66  
DB: 4 Gaps: 8

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-949-016-12412 (1-476044)

Qy 24 LeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyriLeAlaLeuAla 43  
Db 124072 CTACTTTTGTCTAGTATCTAC-----ATTACACCGATTAACTTAATCAGT 124119  
Qy 44 LeuLeu-----SerValThrIleSerPheArgIleTyriysGly 56  
Db 124120 GTCATGTGCTCTGCTAACTGCAATTAATTTGTCTGTATTTTCATTCGGCATCTACAAAATG 124179  
Qy 57 VallileGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyriLeuGluSer 76  
Db 124180 GTAATAAACATA-----GGACATATTTTATAGGGCTATATATTTGAAT 124221  
Qy 77 GluValAlaIleSerGluGluLeuValGlnLysTyriSerAsnSerAlaLeuGlyHisVal 96  
Db 124222 -----GTATTAAATGAGAAATCCTTCAGTATTCCTTAGCACTGTGCTAGAACATGAA 124275  
Qy 97 Asn-----CysThrIleLysGluLeuArgLeuPheLeuValAsp 110  
Db 124276 AACTCTTAATAAGCTTGGCTATTAGTCTGTGTAACCGTAAGACTGTTCTGTCTTAT 124335  
Qy 111 AspLeuValAspSerLeuLysPheAlaValLeuMetTrp-----123  
Db 124336 CCCTTGTGTTATCCCACTTCTTTGCACAGAACTTGTGGCAGCAGATTAATCATAGAAA 124395  
Qy 124 -----ValPheThr-----126  
Db 124396 TTATTGAATAAATTAATGGTCCCATTTTTCCTAGTCCACTGTGGTGAAGTCTCAGAT 124455  
Qy 127 -----TyrValGlyAlaLeuPheAsnGlyLeu-----135  
Db 124456 TCCCAAGGATGTGGTGTGTGCAGATAGTTCCATGTGGCCAGGGCTCTTGTTCAGTTTA 124515  
Qy 136 -----ThrLeuLeuLeuLeuAlaLeuLeuSerLeuPheSerValPro 149  
Db 124516 GTGTATTATTCTGCCACACTTGTCTTAATCCAGATTGAATTTGCTTTTATGAAGATA 124575  
Qy 150 VallileTyriGluArgHis 155  
Db 124576 GTAATATATGGAGGCAT 124593

## RESULT 95

US-09-198-452A-1  
; Sequence 1, Application US/09198452A  
; Patent No. 655294  
; GENERAL INFORMATION:  
; APPLICANT: Griffiths, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
; thereof and uses thereof, in particular for the diagnosis, prevention  
; TITLE OF INVENTION: and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/09/198,452A  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 6849



NAME/KEY: misc feature  
LOCATION: (705001)..(720000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (720001)..(735000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (735001)..(750000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (750001)..(765000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (765001)..(780000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (780001)..(795000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (795001)..(810000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (810001)..(825000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (825001)..(840000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (840001)..(855000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (855001)..(870000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (870001)..(885000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (885001)..(900000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (900001)..(915000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature

Alignment Scores:  
Pred. No.: 7.64e+04 Length: 1230025  
Score: 78.00 Matches: 34  
Percent Similarity: 40.41% Conservative: 25  
Best Local Similarity: 23.29% Mismatches: 65  
Query Match: 8.38% Indels: 23  
DB: 4 Gaps: 5

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-198-452A-1 (1-1230025)

Qy 6 LeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeuPheLeuLeu 25  
Db 1042940 ATGTTTGGATGGACTTCTGCAGGAACC-ATGTCCTTTGCTGCTGGGCTTTATTTC 1042998  
Qy 26 LeuSerLeu-----ThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAla 43  
Db 1042999 CTAGCTCTAAGAAGTTCCTACAAATTCCTATAGCTCAAGATGTGGCTTATGTTTAGCTGCT 1043058  
Qy 44 LeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAlaIleGlnlys 63  
Db 1043059 CTGTAGGGGCTTGTATCGGATTCCTATGTTATGTTTCCCGGCCAGCTCTTCATG 1043118  
Qy 64 SerAspGluGlyHis-----ProPheArgAlaTyrIleuGlu 75  
Db 1043119 GGAGATACCGGGTCACTACTTCTAGGGGCTGCTAGGAGCTCGCTGTTATGCTGCGC 1043178  
Qy 76 SerGlu-----ValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAla 92  
Db 1043179 GCAGATGCATCCTAGTCGTATCGGAGGAGTTTTTTGTTGTTGTAAGCGGATCTGTCATT 1043238

Qy 93 LeuGlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeu 112  
Db 1043239 CTACAGTACTAGTTGTAGATTAAAGGAAA---AAACGCCCTTTCTTATGCTCTCATTTG 1043295  
Qy 113 -----ValAspSerLeuLysPheAlaValLeuMetTrpVal 124  
Db 1043296 CATCACCATTATGAATATCAGGGCTCCAGAGACTAAATCGTCATCGCTTTTGGATC 1043355  
Qy 125 PheThrTyrValGlyAla 130  
Db 1043356 TTTAGTTTGTATGCGCA 1043373  
RESULT 96  
US-09-438-185A-1  
; Sequence 1, Application US/09438185A  
; Patent No. 6822071  
; GENERAL INFORMATION:  
; APPLICANT: Stephens, Richard  
; APPLICANT: Mitchell, Wayne  
; APPLICANT: Kalman, Sue  
; APPLICANT: Davis, Ronald  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence  
; FILE REFERENCE: 018941-000411US  
; CURRENT APPLICATION NUMBER: US/09/438.185A  
; CURRENT FILING DATE: 2002-03-13  
; PRIOR APPLICATION NUMBER: US 60/108,279  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: US 60/128,606  
; PRIOR FILING DATE: 1999-04-08  
; NUMBER OF SEQ ID NOS: 1074  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1230230  
; TYPE: DNA  
; ORGANISM: Chlamydia pneumoniae  
US-09-438-185A-1

Alignment Scores:  
Pred. No.: 7.64e+04 Length: 1230230  
Score: 78.00 Matches: 34  
Percent Similarity: 40.41% Conservative: 25  
Best Local Similarity: 23.29% Mismatches: 65  
Query Match: 8.38% Indels: 23  
DB: 4 Gaps: 5  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-438-185A-1 (1-1230230)  
Qy 6 LeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeuPheLeuLeu 25  
Db 1032818 ATGTTTGGATGGACTTCTGCAGGAACC-ATGTCCTTTGCTGCTGGGCTTTATTTC 1032876  
Qy 26 LeuSerLeu-----ThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAla 43  
Db 1032877 GTAGCTCTAAGAAGTTCCTACAAATTCCTATAGCTCAAGATGTGGCTTATGTTTAGCTGCT 1032936  
Qy 44 LeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAlaIleGlnlys 63  
Db 1032937 CTGTAGGGGCTTGTATCGGATTCCTATGTTATGTTTCCCGGCCAGCTCTTCATG 1032996  
Qy 64 SerAspGluGlyHis-----ProPheArgAlaTyrIleuGlu 75  
Db 1032997 GGAGATACCGGGTCACTACTTCTAGGGGCTGCTAGGAGCTCGCTGTTATGCTGCGC 1033056  
Qy 76 SerGlu-----ValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAla 92  
Db 1033057 GCAGATGCATCCTAGTCGTATCGGAGGAGTTTTTTGTTGTTGTAAGCGGATCTGTCATT 1033116  
Qy 93 LeuGlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeu 112  
Db 1033117 CTACAGTACTAGTTGTAGATTAAAGGAAA---AAACGCCCTTTCTTATGCTCTCCATTG 1033173

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QY 113 -----ValAspSerLeuLysPheAlaValLeuMetTrpVal 124
Db 1033174 CATCACCATTATGAATATCAGGCGCTCCAGAGACTAAATCGTCATGCGCTTTTGGATC 1033233
QY 125 PheThrTyrValGlyAla 130
Db 1033234 TTATGTTTGTATGCGCA 1033251

RESULT 97
US-09-248-796A-730
; Sequence 730, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 730
; LENGTH: 1152
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-730

Alignment Scores:
Pred. No.: 1,22 Length: 1152
Score: 77.50 Matches: 35
Percent Similarity: 34.72% Conservative: 15
Best Local Similarity: 24.31% Mismatches: 27
Query Match: 67 Indels: 67
DB: 5 Gaps: 5

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-248-796A-730 (1-1152)
QY 13 LysThrGlyValValPheGlyAlaSerLeuPheLeuSerLeuThrValPheSer 32
Db 91 AAAACTTCATTAATTCATCAAAACACTC-----CTGACACTATTATT 135
QY 33 IleValSerValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerPheArg 52
Db 136 ATGATTTCCTTAAGGCGAGTAATCGCACTTATCTTTTACCACCTAAATTTATTATTGTT 195
QY 53 IleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisPropheArgAla 72
Db 196 TTAATCAAA-----TATCCATT----- 213
QY 73 TyrLeuGluSerGluValAlaIleSerGluLeuValGlnLysTyrSerAsnSerAla 92
Db 213 ----- 213
QY 93 LeuGlyHisValAsnCysThrIleLysGluLeuArgLeuPheLeuValAspLeu 112
Db 214 TTCGGGGGTAAACCTATATACAAG-----AATGATTG 249
QY 113 ValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyr----- 127
Db 250 GTCAATTCTTGAATTAACCGTTTATCAAGCATTAACTTCCCACTTGATGATGTT 309
QY 128 -----ValGlyAlaLeuPhe 132
Db 310 CATATTTTCAATAATTCTGCTGAATTGTGTTATCAATAAAGCTGTGGTAAATTATAT 369
QY 133 AsnGlyLeuThr 136
Db 370 CCTGGTTTAAACA 381

RESULT 98
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```
US-09-543-681A-215/c
; Sequence 215, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 215
; LENGTH: 1167
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-215

Alignment Scores:
Pred. No.: 1,25 Length: 1167
Score: 77.50 Matches: 30
Percent Similarity: 43.85% Conservative: 27
Best Local Similarity: 23.08% Mismatches: 42
Query Match: 8.32% Indels: 31
DB: 4 Gaps: 5

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-543-681A-215 (1-1167)
QY 30 ValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuSerValThrIle 49
Db 395 GTTTTCTCGTAATCGCGCTTCAATTTTGTTCATCAAGGTTTCATG-----GTA 345
QY 50 SerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisPro 69
Db 344 TCTGGACGAATATCGACAACAACAATAGTCGCCACCAAGTAAACA----- 300
QY 70 PheArgAlaTyr---LeuGluSerGluVal----- 78
Db 299 ---AAGGCGTTCGAAATCGAAACAAAGTGAACACTCGGCATATCATCTTCATCGCGGGT 243
QY 79 -----AlaIleSerGluGluLeuValGlnLysTyrSerAsnSer 91
Db 242 TTGATATCAGAGATAGCCGCCATTCTTAACGATGCTGTACAGAAGGTGTTAACAGC 183
QY 92 AlaLeuGlyHisValAsnCysThrIleLysGluLeuArgLeuPheLeuValAspAsp 111
Db 182 GTCATTATGACAATGAATTTGTTCTTCTTAACCACTTTTTCACATTTTTCGTGAAGTTGCCA 123
QY 112 LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThr-----Tyr 127
Db 122 TCACCACAGAGCTTGCCACTTTCCCATCGCCTGTTTCATATACTACTTAATTTCTGTGCCAACA 63
QY 128 ValGlyAlaLeuPheAsnGlyLeuThrLeu 137
Db 62 ACGGGTGGTTTATTAAACGAATCATATTA 33

RESULT 99
US-09-620-312D-751
; Sequence 751, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
```

APPLICANT: Zhou, Ping  
APPLICANT: Ma, Yungqing  
APPLICANT: Wang, Dunrui  
APPLICANT: Wang, Zhiwei  
APPLICANT: John Tillinghast  
APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: No. 6569662el Nucleic Acids and  
FILE REFERENCE: 784CIP2B  
CURRENT APPLICATION NUMBER: US/09/620,312D  
CURRENT FILING DATE: 2000-07-19  
PRIOR APPLICATION NUMBER: 09/552,317  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 09/488,725  
PRIOR FILING DATE: 2000-01-21  
NUMBER OF SEQ ID NOS: 1105  
SOFTWARE: pt\_FL\_genes Version 1.0  
SEQ ID NO 751  
LENGTH: 2020  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (222)..(1196)  
US-09-620-312D-751

Alignment Scores:  
Pred. No.: Length: 2020  
Score: 3.02  
Percent Similarity: 77.50  
Best Local Similarity: 42.98%  
Query Match: 28.10%  
Indels: 44  
Gaps: 25  
DB: 4

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-620-312D-751 (1-2020)

Qy 75 GluSerGluValAlaIleSer-----GluGluLeuValGlnLysTySerAsnSerAla 92  
Db 189 GAACTGAATTGTCTATTTTCACCTGGAAGAAAATGATAGACAAAATCAAACTGTGGT 248  
Qy 93 LeuGly-----HisValAsnCysThrIleLysGluLeuArgLeuPhe 107  
Db 249 GTAGCAGAGGATTCGTGCCCTATATGATTGTCTGATTTCACATCTCGAAGAATGGTTT 308  
Qy 108 LeuValAspAspLeuValAspSerLeuLysPheAla-----ValLeuMetTrpValPheThr 126  
Db 309 GGTGGGAGCAGTTCGAGGACTATTGTGAATTTGCAAACTATCTCTGTGGGTTTTTACA 368  
Qy 127 TyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPhe 146  
Db 369 -----CCACTAATCTTTTAATCTTCTTACTTCTTACTTACTTCTTT 407  
Qy 147 SerValProVal-----IleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db 408 CTCTCTACCTTACTTATTATTTCCTACATTTTATAGAGAAGAAATGATTGAAAGAA 467  
Qy 161 HisTyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLeuIleGlnAlaLys 180  
Db 468 GCCTAC-----TCTCATAAATTTATGGGATGTGCAAGGAAACACAGTGGCAACT 515  
Qy 181 Ile 181  
Db 516 CTG 518

RESULT 100

US-09-949-016-12735  
Sequence 12735, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12735  
LENGTH: 80355  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-12735  
Alignment Scores:  
Pred. No.: Length: 80355  
Score: 1.13e+03  
Percent Similarity: 77.50  
Best Local Similarity: 57.14%  
Query Match: 42.86%  
Indels: 20  
Gaps: 1  
DB: 4  
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Db 42680 AGATGAGGCTCTGGGATGATACAGCTCTTCTCAG---GACTCTGGGAACCCCTTAAGG 42736  
Qy 72 AlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTySerAsnSer 91  
Db 42737 GCCTGCTTGAACCTCAGAAAGTTGGTGGCTCAGCCAGCAGCTCTCTGCTGTCGCA 42796  
Qy 92 AlaLeuGlyHisValAsnCysThrIle 100  
Db 42797 CGCTTGATATCACACACTTGTGATGTG 42823  
Search completed: June 19, 2005, 05:38:14  
Job time : 2629.5 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 19, 2005, 03:56:06 : Search time 445.5 Seconds  
(without alignments)  
2633.504 Million cell updates/sec

Title: US-09-830-972-29\_COPY\_990\_1178

Perfect score: 931

Sequence: 1 SVDDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRAE 189

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 6054689 seqs, 3103772919 residues

Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:\*

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9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*  
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22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq:\*  
24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	931	100.0	600	21	US-10-956-157-9764 Sequence 9764, Ap
2	931	100.0	1400	21	US-10-956-157-9763 Sequence 9763, Ap
3	931	100.0	2883	21	US-10-956-157-4529 Sequence 4529, Ap
4	931	100.0	3478	21	US-10-956-157-4528 Sequence 4528, Ap
5	931	100.0	3579	9	US-09-789-386-1 Sequence 1, Appli
6	931	100.0	3579	9	US-09-789-386-22 Sequence 22, Appli
7	931	100.0	3579	18	US-10-327-502-212 Sequence 212, App
8	931	100.0	3579	19	US-10-327-213-8 Sequence 8, Appli
9	931	100.0	3579	19	US-10-466-258-8 Sequence 8, Appli
10	931	100.0	3579	20	US-10-810-653-22 Sequence 22, Appli
11	931	100.0	4053	9	US-09-758-140-5 Sequence 5, Appli
12	931	100.0	4053	9	US-09-772-599A-5 Sequence 5, Appli
13	931	100.0	4053	19	US-10-717-597-310 Sequence 310, App
14	931	100.0	4623	21	US-10-956-157-4532 Sequence 4532, Ap
15	931	100.0	4632	14	US-10-060-036-53 Sequence 53, Appli
16	927	99.6	799	18	US-10-660-946-2 Sequence 2, Appli
17	927	99.6	1122	9	US-09-789-386-5 Sequence 5, Appli
18	927	99.6	1160	14	US-10-175-523-156 Sequence 156, App
19	927	99.6	1609	21	US-10-956-157-4527 Sequence 4527, Ap
20	927	99.6	1610	9	US-09-765-205-5 Sequence 5, Appli
21	927	99.6	1610	21	US-10-347-669-5 Sequence 5, Appli
22	927	99.6	1785	17	US-10-439-388-62 Sequence 62, Appli
23	927	99.6	1785	21	US-10-956-157-1705 Sequence 1705, Ap
24	927	99.6	2050	21	US-10-956-157-4530 Sequence 4530, Ap
25	927	99.6	2052	19	US-10-466-258-3 Sequence 3, Appli
26	927	99.6	2226	21	US-10-956-157-4531 Sequence 4531, Ap
27	927	99.6	2235	14	US-10-060-036-54 Sequence 54, Appli
28	921	98.9	1980	17	US-10-220-891-22 Sequence 22, Appli
29	918	98.6	994	11	US-09-978-360A-110 Sequence 110, App
30	914	98.2	2610	18	US-10-641-643-382 Sequence 382, App
31	908	97.5	4684	9	US-09-893-348-17 Sequence 17, Appli
32	908	97.5	4684	20	US-10-810-653-17 Sequence 17, Appli
33	905	97.2	2782	15	US-10-205-194-165 Sequence 165, App
34	904.5	97.2	3492	18	US-10-267-502-214 Sequence 214, App
35	886	95.2	1798	19	US-10-466-258-10 Sequence 10, Appli
36	872	93.7	1400	21	US-10-956-157-9765 Sequence 9765, Ap
37	867	93.1	1514	9	US-09-823-245A-349 Sequence 349, App
38	805	86.5	1400	21	US-10-956-157-9762 Sequence 9762, Ap
39	805	86.5	1400	21	US-10-956-157-9767 Sequence 9767, Ap
40	718	77.1	1400	21	US-10-956-157-9766 Sequence 9766, Ap
41	695	74.7	422	9	US-09-960-352-8477 Sequence 8477, Ap
42	682	73.3	1520	15	US-10-084-817-333 Sequence 333, App
43	682	73.3	2331	18	US-10-267-502-213 Sequence 213, App
44	682	73.3	3202	9	US-09-954-456-210 Sequence 210, App
45	682	73.3	3202	17	US-10-172-118-386 Sequence 386, App

#### ALIGNMENTS

##### RESULT 1

US-10-956-157-9764  
; Sequence 9764, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956.157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9764

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; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-9764

Alignment Scores:
Pred. No.: 2,566-107 Length: 600
Score: 931.00 Matches: 189
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-956-157-9764 (1-600)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
DB 31 TCAGTTGTTGACCTCTCTGCTACTGGAGACATTAAAGAGACTGGAGTGGTGTGGTGC 90
QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 91 AGCCTATTCTCTGCTTTTCATTGACAGTATTTCAGCAATTTGTGAGCGTAAACAGCTACATT 150
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
DB 151 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCT 210
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 211 ATCCAGAAATCAGATGAAAGCCACCCATTTCAGGCATATCTGGAATCTGAAGTTGCTATA 270
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
DB 271 TCTGAGGAGTTGGTTTCAGAAAGTACAGTAATCTCTCTCTGGTTCATGTGAACGTCACGATA 330
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
DB 331 AAGGAACCTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTCAGAGT 390
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
DB 391 TTGATGTGGGTATTTACCTATGTTGGTGCCTTTGTTTAAATGGTCTGACACTACTGATTTTG 450
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
DB 451 GCTCTCAATTCATCTCTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 510
QY 161 HisTyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLys 180
DB 511 CATTTATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTTAAATCCAGCAAAA 570
QY 181 IleProGlyLeuLysArgLysAlaGlu 189
DB 571 ATCCCTGGATTGAAGCGCAAGCTGAA 597

RESULT 2
US-10-956-157-9763
; Sequence 9763, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9763
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens

; Alignment Scores:
Pred. No.: 9,8e-107 Length: 1400
Score: 931.00 Matches: 189
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-956-157-9763 (1-1400)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
DB 488 TCAGTTGTTGACCTCTCTGCTACTGGAGACATTAAAGAGACTGGAGTGGTGTGGTGC 547
QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 548 AGCCTATTCTCTGCTTTTCATTGACAGTATTTCAGCAATTTGTGAGCGTAAACAGCTACATT 607
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
DB 608 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCT 667
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 668 ATCCAGAAATCAGATGAAAGCCACCCATTTCAGGCATATCTGGAATCTGAAGTTGCTATA 727
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
DB 728 TCTGAGGAGTTGGTTTCAGAAAGTACAGTAATCTCTCTCTCTGGTTCATGTGAACGTCACGATA 787
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
DB 788 AAGGAACCTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTCAGAGT 847
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
DB 848 TTGATGTGGGTATTTACCTATGTTGGTGCCTTTGTTTAAATGGTCTGACACTACTGATTTTG 907
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
DB 908 GCTCTCAATTCATCTCTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 967
QY 161 HisTyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLys 180
DB 968 CATTTATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTTAAATCCAGCAAAA 1027
QY 181 IleProGlyLeuLysArgLysAlaGlu 189
DB 1028 ATCCCTGGATTGAAGCGCAAGCTGAA 1054

RESULT 3
US-10-956-157-4529
; Sequence 4529, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4529
; LENGTH: 2883
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4529

; Alignment Scores:
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US-10-956-157-9763

Alignment Scores:
Pred. No.: 9,8e-107 Length: 1400
Score: 931.00 Matches: 189
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-956-157-9763 (1-1400)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
DB 488 TCAGTTGTTGACCTCTCTGCTACTGGAGACATTAAAGAGACTGGAGTGGTGTGGTGC 547
QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 548 AGCCTATTCTCTGCTTTTCATTGACAGTATTTCAGCAATTTGTGAGCGTAAACAGCTACATT 607
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
DB 608 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCT 667
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 668 ATCCAGAAATCAGATGAAAGCCACCCATTTCAGGCATATCTGGAATCTGAAGTTGCTATA 727
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
DB 728 TCTGAGGAGTTGGTTTCAGAAAGTACAGTAATCTCTCTCTCTGGTTCATGTGAACGTCACGATA 787
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
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QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
DB 848 TTGATGTGGGTATTTACCTATGTTGGTGCCTTTGTTTAAATGGTCTGACACTACTGATTTTG 907
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
DB 908 GCTCTCAATTCATCTCTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGAT 967
QY 161 HisTyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLys 180
DB 968 CATTTATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTTAAATCCAGCAAAA 1027
QY 181 IleProGlyLeuLysArgLysAlaGlu 189
DB 1028 ATCCCTGGATTGAAGCGCAAGCTGAA 1054

RESULT 3
US-10-956-157-4529
; Sequence 4529, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4529
; LENGTH: 2883
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4529

; Alignment Scores:
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Pred. No.: 3.08e-106 Length: 2883  
 Score: 931.00 Matches: 189  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 21 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-956-157-4529 (1-2883)

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 DB 2314 TCAGTTGTGACCTCTGCTACTGGAGACATTAAAGAGCTGGAGTGGTGGTGC 2373  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 2374 AGCCTATTCTGCTCTTCATTGACAGTATTGACAGTGTGAGGCTAACAGCTACATT 2433  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 2434 GCCTTGGCCCTGCTCTGTCGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAAGCT 2493  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 2494 ATCCAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGAAAGTTGCTATA 2553  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 DB 2554 TCTGAGGAGTTGGTTCAGAGTACAGTAATCTGCTCTGTCATGTGACTGACAGATA 2613  
 QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 2614 AAGCAACTCAGCGCCTCTCTTAGTTCATGATTAGTTAGTTCTCTGAAAGTTGACGTG 2673  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 DB 2674 TTGATGTGGGTATTACCTATGTTGGTCCCTGTTTAAATGCTGACACTACTGATTTTG 2733  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 DB 2734 GCTCTCATTTCACTCTTCAGTGTCCCTGTTTATTTATGAACGGCATCAGGCACAGATAGT 2793  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 2794 CATTATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAA 2853  
 QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
 DB 2854 ATCCCTGGATTGAAGCGCAAAAGCTGAA 2880

RESULT 4  
 ; US-10-956-157-4528  
 ; Sequence 4528, Application US/10956157  
 ; Publication No. US20050118625A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wyeth  
 ; APPLICANT: Mounts, William  
 ; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
 ; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
 ; FILE REFERENCE: 031896-043000 (AM 101081)  
 ; CURRENT APPLICATION NUMBER: US/10/956.157  
 ; PRIOR FILING DATE: 2004-10-04  
 ; NUMBER OF SEQ ID NOS: 319805  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 4528  
 ; LENGTH: 3478  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-956-157-4528

Alignment Scores:  
 Pred. No.: 4.14e-106 Length: 3478  
 Score: 931.00 Matches: 189  
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 21 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-956-157-4528 (1-3478)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
 DB 2566 TCAGTTGTGACCTCTGCTACTGGAGACATTAAAGAGCTGGAGTGGTGGTGC 2625  
 QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
 DB 2626 AGCCTATTCTGCTCTTCATTGACAGTATTGACAGTGTGAGGCTAACAGCTACATT 2685  
 QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
 DB 2686 GCCTTGGCCCTGCTCTGTCGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAAGCT 2745  
 QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
 DB 2746 ATCCAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGAAAGTTGCTATA 2805  
 QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
 DB 2806 TCTGAGGAGTTGGTTCAGAGTACAGTAATCTGCTCTGTCATGTGAACTGACAGATA 2865  
 QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
 DB 2866 AAGCAACTCAGCGCCTCTCTTAGTTCATGATTAGTTAGTTCTCTGAAAGTTGACGTG 2925  
 QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
 DB 2926 TTGATGTGGGTATTACCTATGTTGGTCCCTGTTTAAATGCTGACACTACTGATTTTG 2985  
 QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
 DB 2986 GCTCTCATTTCACTCTTCAGTGTCCCTGTTTATTTATGAACGGCATCAGGCACAGATAGT 3045  
 QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
 DB 3046 CATTATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAA 3105  
 QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
 DB 3106 ATCCCTGGATTGAAGCGCAAAAGCTGAA 3132

RESULT 5  
 ; US-09-789-386-1  
 ; Sequence 1, Application US/09789386  
 ; Patent No. US20020010324A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MICHALOVICH, DAVID  
 ; APPLICANT: PRINJHA, RABINDER KUMAR  
 ; TITLE OF INVENTION: NOVEL COMPOUNDS  
 ; FILE REFERENCE: GP-30165-C1  
 ; CURRENT APPLICATION NUMBER: US/09/789,386  
 ; CURRENT FILING DATE: 2001-02-21  
 ; PRIOR APPLICATION NUMBER: U.K. 9916898.1  
 ; PRIOR FILING DATE: 1999-07-19  
 ; PRIOR APPLICATION NUMBER: U.K. 9816024.5  
 ; PRIOR FILING DATE: 1998-07-22  
 ; PRIOR APPLICATION NUMBER: US 09/359,208  
 ; PRIOR FILING DATE: 1999-07-22  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 3579  
 ; TYPE: DNA  
 ; ORGANISM: HOMO SAPIENS  
 ; US-09-789-386-1

Alignment Scores:  
 Pred. No.: 4.33e-106 Length: 3579

```
Score: 931.00 Matches: 189
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-789-386-1 (1-3579)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 3010 TCAGTGTGTGACCTCTCTGCTGAGAGACATTAAGAGACTGGAGTGGTGTGGTGGC 3069
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValrile 40
Db 3070 AGCCTATTCTCTGCTCTTTCATTCAGCATTTAGCATTTGAGCGTAAACAGCCTACATT 3129
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 3130 GCCTTGGCCCTCTCTCTGACCATCAGCTTTAGGATATACAAGGTTGTATCCAAGCT 3189
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 3190 ATCCAGAAATCAGATGAAGCCACCCATTTCAGGCGCATATCTGGAATCTGAAGTTGCTATA 3249
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 3250 TCTGAGGAGTTGGTTCAGAAATGACAGTAAATCTCTCTTGGTGTGAACGTCACGATA 3309
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 3310 AAGGAACCTCAGCGGCTCTCTTAGTTAGTATTTAGTTAGTTCTCTGAGTTTCAGAGT 3369
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db 3370 TTGATGTGGGTATTTACCTATGTTGGTGGCTTGTATTAATGCTGACACTACTGATTTTG 3429
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 3430 GCTCTCATTTTCACTCTTCAGTGTCTCTGTTATTAAGACGCGCATCAGCGCGAGATAGAT 3489
QY 161 HistyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 3490 CATTATCTAGGACTTGCAATTAAGAATGTTAAAGATGCTATGGCTAAATCCAGCAAAA 3549
QY 181 IleProGlyLeuLysArgLysAlaGlu 189
Db 3550 ATCCCTGGATTGAAGCGCAAAAGCTGAA 3576

RESULT 6
US-09-893-348-22
; Sequence 22, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
```

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; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3579)
; OTHER INFORMATION:
US-09-893-348-22

Alignment Scores:
Pred. No.: 4,33e-106 Length: 3579
Score: 931.00 Matches: 189
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-893-348-22 (1-3579)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 3010 TCAGTGTGTGACCTCTCTGCTGAGAGACATTAAGAGACTGGAGTGGTGTGGTGGC 3069
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValrile 40
Db 3070 AGCCTATTCTCTGCTCTTTCATTCAGCATTTAGCATTTGAGCGTAAACAGCCTACATT 3129
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 3130 GCCTTGGCCCTCTCTCTGACCATCAGCTTTAGGATATACAAGGTTGTATCCAAGCT 3189
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 3190 ATCCAGAAATCAGATGAAGCCACCCATTTCAGGCGCATATCTGGAATCTGAAGTTGCTATA 3249
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 3250 TCTGAGGAGTTGGTTCAGAAATGACAGTAAATCTCTCTTGGTGTGAACGTCACGATA 3309
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 3310 AAGGAACCTCAGCGGCTCTCTTAGTTAGTATTTAGTTAGTTCTCTGAGTTTCAGAGT 3369
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db 3370 TTGATGTGGGTATTTACCTATGTTGGTGGCTTGTATTAATGCTGACACTACTGATTTTG 3429
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 3430 GCTCTCATTTTCACTCTTCAGTGTCTCTGTTATTAAGACGCGCATCAGCGCGAGATAGAT 3489
QY 161 HistyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 3490 CATTATCTAGGACTTGCAATTAAGAATGTTAAAGATGCTATGGCTAAATCCAGCAAAA 3549
QY 181 IleProGlyLeuLysArgLysAlaGlu 189
Db 3550 ATCCCTGGATTGAAGCGCAAAAGCTGAA 3576

RESULT 7
US-10-267-502-212
; Sequence 212, Application US/10267502
; Publication No. US200400071700A1
; GENERAL INFORMATION:
; APPLICANT: Galant, Ron
; APPLICANT: Kim, Jaeseob
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 212
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; LENGTH: 3579  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-267-502-212

Alignment Scores:  
Pred. No.: 4.33e-106 Length: 3579  
Score: 931.00 Matches: 189  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 18 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-267-502-212 (1-3579)

```
Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 3010 TCAGTTGTGACCTCCCTGCTACTCGAGAGACATTAAGAAGACTGGAGTGGTGGTGGCC 3069
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 3070 AGCCTATTCTCGCTGCTTTCATTCACAGATTTACAGCATTTGAGCGTAACAGCCTACATT 3129
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 3130 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAAGCT 3189
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 3190 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGCGCATATCTGGAATCTGAAGTTGCTATA 3249
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 3250 TCTGAGGAGTTGGTTCAGAGTACAGTAATTCCTGCTCTTGGTCAATGTAAGTGGCAGATA 3309
Qy 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 3310 AAGGAACCTCAGGCGCCCTCTCTTAGTTGATGATTAGTTAGTTCTCTGAAAGTTGCAAGTG 3369
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 3370 TTGATGTGGGTATTTACCTATGTTGGTGGCTTGGTTAATGGTCTGACACTACTGATTTTG 3429
Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 3430 GCTCTCAATTCACCTTCAGTGTCTCTGTTTATTTATGACGGCATCAGGCGCAGATAGAT 3489
Qy 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 3490 CATTATCTAGGACTTGCATAATAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAA 3549
Qy 181 IleProGlyLeuLysArgLysAlaGlu 189
Db 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576
```

RESULT 8

US-10-327-213-8

; Sequence 8, Application US/10327213  
; Publication No. US20040121341A1  
; GENERAL INFORMATION:  
; APPLICANT: FILBIN, MARIE T.  
; APPLICANT: DOMENICONI, MARCO  
; APPLICANT: CAO, ZIXUAN  
; TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)  
; FILE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION  
; FILE REFERENCE: CUNY/003  
; CURRENT APPLICATION NUMBER: US/10/327,213  
; CURRENT FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: Patent in ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 3579  
; TYPE: DNA

; ORGANISM: Homo sapiens  
US-10-327-213-8

Alignment Scores:  
Pred. No.: 4.33e-106 Length: 3579  
Score: 931.00 Matches: 189  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 19 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-327-213-8 (1-3579)

```
Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db 3010 TCAGTTGTGACCTCCCTGCTACTCGAGAGACATTAAGAAGACTGGAGTGGTGGTGGCC 3069
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 3070 AGCCTATTCTCGCTGCTTTCATTCACAGATTTACAGCATTTGAGCGTAACAGCCTACATT 3129
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 3130 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAAGCT 3189
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 3190 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGCGCATATCTGGAATCTGAAGTTGCTATA 3249
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 3250 TCTGAGGAGTTGGTTCAGAGTACAGTAATTCCTGCTCTTGGTCAATGTAAGTGGCAGATA 3309
Qy 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 3310 AAGGAACCTCAGGCGCCCTCTCTTAGTTGATGATTAGTTAGTTCTCTGAAAGTTGCAAGTG 3369
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 3370 TTGATGTGGGTATTTACCTATGTTGGTGGCTTGGTTAATGGTCTGACACTACTGATTTTG 3429
Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 3430 GCTCTCAATTCACCTTCAGTGTCTCTGTTTATTTATGACGGCATCAGGCGCAGATAGAT 3489
Qy 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 3490 CATTATCTAGGACTTGCATAATAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAA 3549
Qy 181 IleProGlyLeuLysArgLysAlaGlu 189
Db 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576
```

RESULT 9

US-10-466-258-8

; Sequence 8, Application US/10466258  
; Publication No. US20040132096A1  
; GENERAL INFORMATION:  
; APPLICANT: GLAXO GROUP LIMITED  
; TITLE OF INVENTION: ASSAY  
; FILE REFERENCE: P80966 GCW  
; CURRENT APPLICATION NUMBER: US/10/466,258  
; CURRENT FILING DATE: 2003-07-15  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 8  
; LENGTH: 3579  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(3579)  
US-10-466-258-8

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Alignment Scores:
Pred. No.: 4,33e-106 Length: 3579
Score: 931.00 Matches: 189
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-466-258-8 (1-3579)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
DB 3010 TCAGTTGTGTGACCTCTGTACTGGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGCC 3069

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 3070 AGCCTATTCTCTGCTGCTTCATTCAGAGTATTCAGCATTTGTGAGGTAAACAGCCTACATT 3129

QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
DB 3130 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCT 3189

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 3190 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3249

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
DB 3250 TCTGAGGAGTTGGTTCAGAGTACAGTAATCTCTGCTTGTGTCATGTGACGACGATA 3309

QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
DB 3310 AAGGAACCTCAGCGCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTCAGTG 3369

QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuIleLeu 140
DB 3370 TTGATGTGGGTATTTACCTATCTTGGTGCCTTGTGTTTAAATGGTCTGACACTACTGATTTTG 3429

QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
DB 3430 GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTATGAACGGCATCAGCGGCGAGATAGAT 3489

QY 161 HistyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
DB 3490 CATTATCTAGGACTTGCATAAATAAGAAATGTTAAAGATGCTATGGCTAAAAATCCAGCAAAA 3549

QY 181 IleProGlyLeuLysArgIlyshAlaGlu 189
DB 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

RESULT 10
US-10-810-653-22
; Sequence 22, Application US/10810653
; Publication No. US20040253218A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Iron R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/10/810,653
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US/09/893,348
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
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; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3579)
; OTHER INFORMATION:
US-10-810-653-22

Alignment Scores:
Pred. No.: 4,33e-106 Length: 3579
Score: 931.00 Matches: 189
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-810-653-22 (1-3579)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
DB 3010 TCAGTTGTGTGACCTCTGTACTGGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGCC 3069

QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 3070 AGCCTATTCTCTGCTGCTTCATTCAGAGTATTCAGCATTTGTGAGGTAAACAGCCTACATT 3129

QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
DB 3130 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAAGCT 3189

QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 3190 ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3249

QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
DB 3250 TCTGAGGAGTTGGTTCAGAGTACAGTAATCTCTGCTTGTGTCATGTGACGACGATA 3309

QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
DB 3310 AAGGAACCTCAGCGCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTCAGTG 3369

QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuIleLeu 140
DB 3370 TTGATGTGGGTATTTACCTATCTTGGTGCCTTGTGTTTAAATGGTCTGACACTACTGATTTTG 3429

QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
DB 3430 GCTCTCATTTCACTCTTCAGTGTCTCTGTTATTATGAACGGCATCAGCGGCGAGATAGAT 3489

QY 161 HistyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
DB 3490 CATTATCTAGGACTTGCATAAATAAGAAATGTTAAAGATGCTATGGCTAAAAATCCAGCAAAA 3549

QY 181 IleProGlyLeuLysArgIlyshAlaGlu 189
DB 3550 ATCCCTGGATTGAAGCGCAAGCTGAA 3576

RESULT 11
US-09-758-140-5
; Sequence 5, Application US/09758140
; Patent No. US20020012965A1
; GENERAL INFORMATION:
; APPLICANT: Strittmatter, Stephen M.
; TITLE OF INVENTION: No. US20020012965A10 Receptor-Mediated Blockade of Axonal Growth
; FILE REFERENCE: 44574-5073-US
; CURRENT APPLICATION NUMBER: US/09/758,140
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; CURRENT FILING DATE: 2001-01-12  
; PRIOR FILING DATE: US 60/175,707  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: US 60/207,366  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/236,378  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5

LENGTH: 4053

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (135)..(3710)

; OTHER INFORMATION: Human mRNA for No. US20020012965A1 protein (KIAA0886, GenBank  
; OTHER INFORMATION: Accession No. US20020012965A1 AB020693)

US-09-758-140-5

Alignment Scores:  
Pred. No.: 5,28e-106 Length: 4053  
Score: 931.00 Matches: 189  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-758-140-5 (1-4053)

Qy	1	SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla	20
Db	3144	TCAGTTGTTGACCTCTCTGACTGGAGAGACATTAAAGAGACTGGAGTGGTGGTGGCC	3203
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	3204	AGCCTATTCTCTGCTCTTCAATTCACAGTATTTCAGCATTTGTGACGCTAACAGCCTACATT	3263
Qy	41	AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
Db	3264	GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT	3323
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
Db	3324	ATCAGAAATCAGATGAAGCCACCCATTGAGGCATATCTGGAATCTGGAATGCTGCTATA	3383
Qy	81	SerGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle	100
Db	3384	TCTGAGGAGTTGGTTTCAGAAAGTACAGTAATCTCTGCTCTGTCATGTGAAGTGGCAGGAT	3443
Qy	101	LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal	120
Db	3444	AAGAACTCAGAGCCCTCTTCTTAGTTGATGATTAGTTGATTTCTGGAAGTTTGCAGTG	3503
Qy	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
Db	3504	TTGATGGGGTATTACTATGTTGGTGGCTTGTAAATGGTCTGACACTACTGATTTTG	3563
Qy	141	AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp	160
Db	3564	GCTCTCATTTTCACTCTTCAGTGTTCCTGTTATTATGAACGGCATCAGGCACACATAGAT	3623
Qy	161	HistyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys	180
Db	3624	CATTATCTAGGACTTGCATAATGAAGTGTAAAGATGCTATGGCTAAATCCAGCAAA	3683
Qy	181	IleProGlyLeuLysArgLysAlaGlu	189
Db	3684	ATCCCTGGATTGAACGGCAAGCTGAA	3710

RESULT 12

US-09-972-599A-5

; Sequence 5, Application US/09972599A

; Patent No. US20020077295A1

; GENERAL INFORMATION:

; APPLICANT: STRITTMATTER, STEPHEN M.

; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH

; FILE REFERENCE: C077 CIP US

; CURRENT APPLICATION NUMBER: US/09/972,599A

; CURRENT FILING DATE: 2001-10-06

; PRIOR APPLICATION NUMBER: PCT/US01/01041

; PRIOR FILING DATE: 2001-01-12

; PRIOR APPLICATION NUMBER: 09/758,140

; PRIOR FILING DATE: 2001-01-12

; PRIOR APPLICATION NUMBER: 60/236,378

; PRIOR FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: 60/207,366

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/175,707

; PRIOR FILING DATE: 2000-01-12

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

LENGTH: 4053

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (135)..(3710)

; OTHER INFORMATION: Human DNA encoding for No. US20020077295A1 protein (KIAA0886, Ge

; OTHER INFORMATION: Accession No. US20020077295A1 AB020693)

US-09-972-599A-5

Alignment Scores:  
Pred. No.: 5,28e-106 Length: 4053  
Score: 931.00 Matches: 189  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-972-599A-5 (1-4053)

Qy	1	SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla	20
Db	3144	TCAGTTGTTGACCTCTCTGACTGGAGAGACATTAAAGAGACTGGAGTGGTGGTGGCC	3203
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	3204	AGCCTATTCTCTGCTCTTCAATTCACAGTATTTCAGCATTTGTGACGCTAACAGCCTACATT	3263
Qy	41	AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
Db	3264	GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCT	3323
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
Db	3324	ATCAGAAATCAGATGAAGCCACCCATTGAGGCATATCTGGAATCTGGAATGCTGCTATA	3383
Qy	81	SerGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle	100
Db	3384	TCTGAGGAGTTGGTTTCAGAAAGTACAGTAATCTCTGCTCTGTCATGTGAAGTGGCAGGAT	3443
Qy	101	LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal	120
Db	3444	AAGAACTCAGAGCCCTCTTCTTAGTTGATGATTAGTTGATTTCTGGAAGTTTGCAGTG	3503
Qy	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
Db	3504	TTGATGGGGTATTACTATGTTGGTGGCTTGTAAATGGTCTGACACTACTGATTTTG	3563
Qy	141	AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp	160
Db	3564	GCTCTCATTTTCACTCTTCAGTGTTCCTGTTATTATGAACGGCATCAGGCACACATAGAT	3623
Qy	161	HistyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys	180

Db 3624 CATTATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATAATCCAGCAAAA 3683  
QY 181 ileProGlyLeuLysArgLysAlaGlu 189  
Db 3684 ATCCCTGGATTGAAGCGCAAAAGCTGAA 3710  
RESULT 13  
US-10-717-597-310  
; Sequence 310, Application US/10717597  
; Publication No. US20040110221A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Burczynski, Michael E.  
; APPLICANT: Twine, Natalie C.  
; APPLICANT: Dornier, Andrew J.  
; APPLICANT: Trepicchio, William L.  
; APPLICANT: Slonim, Donna K.  
; APPLICANT: Stover, Jennifer A.  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS  
; FILE REFERENCE: AM101080L  
; CURRENT APPLICATION NUMBER: US/10/717,597  
; PRIORITY FILING DATE: 2003-11-21  
; PRIOR APPLICATION NUMBER: US 60/459,782  
; PRIORITY FILING DATE: 2003-04-03  
; PRIOR APPLICATION NUMBER: US 60/427,982  
; PRIORITY FILING DATE: 2002-11-21  
; NUMBER OF SEQ ID NOS: 4904  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 310  
; LENGTH: 4053  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-717-597-310

Alignment Scores:  
Pred. No.: 5,286-106 Length: 4053  
Score: 931.00 Matches: 189  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 19 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-717-597-310 (1-4053)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 3144 TCAGTTGTTGACCTCTCTGACTGGAGACATTAAAGACACTGGAGTGGTGTGGTGCC 3203  
QY 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 3204 AGCCTATTCTCTGCTGCTTTTCATTGACAGTATTTCAGCATTTGTGAGCGTAAACAGCCTACATT 3263  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 3264 GCCTTTGGCCCTCTCTCTGTGACCAATCAGCTTTAGGATATACAGGTTGTGATCCAGCT 3323  
QY 61 ileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 3324 ATCCAGAAATCAGATGAAGCGCCACCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3383  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 3384 TCTGAGGAGTTGGTTTCAGAAAGTACAGTAAATCTCTGCTTTGGTCAATGTGAACGTGCACGATA 3443  
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3444 AAGGAACCTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTCAGTG 3503  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 3504 TTGATGTGGGTTATTTACCTATGTTGGTGGCTTTGTTTAAATGGTCTGCACACTACTGATTTTG 3563

QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db 3564 GCTCTCATTTTCACTCTTCACTGTTCTCTGTTATTTATGAACCGCATCAGGCACAGATAGAT 3623  
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 3624 CATTTATCTAGGACTTGCAATAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAA 3683  
QY 181 ileProGlyLeuLysArgLysAlaGlu 189  
Db 3684 ATCCCTGGATTGAAGCGCAAAAGCTGAA 3710

## RESULT 14

US-10-956-157-4532  
; Sequence 4532, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4532  
; LENGTH: 4623  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-956-157-4532

## Alignment Scores:

Pred. No.: 6,5e-106 Length: 4623  
Score: 931.00 Matches: 189  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 21 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-956-157-4532 (1-4623)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 3151 TCAGTTGTTGACCTCTCTGACTGGAGACATTAAAGACACTGGAGTGGTGTGGTGCC 3210  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 3211 AGCCTATTCTCTGCTGCTTTTCATTGACAGTATTTCAGCATTTGTGAGCGTAAACAGCCTACATT 3270  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 3271 GCCTTTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAGGTTGTGATCCAGCT 3330  
QY 61 ileGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 3331 ATCCAGAAATCAGATGAAGCGCCACCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3390  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 3391 TCTGAGGAGTTGGTTTCAGAAAGTACAGTAAATCTCTGCTTTGGTCAATGTGAACGTGCACGATA 3450  
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3451 AAGGAACCTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTCAGTG 3510  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 3511 TTGATGTGGGTTATTTACCTATGTTGGTGGCTTTGTTTAAATGGTCTGCACACTACTGATTTTG 3570  
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db 3571 GCTCTCATTTTCACTCTTCACTGTTTCTCTGTTATTTATGAACCGCATCAGGCACAGATAGAT 3630



QY 161 HistyLeuGlyLeuAlaAsnLysenValLysAspAlaMetAlaLysleleGlnAlaLys 180  
Db 3631 CATTATCTAGGACTTGCAGAAATGAAGAATGTTAAAGATGCTATGGCTAAATAATCCAGCAAAA 3690  
QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
Db 3691 ATCCCTGGATTGAAGCGCAAAAGCTGAA 3717

## RESULT 15

US-10-060-036-53  
; Sequence 53, Application US/10060036  
; Publication No. US20030073144A1  
; GENERAL INFORMATION:  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Persing, David H.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Jiang, Yugu  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER  
; FILE REFERENCE: 210121.566  
; CURRENT APPLICATION NUMBER: US/10/060,036  
; CURRENT FILING DATE: 2002-01-30  
; NUMBER OF SEQ ID NOS: 4560  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 53  
; LENGTH: 4632  
; TYPB: DNA  
; ORGANISM: Homo sapiens  
US-10-060-036-53

Alignment Scores:  
Pred. No.: 6.52e-106 Length: 4632  
Score: 931.00 Matches: 189  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-09-830-972-29\_copy\_990\_1178 (1-189) x US-10-060-036-53 (1-4632)

QY 1 SerValAlaLeuLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyVala 20  
Db 3151 TCAGTTGTGACCTCTCTGTACTGGAGACATTAGAGACTGGAGTGGTGTGGTGGCC 3210  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 3211 AGCCTATTCTCTGCTCTTCATTGACAGTATTTCAGCATTTGTGAGCGTAAACAGCTACATT 3270  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 3271 GCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTTAGGATATACAAGGGTGTGATCCAAAGCT 3330  
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 3331 ATCCAGAAATCAGATGAAGGCCACCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATA 3390  
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnLysThrIle 100  
Db 3391 TCTGAGGAGTGGTTTCAGAGTACAGTAATCTCTGCTCTGTCATGTGACACTGACAGATA 3450  
QY 101 LysGluLeuArgArgLeuPheLeuValAlaAspLeuValAspSerLeuLysPheAlaVal 120  
Db 3451 AAGGAACCTCAGCGCCCTCTCTTAGTATGATGATTTAGTTGATTCCTGAAAGTTTCAGGTG 3510  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 3511 TTGATGTGGGTATTTACCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3570  
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160

Db 3571 GCTCTCATTTCACTCTTCAGTGTTCCTCTTATTTATGAACGGCATCAGGCACAGATAGAT 3630  
QY 161 HistyLeuGlyLeuAlaAsnLysenValLysAspAlaMetAlaLysleleGlnAlaLys 180  
Db 3631 CATTATCTAGGACTTGCAGAAATGAAGAATGTTAAAGATGCTATGGCTAAATAATCCAGCAAAA 3690  
QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
Db 3691 ATCCCTGGATTGAAGCGCAAAAGCTGAA 3717

## RESULT 16

US-10-660-946-2  
; Sequence 2, Application US/10660946  
; Publication No. US20040063131A1  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; Au-Young, Janice  
; Goli, Surya K.  
; Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/660,946  
FILING DATE: 12-Sep-2003  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/228,213A  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/700,607  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0114 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 799 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: Consensus  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-660-946-2  
Alignment Scores:  
Pred. No.: 1.29e-106 Length: 799  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 18 Gaps: 0  
US-09-830-972-29\_copy\_990\_1178 (1-189) x US-10-660-946-2 (1-799)  
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21

Db 108 GTTGTGACCTCTCTGACTGGAGACATTAAGAACACTGGAGTGTGTTTGGTGCCAGC 167  
QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValrileAla 41  
Db 168 CTATTCTCTGCTGCTTCAITGACAGTATTGACGATTTGAGCGTAACAGCCTACATTTGCC 227  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrlsGlyValIleGlnAlaIle 61  
Db 228 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 287  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaValrLeuGluSerGluValAlaIleSer 81  
Db 288 CAGAAATCAGATGAAGCCACCCATTCAGGGCATATCTGGAATCTGGAATCTGCTATATCT 347  
QY 82 GluGluLeuValGlnLysTyrlsSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 348 GAGGAGTTGGTTTCAGAAATACAGTAATCTCTGCTCTTGGTCTGATGAACTGCAGATAAG 407  
QY 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 408 GAACTCAGCGGCTCTCTTCTAGTTGATGATTTAGTTGATTTCTGAAAGTTTCAGGTGTTG 467  
QY 122 MetTrpValPheThrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
Db 468 ATGTGGGTATTTACCTATGTTGGTGGCTTGTGTTTAAATGGTCTGACACTACTGATTTGGCT 527  
QY 142 LeuIleSerLeuPheSerValProValIleTyrlsGluArgHisGlnAlaGlnIleAspHis 161  
Db 528 CTCAATTCATCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 587  
QY 162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 588 TATCTAGGACTTGCATAAATGAAGATGTTAAAGATGCTATGGCTAAATCCCAAGCAAAATC 647  
QY 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 648 CTGGATTGAAGCGCAAAAGCTGAA 671

## RESULT 17

US-09-789-386-5  
; Sequence 5, Application US/09789386  
; Patent No. US20020010324A1  
; GENERAL INFORMATION:  
; APPLICANT: MICHALOVICH, DAVID  
; TITLE OF INVENTION: PRINJHA, RABINDER KUMAR  
; FILE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP-30165-C1  
; CURRENT APPLICATION NUMBER: US/09/789,386  
; CURRENT FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: U.K. 9916898.1  
; PRIOR FILING DATE: 1999-07-19  
; PRIOR APPLICATION NUMBER: U.K. 9816024.5  
; PRIOR FILING DATE: 1998-07-22  
; PRIOR APPLICATION NUMBER: US 09/359,208  
; PRIOR FILING DATE: 1999-07-22  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 1122  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
US-09-789-386-5

Alignment Scores:  
Pred. No.: 2,21e-106 Length: 1122  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 9 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-789-386-5 (1-1122)

QY 2 ValValAspLeuLeuTyrlsTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 556 GTTGTGACCTCTCTGACTGGAGACATTAAGAACACTGGAGTGTGTTTGGTGCCAGC 615  
QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValrileAla 41  
Db 616 CTATTCTCTGCTGCTTCAITGACAGTATTGACGATTTGAGCGTAACAGCCTACATTTGCC 675  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrlsGlyValIleGlnAlaIle 61  
Db 676 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 735  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaValrLeuGluSerGluValAlaIleSer 81  
Db 736 CAGAAATCAGATGAAGCCACCCATTCAGGGCATATCTGGAATCTGGAATCTGCTATATCT 795  
QY 82 GluGluLeuValGlnLysTyrlsSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 796 GAGGAGTTGGTTTCAGAAATACAGTAATCTCTGCTCTTGGTCTGATGAACTGCAGATAAG 855  
QY 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 856 GAACTCAGCGGCTCTCTTCTAGTTGATGATTTAGTTGATTTCTGAAAGTTTCAGGTGTTG 915  
QY 122 MetTrpValPheThrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
Db 916 ATGTGGGTATTTACCTATGTTGGTGGCTTGTGTTTAAATGGTCTGACACTACTGATTTGGCT 975  
QY 142 LeuIleSerLeuPheSerValProValIleTyrlsGluArgHisGlnAlaGlnIleAspHis 161  
Db 976 CTCAATTCATCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1035  
QY 162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 1036 TATCTAGGACTTGCATAAATGAAGATGTTAAAGATGCTATGGCTAAATCCCAAGCAAAATC 1095  
QY 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 1096 CTGGATTGAAGCGCAAAAGCTGAA 1119

## RESULT 18

US-10-175-523-156  
; Sequence 156, Application US/10175523  
; Publication No. US20030096264A1  
; GENERAL INFORMATION:  
; APPLICANT: Brockman, Jeffrey  
; APPLICANT: Evans, David  
; APPLICANT: Hook, Derek  
; APPLICANT: Klimczak, Leszek  
; APPLICANT: Laeng, Pascal  
; APPLICANT: Palfreyman, Michael  
; APPLICANT: Rajan, Prithi  
; TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)  
; FILE REFERENCE: 3235/IJ795-US3  
; CURRENT APPLICATION NUMBER: US/10/175,523  
; CURRENT FILING DATE: 2002-06-18  
; PRIOR APPLICATION NUMBER: US 60/299,151  
; PRIOR FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: US 60/317,828  
; PRIOR FILING DATE: 2001-09-07  
; PRIOR APPLICATION NUMBER: US 60/325,150  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US 60/333,047  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: US 60/349,936  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: US 60/361,834  
; PRIOR FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 156  
; LENGTH: 1160  
; TYPE: DNA

ORGANISM: Homo sapiens  
US-10-175-523-156

Alignment Scores:  
Pred. No.: 2,338-106 Length: 1160  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 14 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-175-523-156 (1-1160)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 228 GTTGTGACCTCCTGCTACTGGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGGCCAGC 287  
QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 288 CTATTCTCTGCTGCTTCTCATTCAGCATTTAGCATTTGAGCGTAACAGCCTACATTGCC 347  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 348 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 407  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 408 CAGAAATCAGATGAAGGCCACCCATTCAAGGCATATCTGGAATCTGGAAGTTGCTATATCT 467  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
DB 468 GAGGAGTTGGTTTCAGAACTACAGTAATCTGCTCTGTGTCATCAAGCTGCAAGTAAG 527  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspLeuLysPheAlaValLeu 121  
DB 528 GAACCTACGGCCCTCTCTTCTAGTTAGTATGATTTAGTATCTCTGAAGTTGCAAGTGTG 587  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
DB 588 ATGTGGGTATTTACCTATGTTGGTGGCTTTTAAATGCTGACACTACTGATTTGGCT 647  
QY 142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
DB 648 CTCATTTTCACCTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 707  
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 708 TATCTAGGACTTGCATAATGAAGTGTAAAGATGCTATGGCTAAATAATCAAGCAAAATC 767  
QY 182 ProGlyLeuLysArgLysAlaGlu 189  
DB 768 CTGGATTGAAGCGCAAGCTGAA 791

RESULT 19

US-10-956-157-4527  
; Sequence 4527, Application US/10956157  
; Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Mounts, William

TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

FILE REFERENCE: 031896-043000 (AM 101081)

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE: PatentIn version 3.2

SEQ ID NO 4527

LENGTH: 1609

TYPE: DNA

ORGANISM: Homo sapiens

US-10-956-157-4527

Alignment Scores:

Pred. No.: 3,918-106 Length: 1609  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 21 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-956-157-4527 (1-1609)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 140 GTTGTGACCTCCTGCTACTGGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGGCCAGC 199  
QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 200 CTATTCTCTGCTGCTTCTCATTCAGCATTTAGCATTTGAGCGTAACAGCCTACATTGCC 259  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 260 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 319  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 320 CAGAAATCAGATGAAGGCCACCCATTCAAGGCATATCTGGAATCTGGAAGTTGCTATATCT 379  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
DB 380 GAGGAGTTGGTTTCAGAACTACAGTAATCTGCTCTGTGTCATCAAGCTGCAAGTAAG 439  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspLeuLysPheAlaValLeu 121  
DB 440 GAACCTACGGCCCTCTCTTCTAGTTAGTATGATTTAGTATCTCTGAAGTTGCAAGTGTG 499  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
DB 500 ATGTGGGTATTTACCTATGTTGGTGGCTTTTAAATGCTGACACTACTGATTTGGCT 559  
QY 142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
DB 560 CTCATTTTCACCTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 619  
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 620 TATCTAGGACTTGCATAATGAAGTGTAAAGATGCTATGGCTAAATAATCAAGCAAAATC 679  
QY 182 ProGlyLeuLysArgLysAlaGlu 189  
DB 680 CTGGATTGAAGCGCAAGCTGAA 703

RESULT 20

US-09-765-205-5

; Sequence 5, Application US/09765205

; Patent No. US20020034800A1

GENERAL INFORMATION:

APPLICANT: Cao, Li

TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES

FILE REFERENCE: 1458.004/200130.449

CURRENT APPLICATION NUMBER: US/09/765,205

CURRENT FILING DATE: 2001-01-17

PRIOR APPLICATION NUMBER: US/09/212,440

PRIOR FILING DATE: 1998-12-16

NUMBER OF SEQ ID NOS: 46

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 5

LENGTH: 1610

TYPE: DNA

ORGANISM: human

US-09-765-205-5

Alignment Scores:

Pred. No.: 3,918-106 Length: 1610  
Score: 927.00 Matches: 188

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.57%	Indels:	0
DB:	9	Gaps:	0

US-09-830-972-29 COPY 990 1178 (1-189) x US-09-765-205-5 (1-1610)

Qy	2	ValValAspLeuLeuTyrTrpArgAspIleValSerThrGlyValValPheGlyAlaSer	21
Db	687	GTGTGTCACCTCCTGTACTGCGAGACACATTAAAGAAGACTGGAGTGGTGTGGTGGCCAGC	746
Qy	22	LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla	41
Db	747	CTATTCTCTGCTCTTTTCATTGACAGTATTGAGCAATTGTGACGGTAAACAGCTACATTGCC	806
Qy	42	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAlaIle	61
Db	807	TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC	866
Qy	62	GlnIysSerAspGluGlyHisProPheArgAlaTyrIeuGluSerGluValAlaIleSer	81
Db	867	CAGAAATCAGATGAAGGCCACCCATTTCAGGCGCATATCTGGAATCTGAAGTTGCTATATCT	926
Qy	82	GluGluLeuValGlnIysTyrSerAsnSerAlaIleuGlyHisValaenCysThrIleLys	101
Db	927	GAGGAGTTGGTTTCAGAAGTACAGTAAATTCCTGCTCTGGTCATGTCAACTGCACGATAAAG	986
Qy	102	GluLeuArgArgLeuPheLeuValAlaAspLeuValAspSerLeuLysPheAlaValLeu	121
Db	987	GAACCTCAGGGCCCTCTCTTAGTTGATGATTTAGTTGATCTCTGAGATTTGCAGTGTG	1046
Qy	122	MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla	141
Db	1047	ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGCTCTGACACACTACTGATTTGGCT	1106
Qy	142	LeuIleSerLeuPheSerValProValIleTyrGlnuArgHisGlnAlaGlnIleAspHis	161
Db	1107	CTCATTTTCACTCTTCAGTGTTCCTGTGTTATTATTAGACGGCATCAGGCACAGATAGATCAT	1166
Qy	162	TyrLeuGlyLeuAlaAsnLysAsnValIysAspAlaMetAlaIysIleGlnAlaLysIle	181
Db	1167	TATCTAGACTTGGCAATATAGATGTTTAAAGATGCTATGCTAAATCCAAGCAAAAATC	1226
Qy	182	ProGlyLeuLysArgLysAlaGlu	189
Db	1227	CCTGGATTGAAGCGCAAGCTGAA	1250

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RESULT 21
US-10-347-669-5
; Sequence 5, Application US/10347669
; Publication No. US20050084850A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/10/347,669
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1610
; TYPE: DNA
; ORGANISM: human
US-10-347-669-5

```

Alignment Scores:	
Pred. No.:	3.91e-106
Score:	927.00
Length:	1610
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	99.57%
Mismatches:	0
Indels:	0
Conservative:	0
Matches:	188

DB:	21	0	Gaps:
US-09-830-972-29_COPY_990_1178 (1-189) x US-10-347-669-5 (1-1610)			
Qy	2	ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer	21
Db	687	GTGTGGACCTCTCTGCTACTGGAGACATTAAGAGACTGGAGTGGTGTGTGGTGGCAGC	746
Qy	22	LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla	41
Db	747	CTATTCTCGTGTCTTTCACTTACAGTATTACAGCATTTGAGCGTAACAGCCTACATTGCC	806
Qy	42	LeuAlaIleuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle	61
Db	807	TTGGCCCTCGTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAAGCTATC	866
Qy	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer	81
Db	867	CAGAAATCAGATGAAGGCCACCCATTTCAGGCATATCTGGAATCTGAGTTGCTATATCT	926
Qy	82	GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys	101
Db	927	GAGGAGTTGGTTTCAGAAAGTACAGTAATTCCTGCTCTTGGTCAATCTCAACTGCACGATAAAG	986
Qy	102	GluLeuArgArgLeuPheLeuValAspAsnLeuValAspSerLeuLysPheAlaValLeu	121
Db	987	GAATCTCAGGGCCCTCTCTTAGTTGATGATTTAGTTGATTCCTCGAAGTTTCAGATGTTG	1046
Qy	122	MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla	141
Db	1047	ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAAATGGTCTGCACACTACTGATTTTGGCT	1106
Qy	142	LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis	161
Db	1107	CTCATTTTCACTCTTCAGTGTTCCTGTTATTATGAACGGCATCAGGCACAGATAGATCAT	1166
Qy	162	TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle	181
Db	1167	TATCTAGGACTTCGAATATAGATGTTAAAGATGCTATGGCTTAATAATCCNAGCAAAATC	1226
Qy	182	ProGlyLeuLysArgLysAlaGlu	189
Db	1227	CCTGGATTGAAGCGCAAGCTGAA	1250

```

RESULT 22
US-10-439-388-62
; Sequence 62, Application US/10439388
; Publication No: US20030228617A1
; GENERAL INFORMATION:
; APPLICANT: Aune, Thomas M
; APPLICANT: Olsen, Nancy J
; TITLE OF INVENTION: Method for Predicting Autoimmune Disease
; FILE REFERENCE: 1242/68
; CURRENT APPLICATION NUMBER: US/10/439,398
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/381,055
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-439-388-62

Alignment Scores:
Pred. No.: 4, 61e-106 Length: 1785
Score: 927.00 Matches: 188
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.57% Indels: 0
DB: 17 Gaps: 0

```

Alignment Scores:	
Pred. No.:	4.61e-106
Score:	927.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	99.57%
DB:	17
	Gaps: 0
	Indels: 0
	Mismatches: 0
	Conservative: 0
	Matches: 188
	Length: 1785

US-09-830-972-29 COPY 990 1178 (1-189) x US-10-439-388-62 (1-1785)

Qy	2	ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer	21
Db	247	GTGTGTGACCTCTCTACTCGGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGGCAGC	306
Qy	22	LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla	41
Db	307	CTATTCCTGCTGCTTTCAATTGACAGTATTCAGCATTTGTGAGCGTAAACGCTACATTGCC	366
Qy	42	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle	61
Db	367	TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC	426
Qy	62	GlnLysSerAspGluGlnIleHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer	81
Db	427	CAGAAATCAGATGAAGGCCACCCCATTCAGGGCATATCTGGAATCTGAAGTTCGTATATCT	486
Qy	82	GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys	101
Db	487	GAGAGTTGGTTCAGNAGTACAGTAATTCCTGCTCTTGGTCATGTGAACTCGACGATAAAG	546
Qy	102	GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu	121
Db	547	GAACTCAGCGCCCTCTCTTAGTTCGATGATTTAGTTGATCTCTGAGTTTGCAGTGTG	606
Qy	122	MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla	141
Db	607	ATGTGGGTATTACCTATGTGTGGTCCCTGTTTAATGTGCTGCACACTACTGATTTTGGCT	666
Qy	142	LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis	161
Db	667	CTCATTTTCACCTCTCAGTGTTCCCTGTATTTATGAACGGCATCAGCGCACAGATGATCAT	726
Qy	162	TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle	181
Db	727	TATCTAGGACTTGCDAATAAGATGTTAAAGATGCTATGGCTTAAATCCAACCAAAATC	786
Qy	182	ProGlyLeuLysArgLysAlaGlu	189
Db	787	CCTGGATTGAAGCGCAAAAGCTGAA	810

RESULT 23  
 US-10-956-157-1705  
 ; Sequence 1705, Application US/10956157  
 ; Publication No. US20050118625A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wyeth  
 ; APPLICANT: Mounts, William  
 ; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
 ; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
 ; FILE REFERENCE: 031896-043000 (AM 101081)  
 ; CURRENT APPLICATION NUMBER: US/10/956.157  
 ; CURRENT FILING DATE: 2004-10-04  
 ; NUMBER OF SEQ ID NOS: 319805  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 1705  
 ; LENGTH: 1785  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-956-157-1705

Alignment Scores:		
Pred. No.:	4,618-106	Length:
Score:	927.00	Matches:
Percent Similarity:	100.00%	Conservative:
Best Local Similarity:	100.00%	Mismatches:
Query Match:	95.57%	Indels:
DB:	21	Gaps:
		0
		0
		1785

US-09-830-972-29 COPY 990 1178 (1-189) x US-10-956-157-1705 (1-1785)

QY 2 ValValAspLeuLeuTyrTrpArqAspIleLysLysThrGlyValValPheGlyAlaSer 21

247	Db	GTGTGTGACCTCCCTGCTACTGAGAGACATTAAGAAGACTGGAGTGGGTGTGGTGGCCAGC	308
22	Qy	LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrlleAla	41
307	Db	CTATTTCCTGCTGCTTTTCATTGACAGTATTACAGCTTTGAGCGTAACAGCCTACATTGGC	366
42	Qy	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrlsGlyValIleGlnAlaIle	61
367	Db	TTGGCCCTGCTCTCTGTGACCATCAGCTTTTAGGATATACAAGGGTGTGATCCAAGCTATC	426
62	Qy	GlnIysSerAspGluGlyHisProPheArgAlaTyrlsLeuGluSerGluValAlaIleSer	81
427	Db	CAGAAATCAGATGAAGGCCACCCCATTCAGGGCATATCTGGAAATCTGGAAGTTCCTATATCT	486
82	Qy	GluGluLeuValGlnLysTyI-SerAsnSerAlaLeuGlyHisValAsnCysThrIleLys	101
487	Db	GAGGAGTTGGTTCAGAGTACAGTAATTCCTGCTCTTGCTCATGTGNACTGCACGATTAAG	546
102	Qy	GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu	121
547	Db	GAACTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTG	606
122	Qy	MetTrpValPheThrTyrlValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla	141
607	Db	ATGTGGGTATTACCTATGTTGGTGCCCTGTTTAAATGCTCTGACACTACTGATTTTGGCT	666
142	Qy	LeuIleSerLeuPheSerValProValIleTyrlGluArgHisGlnAlaGlnIleAspHis	161
667	Db	CTCATTTTCACCTCTTCAGTGTTCTCGTTATTATGAACGGCATCAGGCACAGATGATCAT	726
162	Qy	TyrLeuGlyLeuAlaAsnLysAsnValIysAspAlaMetAlaLysIleGlnAlaLysIle	181
727	Db	TATCTAGGACTTGCAATAAGAATGTTAAAGATGCTATGGCTTAAATCCAAGCAAAATC	786
182	Qy	ProGlyLeuLysArgLysAlaGlu	189
787	Db	CCTGGATTGAAGCGCAAGCTGAA	810

## RESULT 24

US-10-956-157-4530  
; Sequence 4530, Application US/10956157  
; Publication No. US20050118625A1

**GENERAL INFORMATION:**

APPLICANT: Wyeth

APPLICANT: Mounts, William

1. TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956,157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

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; SOFTWARE: Pat
; GEO ID: NO 4530

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; SEQ ID NO 4530
: 1 ENCTH: 2050

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; LENGTH: 2050
; TYPE: DNA

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TYPE: DNA  
ORGANISM: Homo sapiens

ORGANISM: HOMO  
;  
IIS-10-956-157-4530

US-10-956-13 / -4530

Alignment Scores:

Assignment scores:	
Pred. No.:	Length:
5.74e-106	2050

Filed: NO.:	3:74e-106	Demysti:	2030
Score:	927.00	Matches:	188

Percent Similarity: 100.00%  
 Conservative: 0

Best Local Similarity: 100.00%

Query Match: 99.57% Indels: 0

DB:	21	Gaps:	0
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US-09-830-972-29 COPY 990 1178 (1-189) x US-10-956-157-4530 (1-2050)

Qv 2 ValValAspLeuLeuTyrTrpArgAspIleIleValIleValThrGlyValValPheGlyAlaSer 21

[illegible]

622 GTTGTGACCTCCTGTACTGGAGAGACATTAAAGAAGACTGGAGTGGTGTGGTGCCAGC 68



Db 817 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTTGTATCCAAAGCTATC 876  
Qy 62 GlnlysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 877 CAGAAATCAGATGAAGGCCACCATTTCAAGGCATATCTGGAATCTGAAAGTTGCTATATCT 936  
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 937 GAGGAGTTGGTTCAAGAGTACAGTAATTTCTGCTCTTGTGTCATGTGAATCTGCACGATAAG 996  
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 997 GAACTCAGCGCGCTCTCTTCTAGTGATGATTTAGTTAGTTCTCTCAAGTTTGCAGTGTG 1056  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
Db 1057 ATGTGGGTATTTACCTATGTTGGTGCCTTGTATTAATGCTCTGACACTACTGATTTTGGCT 1116  
Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 1117 CTCATTTTCACTTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1176  
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 1177 TATCTAGGACTTGCAAAATAAGAACTGTTAAAGATGCTATGGCTTAAATCCAAAGCAAATC 1236  
Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 1237 CCTGGATTGAAGCGCAAGCTGAA 1260

## RESULT 27

US-10-060-036-54

; Sequence 34, Application US/10060036

; Publication No. US20030073144A1

; GENERAL INFORMATION:

; APPLICANT: Benson, Darin R.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Persing, David H.

; APPLICANT: Hepler, William T.

; APPLICANT: Jiang, Yugu

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

; FILE REFERENCE: 210121.566

; CURRENT APPLICATION NUMBER: US/10/060,036

; CURRENT FILING DATE: 2002-01-30

; NUMBER OF SEQ ID NOS: 4560

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 54

; LENGTH: 2235

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-10-060-036-54

Alignment Scores:  
Pred. No.: 6,588-106 Length: 2235  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 14 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-060-036-54 (1-2235)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 697 GTTGTGTGACCTCTGCTACTGAGAGACATTAAGAGACTGGAGTGTGTTTGGTGCCAGC 756  
Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 757 CTATTCTCTGCTGCTTTCTATTCAGACTATTACAGCATTTGAGCGTAACAGCCTACATTCGCC 816

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 817 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTTGTATCCAAAGCTATC 876  
Qy 62 GlnlysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 877 CAGAAATCAGATGAAGGCCACCATTTCAAGGCATATCTGGAATCTGAAAGTTGCTATATCT 936  
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 937 GAGGAGTTGGTTCAAGAGTACAGTAATTTCTGCTCTTGTGTCATGTGAATCTGCACGATAAG 996  
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 997 GAACTCAGCGCGCTCTCTTCTAGTGATGATTTAGTTAGTTCTCTCAAGTTTGCAGTGTG 1056  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
Db 1057 ATGTGGGTATTTACCTATGTTGGTGCCTTGTATTAATGCTCTGACACTACTGATTTTGGCT 1116  
Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 1117 CTCATTTTCACTTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1176  
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 1177 TATCTAGGACTTGCAAAATAAGAACTGTTAAAGATGCTATGGCTTAAATCCAAAGCAAATC 1236  
Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 1237 CCTGGATTGAAGCGCAAGCTGAA 1260

## RESULT 28

US-10-220-891-22

; Sequence 22, Application US/10220891

; Publication No. US20030207286A1

; GENERAL INFORMATION:

; APPLICANT: NAKAGAWARA, AKIRA

; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES HAVING CHARACTERISTICS OF ENHANCED

; TITLE OF INVENTION: EXPRESSION IN HUMAN NEUROBLASTOMA WITH FAVORABLE PROGNOSIS

; TITLE OF INVENTION: BASED ON COMPARISON BETWEEN HUMAN NEUROBLASTOMA WITH FAVORABLE

; TITLE OF INVENTION: PROGNOSIS AND HUMAN NEUROBLASTOMA WITH UNFAVORABLE PROGNOSIS

; FILE REFERENCE: 73888-73435

; CURRENT APPLICATION NUMBER: US/10/220,891

; CURRENT FILING DATE: 2003-03-07

; PRIOR APPLICATION NUMBER: JP 2000/140387

; PRIOR FILING DATE: 2000-05-12

; PRIOR APPLICATION NUMBER: JP 2000/159195

; PRIOR FILING DATE: 2000-03-07

; NUMBER OF SEQ ID NOS: 108

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 22

; LENGTH: 1980

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-10-220-891-22

Alignment Scores:  
Pred. No.: 3,188-105 Length: 1980  
Score: 921.00 Matches: 187  
Percent Similarity: 99.47% Conservative: 1  
Best Local Similarity: 98.94% Mismatches: 1  
Query Match: 98.93% Indels: 0  
DB: 17 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-220-891-22 (1-1980)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 1006 TCAGTGTGTGACCTCTGCTACTGGAGAGACATTAAGAGACTGGAGTGTGTTTGGTGCC 1065  
Qy 21 SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40

Db	1066	AGCCTATTCCAGCTGCTTTTCATTGACAGTATTTCAGACGTATGTGACGGTAACAGCCTACACTT	1125
Qy	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
Db	1126	GCCTTGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATATCAAGGGTGTGATCCAAGCT	1185
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
Db	1186	ATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAAGTTGCTGATA	1245
Qy	81	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle	100
Db	1246	TCTCAGGAGTGGTTTCAGAAGTCACAGTAATTCCTGCTCTGGTCATGTCAACTGCACGATA	1305
Qy	101	LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal	120
Db	1306	AAGGAACCTCAGCGCCCTCTCTTCTAGTTGATGATTTAGTTGATCTCTCGAGTTTTCAGTG	1365
Qy	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
Db	1366	TTGATCTGGGTATTTACCTATGTTGGTGCCCTGTTTAATGGTCTGCACACTACTGATTTTG	1425
Qy	141	AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp	160
Db	1426	GCTCTCATTTTCACCTCTTCAGTGTGCTCTGTTATTTATGAACGGCATCAGGCACAGATAGAT	1485
Qy	161	HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys	180
Db	1486	CATTATCTAGACACTTGCAAAATAGAGATGTTAAGATGCTATGGCTTAAATCCACGACAAA	1545
Qy	181	IleProGlyLeuLysArgLysAlaGlu	189
Db	1546	ATCCCTCGATTGAAGCGCAAAAGCTCAA	1572

## RESULT 29

```

US-09-978-360A-110
; Sequence 110, Application US/09978360A
; Publication No. US20040110939A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56.US4.CIP
; CURRENT APPLICATION NUMBER: US/09/978,360A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/IB98/02122
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; PRIOR FILING DATE: 1999-02-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.pm
; SEQ ID NO 110
; LENGTH: 994

```



GENERAL INFORMATION:  
APPLICANT: Cocks, Benjamin G.  
Suan G. Stuart  
Jeffrey J. Seilhamer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL  
GENE EXPRESSION  
NUMBER OF SEQUENCES: 1508  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/641,643  
FILING DATE: 14-Aug-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 382:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2610 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: LUNGNOT14  
CLONE: 1508778  
SEQUENCE DESCRIPTION: SEQ ID NO: 382 :  
US-10-641-643-382  
Alignment Scores:  
Pred. No.: 3,688-104 Length: 2610  
Score: 914.00 Matches: 188  
Percent Similarity: 99.47% Conservative: 0  
Best Local Similarity: 99.47% Mismatches: 0  
Query Match: 98.17% Indels: 1  
DB: 18 Gaps: 0  
US-09-830-972-29\_copy\_990\_1178 (1-189) x US-10-641-643-382 (1-2610)  
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 1311 GTTGTGACCTCTCTGTTGAGGACATTAAGAGACTGGAGTGTGTGTGGTCCAGC 1370  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr-IleAl 41  
DB 1371 CTATTCTCTGCTCTTCTTATTGACATTTACGATTTGTGAGCGTAACAGCCTACAAATTC 1430  
QY 41 aleuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaI 61  
DB 1431 CTTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAAGCTAT 1490  
QY 61 ecInLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 81  
DB 1491 CAGAAATCAGATGAAGGCCACCCATTACAGGCATATCTGGAATCTGAAGTTGCTATATC 1550  
QY 81 rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIlely 101

DB 1551 TCAGGAGTTGGTTCAGAAAGTACAGTAATTCCTCTCTTGGTGTGAACTGCACGATAA 1610  
QY 101 sGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 121  
DB 1611 GGAACCTCAGGCGCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGT 1670  
QY 121 uMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAl 141  
DB 1671 GATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGCACACTACTGATTTTGGC 1730  
QY 141 aleuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHi 161  
DB 1731 TCTCATTTCACTCTCTCAGTGTTCCTGTTATTATTAACGGCATCAGGCACAGATGATCA 1790  
QY 161 sTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysI 181  
DB 1791 TTATCTAGGACTTGCAATAAGAAATGTTAAAGATGCTATGGCTAATAATCCAAAGCAAAAT 1850  
QY 181 eProGlyLeuLysArgLysAlaGlu 189  
DB 1851 CCCTGGGTGGAAGCGCAAGCTGAA 1875  
RESULT 31  
US-09-893-348-17  
; Sequence 17, Application US/09893348  
; Patent No. US20020072493A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN, Irun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR US-  
; FILE REFERENCE: EIS-SCHWARTZ-2A  
; CURRENT APPLICATION NUMBER: US/09/893,348  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 4684  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (253)..(3744)  
; OTHER INFORMATION:  
US-09-893-348-17  
Alignment Scores:  
Pred. No.: 5,318-103 Length: 4684  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3  
Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 97.53% Indels: 0  
DB: 9 Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-893-348-17 (1-4684)  
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
DB 3175 TCAGTTGTGACCTCTCTCTGAGAGACATTAAGAGACTGGAGTGTGTGTGGTCC 3234  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
DB 3235 AGCTTATTCCTGCTGCTCTCTGACAGTGTTCAGCATTTGTCAGTGTAAACGCGCTACATT 3294

QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60  
Db GCCTGGCCCTGCTCTCGGTGACTATCAGCTTAGGATATATAAGGCGGTGATCCAGGCT 3354  
QY 61 IleGlnIleSerAspGluGlyHisProPheArgAlaTyrIleGluSerGluValAlaIle 80  
Db ATCCAGAAATCAGATGAAGCCACCCATTCAGGGCATATTTAGAAATCTGAAGTTGCTATA 3414  
QY 81 SerGluGluLeuValGlnIleTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db TCAGAGGAATTTGGTTCAGAAATACAGTAATTCCTGCTCTGGTCATGTGACACCAATA 3474  
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
Db AAGAACTGAGCGCGCTTTCTTAGTTGATGATTTAGTTGATTCCTCGAAGTTGCGAGTG 3534  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeu 140  
Db TTGATGTGGGTGTTTACTTATGTGTGGTCTGTTCAATGGTCTGACACTACTGATTTTA 3594  
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db GCTCTGATCTCACTCTCTCAGTATCTCTGTTATTAAGACGCATCAGGTGCAGATAGAT 3654  
QY 161 HisTyrLeuGlyLeuAlaLeuIleAsnValLysAsnValLysAsnAlaMetAlaLysIleGlnAlaLys 180  
Db CATTATCTAGGACTTGCAAAACAGAGTGTAAAGGATGCCATGGCCAAAATCCAAGCAAAA 3714  
QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
Db ATCCCTGGATTGAAGCGCAAGCAGAT 3741  
RESULT 32  
US-10-810-653-17  
; Sequence 17, Application US/10810653  
; Publication No. US20040253218A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michel  
; APPLICANT: COHEN, Irun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SCHWARTZ=2A  
; CURRENT FILING DATE: 2004-03-29  
; PRIOR APPLICATION NUMBER: US/09/893,348  
; PRIOR FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 4684  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (253)..(3744)  
; OTHER INFORMATION:  
US-10-810-653-17  
Alignment Scores:  
Pred. No.: 5,31e-103 Length: 4684  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3

Best Local Similarity: 97.35% Mismatches: 2  
Query Match: 97.53% Indels: 0  
DB: 20 Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-810-653-17 (1-4684)  
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db TCAGTTGTTGACCTCTCTACTGAGAGACATTAAGAAAGACTGGAGTGGTGTGGTGCC 3234  
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db ACCTTATTCCTGCTGCTCTGACAGTTCAGCAATTCAGTGTAAAGCGCCCTACAT 3294  
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60  
Db GCCTTGGCCCTGCTCTCGGTGACTATCAGCTTAGGATATATAAGGCGGTGATCCAGGCT 3354  
QY 61 IleGlnIleSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db ATCCAGAAATCAGATGAAGCCACCCATTCAGGGCATATTTAGAAATCTGAAGTTGCTATA 3414  
QY 81 SerGluGluLeuValGlnIleTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db TCAGAGGAATTTGGTTCAGAAATACAGTAATTCCTGCTCTGGTCATGTGACACCAATA 3474  
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120  
Db AAGAACTGAGCGCGCTTTCTTAGTTGATGATTTAGTTGATTCCTCGAAGTTGCGAGTG 3534  
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeu 140  
Db TTGATGTGGGTGTTTACTTATGTGTGGTCTGTTCAATGGTCTGACACTACTGATTTTA 3594  
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db GCTCTGATCTCACTCTCTCAGTATCTCTGTTATTAAGACGCATCAGGTGCAGATAGAT 3654  
QY 161 HisTyrLeuGlyLeuAlaLeuIleAsnValLysAsnValLysAsnAlaMetAlaLysIleGlnAlaLys 180  
Db CATTATCTAGGACTTGCAAAACAGAGTGTAAAGGATGCCATGGCCAAAATCCAAGCAAAA 3714  
QY 181 IleProGlyLeuLysArgLysAlaGlu 189  
Db ATCCCTGGATTGAAGCGCAAGCAGAT 3741  
RESULT 33  
US-10-205-194-165  
; Sequence 165, Application US/10205194  
; Publication No. US20030134301A1  
; GENERAL INFORMATION:  
; APPLICANT: Warner-Lambert Company  
; APPLICANT: Lee, Kevin  
; APPLICANT: Dixon, Alistair  
; APPLICANT: Brooksbank, Robert  
; APPLICANT: Finnock, Robert  
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain  
; FILE REFERENCE: WL-A-018201  
; CURRENT APPLICATION NUMBER: US/10/205,194  
; CURRENT FILING DATE: 2000-07-24  
; PRIOR APPLICATION NUMBER: GB 0118354.0  
; PRIOR FILING DATE: 2001-07-27  
; NUMBER OF SEQ ID NOS: 177  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 165  
; LENGTH: 2782  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: Foccen-m2 reticulon  
US-10-205-194-165  
Alignment Scores:  
Pred. No.: 5,31e-103 Length: 4684  
Score: 908.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 3

Pred. No.:	5.57e-103	Length:	2782
Score:	905.00	Matches:	183
Percent Similarity:	98.94%	Conservative:	4
Best Local Similarity:	96.83%	Mismatches:	2
Query Match:	97.21%	Indels:	0
DB:	15	Gaps:	0
US-09-830-972-29_COPV_990_1178 (1-189) x US-10-205-194-165 (1-2782)			
QY	1	SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla	20
DB	1271	GCAGTTGTTGACCTCCTCTACTCGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGCC	1330
QY	21	SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
DB	1331	AGCTTATTCTCGTGTCTCTCGACAGTGTTCAGCATTTGTCAGTGTAAACGGCTACATT	1390
QY	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
DB	1391	GCCTTGGCCCTGCTTCGGTGACTATCAGCTTTAGGATATATAGGCGGTGATCCAGGCT	1450
QY	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
DB	1451	ATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATTTTACAATCTGAAGTTGCTATA	1510
QY	81	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValIleAsnCysThrIle	100
DB	1511	TCAGAGGAATTGGTTTCAGAAATACAGTAATTCCTTGCTCTTGTCATGTGAACACGACAATA	1570
QY	101	LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal	120
DB	1571	AAGAAGACTGAGGCGGCTTTCTTAGTTGATGATTTAGTTGATTCCTCGAAGTTTCAGATG	1630
QY	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
DB	1631	TTGATGTGGGTGTTTACTTATGTTGGTGGCTTGTTCATGTGCTGCACACTACTGATTTTATA	1690
QY	141	AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp	160
DB	1691	GCCTCATCTCTCTTCAGTATTCCTGTTATTATTCATGACGGCATCAGGTGCAGATAGAT	1750
QY	161	HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys	180
DB	1751	CATTATCTAGGACTTGCAACAACAGAGTGTTAAGATGCCATGCGCAAAATCCAAAGCAAAA	1810
QY	181	IleProGlyLeuLysArgLysAlaGlu	189
DB	1811	ATCCCTTGGATTGAAGCGCAAGACAGAT	1837

## RESULT 34

```

US-10-267-502-214
; Sequence 214, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 214
; LENGTH: 3492
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-267-502-214

```

Query Match:	97.15%	Indels:	1
DB:	18	Gaps:	1
US-09-830-972-29_COPY_990_1178 (1-189) x US-10-267-502-214 (1-3492)			
Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValVal---PheGly 19			
Db 2920 TCAGTGTGTGACCTCTCTACTCGGAGAGACATTAAGAAGCTGGAGTGGTGTATTGTGGT 2979			
Qy 20 AlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyr 39			
Db 2980 GCCAGCTTATTCCTGCTGTCTCTGACAGTGTTCAGCATTTGTCAGTGTAAACGGGCTAC 3039			
Qy 40 IleAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGln 59			
Db 3040 AITGGCTTTGGCCCTGCTCTCTGTGACTATACAGCTTTAGGATATATAAGGGTGTGATCCAA 3099			
Qy 60 AlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleuGlnSerGluValAla 79			
Db 3100 GCTATTCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTTGGAAATCTGAAGTTGCC 3159			
Qy 80 IleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThr 99			
Db 3160 ATATCAGAGAAATTGGTTTCAGAAATATAGTAATTCCTGCTCTGGTCACTGTGAACGCACA 3219			
Qy 100 IleLysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAla 119			
Db 3220 ATAAAAGAATTGAGGCGTCTCTCTTAGTTGATGATTTAGTTGATTTCCCTGAAGTTTGCA 3279			
Qy 120 ValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIle 139			
Db 3280 GTGTTGATGGGTATTACTTACGTTGGTGCGCTGTTCAATGGTTTGACACTACTGATTT 3339			
Qy 140 LeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIle 159			
Db 3340 TTAGCTCTGATCTCACTTCTAGTATTCCTGTATATATATGAACGGCATCAGGCGCAGATA 3399			
Qy 160 AspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAla 179			
Db 3400 GATCATTTACTAGGACTTGCAAACAGAGCGTTAGGTGCCATGTGCCAAATATCCAGCA 3459			
Qy 180 LysIleProGlyLeuLysArgLysAlaGlu 189			
Db 3460 AAAATCCCTTGGATTGAAGCGCAAGCAGAA 3489			

RESULT 35

```

US-10-466-258-10
; Sequence 10, Application US/10466258
; Publication No. US20040132096A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: ASSAY
; FILE REFERENCE: P80966 GCW
; CURRENT APPLICATION NUMBER: US/10/466,258
; CURRENT FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 1798
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (215)..(814)
US-10-466-258-10

```

Alignment Scores:		
Pred. No.:	6.98e-101	1798
Score:	886.00	187
Percent Similarity:	98.94%	Conservative: 0
Best Local Similarity:	98.94%	Mismatches: 1
Query Match:	95.17%	Indels: 2
DB:	19	Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-466-258-10 (1-1798)

QY 2 ValValAspLeuLeuTyrTrpArgAspLeuLysThrGlyValValPheGlyAlaSer 21  
DB 248 GTTGTGACCTCTCTGACTGGAGACATTAAGAGACTGGAGTGGTGTGGTCCAGC 307  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 308 CTATTCTGCTGCTCTTCATGTGACAGTATTTCAGCATTTGTGAGCGTAACAGCCTACATTGCC 367  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 368 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCAAGCTATC 427  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 428 CAGAAATCAGATGAAGCCACCCATTCAGGCGCATATCTGGAATCTGGAATCTGATATCT 487  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
DB 488 GAGGAGTGTGTTTCAGAAAGTACAGTAATCTGCTCTTGTGTCATGTGAACCTGCACGATAAG 547  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspLeuPheAlaValLeu 121  
DB 548 GAACCTCAGCGCGCTCTCTTAGTGTGATGATTTAGTGTGATTTCTGAAAGTTTCAGTGTG 607  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
DB 608 ATGTGGGTATTTACCTATGTTGGTGGCTGCTGTTTAAATGTTCTGACACTACTGATTTGGCT 667  
QY 142 LeuIleSerLeu-PheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
DB 668 CTCATTCTCACTCTTCAGGTTCCTGTTATTTA-GAAACGGCATCAGGCACAGATAGATCA 726  
QY 161 sTyrLeuGlyLeuAlaAsnLysValIleAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 727 TTATCTAGGACTTGCAATTAAGATGTTAAAGATGCTATGGCTAAATCCAAGCAAAAT 786  
QY 181 eProGlyLeuLysArgLysAlaGlu 189  
DB 787 CCTGTGATTGAAGCGCAAGCTGAA 811

## RESULT 36

US-10-956-157-9765  
; Sequence 9765, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9765  
; LENGTH: 1400  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-956-157-9765

Alignment Scores:  
Pred. No.: 2,75e-99 Length: 1400  
Score: 872.00 Matches: 178  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 93.66% Indels: 0  
DB: 21 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-956-157-9765 (1-1400)

QY 12 LysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPhe 31  
DB 2 AAGAAGACTGGAGTGGTGTGGTGCCAGCCTATTCTGCTGCTTCTATTGACAGATTTC 61  
QY 32 SerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerPhe 51  
DB 62 AGCATTTGAGCGGTAAACAGCCTACATTGCTTGGCTTGGCTCTCTGTGACCATCAGCTTT 121  
QY 52 ArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArg 71  
DB 122 AGGATATCAAGGGTGTGATCCAGCTATCCAGAAATCAGATGAAGGCCACCCATTCCAG 181  
QY 72 AlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSer 91  
DB 182 GCATATCTGGAATCTGAAAGTTGCTATATCTGAGGAGTTGGTTCAAGAGTACAGTAATCT 241  
QY 92 AlaLeuGlyHisValAsnCysThrIleLysGlnLeuArgArgLeuPheLeuValAspAsp 111  
DB 242 GCTCTTGTGTCATGTGAACCTGCACGATAAAGAACTCAGCGGCTCTCTTAGTGTGATG 301  
QY 112 LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeu 131  
DB 302 TTAGTTGATTTCTCTGAAGTTTGCAGTGTGATGTGGTATTTACCTATGTTGGTGGCTTG 361  
QY 132 PheAsnGlyLeuThrLeuLeuIleLeuAlaIleSerLeuPheSerValProValIle 151  
DB 362 TTATATGCTGTGACACTACTGATTTTGGCTCTCACTTCTCAGTGTTCCTGTTATT 421  
QY 152 TyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLys 171  
DB 422 TATGAACGGCATCAGGCACAGATAGATCATTTATCTAGGACTTGCAATTAAGATGTTAAA 481  
QY 172 AspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLysArgLysAlaGlu 189  
DB 482 GATGCTATGGCTAAATCCAAGCAAAATCCCTGATTCAAGCGCAAGCTGAA 535

## RESULT 37

US-09-823-245A-349  
; Sequence 349, Application US/09823245A  
; Publication No. US20020039760A1  
; GENERAL INFORMATION:  
; APPLICANT: Wong, Gordon G.  
; APPLICANT: Clark, Hilary  
; APPLICANT: Fecthel, Kim  
; APPLICANT: Agostino, Michael J.  
; APPLICANT: Howes, Steven H.  
; APPLICANT: Resnick, Richard J.  
; APPLICANT: Gulukota, Kamalakur  
; APPLICANT: Graham, James R.  
; APPLICANT: Genetics Institute, Inc.  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS  
; FILE REFERENCE: GIN 6401  
; CURRENT APPLICATION NUMBER: US/09/823,245A  
; CURRENT FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: 60/194,941  
; PRIOR FILING DATE: 2000-04-06  
; NUMBER OF SEQ ID NOS: 631  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 349  
; LENGTH: 1514  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-823-245A-349

Alignment Scores:  
Pred. No.: 1.33e-98 Length: 1514  
Score: 867.00 Matches: 177  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 93.13% Indels: 0  
DB: 9 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-823-245A-349 (1-1514)



Db 183 CAGAAGTACAGTAATCTCTCTTGGTCATGTGAAGTGCACGATTAAGAACTCAGGCGC 242  
Qy 106 LeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPhe 125  
Db 243 CTCCTCTAGTTGATGATTTAGTTAGTTCTCTGAAGTTTGCAGTTTGGTGGTATTT 302  
Qy 126 ThrTyValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeuLeuSerLeu 145  
Db 303 ACTATGTTGGTGGCTTGTATTAATGCTCTGACACTACTGATTTGGCTCTCAATTCACATC 362  
Qy 146 PheSerValProValIleTyGluArgHisGlnAlaGlnIleAspHisTyLeuGlyLeu 165  
Db 363 TTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACATAGATCATTTATCTAGGACTT 422  
Qy 166 AlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 185  
Db 423 GCATAATAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAATCCCTGGATTGAAG 482  
Qy 186 ArgLysAlaGlu 189  
Db 483 CGCAAAAGCTGAA 494

## RESULT 40

US-10-956-157-9766  
; Sequence 9766, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9766  
; LENGTH: 1400  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-956-157-9766

## Alignment Scores:

Pred. No.: 7,566-80 Length: 1400  
Score: 718.00 Matches: 144  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 77.12% Indels: 0  
DB: 21 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-956-157-9766 (1-1400)

Qy 46 SerValThrIleSerPheArgIleTyLysGlyValIleGlnAlaIleGlnLysSerAsp 65  
Db 3 TCTGTGACCATCAGCTTTTAGGATATACAAAGGGTGTGATCCAGCTATCCAGAAATCAGAT 62  
Qy 66 GluGlyHisProPheArgAlaTyLeuGluSerGluValAlaIleSerGluGluLeuVal 85  
Db 63 GAAGGCCACCCATTCAGGCGCATCTCGAATCTGAAGTTGCTATATCTCAGGAGTTGGTT 122  
Qy 86 GlnLysTySerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgArg 105  
Db 123 CAGAAGTACAGTAATCTCTCTTGGTCATGTGAATGTCAGCTGACGATTAAGAACTCAGGCGC 182  
Qy 106 LeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPhe 125  
Db 183 CTCCTCTTAGTTGATTTAGTTGATTTCTGAAGTTTGCAGTTTGGTGGTATTT 242  
Qy 126 ThrTyValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeuLeuSerLeu 145  
Db 243 ACTATGTTGGTGGCTTGTATTAATGCTCTGACACTACTGATTTGGCTCTCAATTCACATC 302

Qy 146 PheSerValProValIleTyGluArgHisGlnAlaGlnIleAspHisTyLeuGlyLeu 165  
Db 303 TTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACATAGATCATTTATCTAGGACTT 362  
Qy 166 AlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 185  
Db 363 GCATAATAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAATCCCTGGATTGAAG 422  
Qy 186 ArgLysAlaGlu 189  
Db 423 CGCAAAAGCTGAA 434

## RESULT 41

US-09-960-352-8477  
; Sequence 8477, Application US/09960352  
; Patent No. US20020137139A1  
; GENERAL INFORMATION:

; APPLICANT: Warren, Wesley C.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Byatt, John C.  
; APPLICANT: Mathialagan, Nagappan  
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
; FILE REFERENCE: 16511.006/37-21(10298)C  
; CURRENT APPLICATION NUMBER: US/09/960,352  
; CURRENT FILING DATE: 2001-09-24  
; NUMBER OF SEQ ID NOS: 15112  
; SEQ ID NO 8477  
; LENGTH: 422  
; TYPE: DNA  
; ORGANISM: Bos taurus  
; OTHER INFORMATION: Clone ID: 36-LIB34-048-Q1-E1-A8  
US-09-960-352-8477

## Alignment Scores:

Pred. No.: 9,066-78 Length: 422  
Score: 695.00 Matches: 140  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 74.65% Indels: 0  
DB: 9 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-960-352-8477 (1-422)

Qy 37 ThrAlaTyIleAlaLeuAlaLeuSerValThrIleSerPheArgIleTyLysGly 56  
Db 2 ACGGCTACATTCGCTTGGCCCTGCTCTGTGACTATCAGCTTTAGGATATAAAGGCT 61  
Qy 57 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyLeuGluSer 76  
Db 62 GTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTCAGGCGCATTTTGAATCT 121  
Qy 77 GluValAlaIleSerGluGluLeuValGlnLysTySerAsnSerAlaLeuGlyHisVal 96  
Db 122 GAAGTTGCTATATCTGAGAGTTGGTTGAGAGTACAGCAATTCCTCTGGTCATGTT 181  
Qy 97 AsnCysThrIleLysGluLeuArgLeuPheLeuValAspAspLeuValAspSerLeu 116  
Db 182 AACTGCACAATAAAGAACTCAGACGCTCTCTTGTAGTTGATGATTTAGTTGATCTCTG 241  
Qy 117 LysPheAlaValLeuMetTrpValPheThrTyValGlyAlaLeuPheAsnGlyLeuThr 136  
Db 242 AAGTTGACAGTTGATGTTGGGTATTTACCTATGTTGGTGCCTTGTTCATGGTCTGACA 301  
Qy 137 LeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyGluArgHisGln 156  
Db 302 CTACTAAATTTGGCTCTGATTTCACTTTCAGTGTTCCTGTATTATTATGACGGCATCAG 361  
Qy 157 AlaGlnIleAspHisTyLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLys 176  
Db 362 GCGCAAAATAGATCATTTCTGGGACTTGCATAAAGAAATGTTAAAGATGCTATGGCTAAA 421

## RESULT 42







```
QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLeuPheAlaValLeuMet 122
Db 2190 CTGAGGAGGCTCTCTCTGTCAGGACCTGGTGGATTCCTTAAATTTGCAGTCTGATG 2249
QY 123 TrpValPheThrTyrValGlyAlaLeuPheAngLeuThrLeuLeuLeuAlaLeu 142
Db 2250 TGGCTCTGACCTAGCTGGGCGCTCTCTCAATGGCGCTGACCTGCTGCTGCTGCTG 2309
QY 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162
Db 2310 GTTTCATGTTTACTCTACTCTAGCTAGTGTATGTATAGCAGCCAGGCACAGTTGACCAATAT 2369
QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
Db 2370 CTGGGACTTGTGAGGACTCACATAAATGCTGTGTGGCAAGATTTCAGGCTAAATCCCA 2429
QY 183 GlyLeuLysArgLysAlaGlu 189
Db 2430 GCGCTAAGAGGCACGCTGAG 2450
RESULT 46
US-10-342-887-386
; Sequence 386, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 386
; LENGTH: 3202
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-386
Alignment Scores:
Pred. No.: 9.8e-75 Length: 3202
Score: 682.00 Matches: 128
Percent Similarity: 85.03% Conservative: 31
Best Local Similarity: 68.45% Mismatches: 28
Query Match: 73.25% Indels: 0
Gaps: 0
US-09-830-972-29_COPY_990_1178 (1-189) x US-10-342-887-386 (1-3202)
QY 3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22
Db 1890 ATTGACCTGTGTATTGGCGGACATCAAGCAGCGGCATCGTGTGGAGTTCTCTG 1949
QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerIleValThrAlaTyrIleAlaLeu 42
Db 1950 CTGCTGCTCTCTCTGACCCAGTTTCAGCGGGTGGAGCGTGTGCTGCTGCTGCTG 2009
QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62
Db 2010 GCCGCACTCTCAGCCACCATCATGTTCCGCATCTACAAGTCTGTGTTTACAAGCAGTG 2069
QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
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Db 2070 AAAACCCAGCAGGCGCACCCCTTTCAAGGCCTACTTGGAGCTTGAGATCACCCCTTCTCAG 2129
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102
Db 2130 GAGCAGATTCTAGAGTACACGAGCTGCTGAGTTCTACGTTCAACGTAACAGCACACTTAAGGAA 2189
QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122
Db 2190 CTGAGGAGGCTCTCTCTGTCAGGACCTGGTGGATTCCTTAAATTTGCAGTCTGATG 2249
QY 123 TrpValPheThrTyrValGlyAlaLeuPheAngLeuThrLeuLeuLeuAlaLeu 142
Db 2250 TGGCTCTGACCTAGCTGGGCGCTCTCTCAATGGCGCTGACCTGCTGCTGCTGCTG 2309
QY 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162
Db 2310 GTTTCATGTTTACTCTACTCTAGCTAGTGTATGTATAGCAGCCAGGCACAGTTGACCAATAT 2369
QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
Db 2370 CTGGGACTTGTGAGGACTCACATAAATGCTGTGTGGCAAGATTTCAGGCTAAATCCCA 2429
QY 183 GlyLeuLysArgLysAlaGlu 189
Db 2430 GCGCTAAGAGGCACGCTGAG 2450
RESULT 47
US-10-723-860-1480
; Sequence 1480, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nataasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods for Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1480
; LENGTH: 3202
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-1480
Alignment Scores:
Pred. No.: 9.8e-75 Length: 3202
Score: 682.00 Matches: 128
Percent Similarity: 85.03% Conservative: 31
Best Local Similarity: 68.45% Mismatches: 28
Query Match: 73.25% Indels: 0
Gaps: 0
US-09-830-972-29_COPY_990_1178 (1-189) x US-10-723-860-1480 (1-3202)
QY 3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22
Db 1890 ATTGACCTGTGTATTGGCGGACATCAAGCAGCGGCATCGTGTGGAGTTCTCTG 1949
QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerIleValThrAlaTyrIleAlaLeu 42
Db 1950 CTGCTGCTCTCTCTGACCCAGTTTCAGCGGGTGGAGCGTGTGCTGCTGCTGCTG 2009
QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62
Db 2010 GCCGCACTCTCAGCCACCATCATGTTCCGCATCTACAAGTCTGTGTTTACAAGCAGTG 2069
QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
```

DB: 2070 AAAACCGACGAGGACACCTTTTCAGGCTTACTTGAGCTTGAGATCACTTCTCAG 2129  
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102  
DB 2130 GAGCAGATTGAGAGTACAGGACTGCTGAGTTCACGTGAAACAGCACCTTAAGGAA 2189  
QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
DB 2190 CTGAGGAGGCTTCTCTTCCAGGACCTGGTGGATTCCTAAATTTTCAGTCTCTGATG 2249  
QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeu 142  
DB 2250 TGGCTCCTGACCTACCTGCTGCTCTCTCAATGGCTGACCTGCTGCTGCTGCTG 2309  
QY 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162  
DB 2310 GTTTCATGTTTACTTCTACCTGTAGTGTATGTTAAGCACCAGCACAGATTGACCAATAT 2369  
QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
DB 2370 CTGGGACTTGTGAGGACTCACATAATGCTGTGTGGCAAGATTTCAGGCTAAATCCCA 2429  
QY 183 GlyLeuLysArgLysAlaGlu 189  
DB 2430 GCGCTTAAGGACGCTGAG 2450

## RESULT 48

US-10-843-641A-3237  
; Sequence 3237, Application US/10843641A  
; Publication No. US20050064454A1  
; GENERAL INFORMATION:  
; APPLICANT: Avalon Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using  
; TITLE OF INVENTION: Signature Gene Sets  
; FILE REFERENCE: 689290-189  
; CURRENT APPLICATION NUMBER: US/10/843,641A  
; CURRENT FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: US/09/873,367  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US/09/954,531  
; PRIOR FILING DATE: 2001-09-18  
; PRIOR APPLICATION NUMBER: US/09/954,456  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US/09/962,436  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US/09/962,832  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US/09/964,824  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: US/09/967,768  
; PRIOR FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: US/09/968,007  
; PRIOR FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US/09/969,347  
; PRIOR FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US/09/969,708  
; PRIOR FILING DATE: 2001-10-03  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 8447  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3237  
; LENGTH: 3202  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-843-641A-3237

Alignment Scores:  
Pred. No.: 9,8e-75 Length: 3202  
Score: 682.00 Matches: 128  
Percent Similarity: 85.03% Conservative: 31  
Best Local Similarity: 68.45% Mismatches: 28  
Query Match: 73.25% Indels: 0

DB: 21 Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-843-641A-3237 (1-3202)  
QY 3 ValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeu 22  
DB 1890 ATTGACCTGTTGTTATTTGGCGGACATCAAGCAGACGGCATCGTGTGTTGGAGATTTCCTG 1949  
QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerIleValSerValThrAlaTyrIleAlaLeu 42  
DB 1950 CTGCTGCTCTTCTCCTGACCTACCCAGTTACGCGTGGTGGAGCTGCTGGCCTTACCTGGCCCTG 2009  
QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
DB 2010 GCGGCACCTCTCAGCCACCACATCATGTTTCGCATCTCAAGTCTGTTTTCACAGAGTGCAG 2069  
QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
DB 2070 AAAACCGAGGAGGCCACCTTTTCAAGGCTTACTTTGGAGCTTGAGATCACCTTCTCTCAG 2129  
QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102  
DB 2130 GAGCAGATTGAGAGTACAGGACTGCTGAGTTCACGTGAAACAGCACCTTAAGGAA 2189  
QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
DB 2190 CTGAGGAGGCTTCTCTTGTCCAGGACCTGGTGGATTCCTAAATTTTCAGTCTCTGATG 2249  
QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeu 142  
DB 2250 TGGCTCCTGACCTACCTGTTGGGCTCTCTTCAATGGCTGACCTGCTGCTGCTGCTG 2309  
QY 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162  
DB 2310 GTTTCATGTTTACTTCTACCTGTAGTGTATGTTAAGCACCAGCACAGATTGACCAATAT 2369  
QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
DB 2370 CTGGGACTTGTGAGGACTCACATAATGCTGTGTGGCAAGATTTCAGGCTAAATCCCA 2429  
QY 183 GlyLeuLysArgLysAlaGlu 189  
DB 2430 GCGCTTAAGGACGCTGAG 2450  
RESULT 49  
US-10-723-860-5926  
; Sequence 5926, Application US/10723860  
; Publication No. US20040253606A1  
; GENERAL INFORMATION:  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Ginsburg, Wendy M.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators  
; FILE REFERENCE: 05882.0193.NPUS01  
; CURRENT APPLICATION NUMBER: US/10/723,860  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 60/429,739  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 8393  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5926  
; LENGTH: 3305  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-723-860-5926  
Alignment Scores:  
Pred. No.: 1.03e-74 Length: 3305  
Score: 682.00 Matches: 128  
Percent Similarity: 85.03% Conservative: 31  
Best Local Similarity: 68.45% Mismatches: 28  
Query Match: 73.25% Indels: 0

DB: 20 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-723-860-5926 (1-3305)

QY 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22  
DB 1890 ATTGACCTGTTGTTATGGCGGACATCAAGCAGCGGATGTTGGAGTTCCTG 1949

QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
DB 1950 CTGCTGCTCTCTCCCTGACCCAGTTACGCGTGGGAGCGTCTGCTGACCTTACCTGCCCTG 2009

QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
DB 2010 GCGGACCTCTCAGCCACCATCAGTTCCGCATCTACAGTCTGTTTACAGCAGTGCAG 2069

QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
DB 2070 AAACCGAGAGGCGACCCCTTCAAGGCTTCTTGGAGCTTGAGATCACCCCTTCTCAG 2129

QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102  
DB 2130 GAGCAGATTCAGAGTACAGGACTGCTGCTGAGTCTACGTGAACAGCAGCATTAAAGAA 2189

QY 103 LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
DB 2190 CTGAGGAGCTCTCTCTGTCAGGACCTGCTGAGTCTCTTAAATTTGAGTCTGATG 2249

QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeu 142  
DB 2250 TGGCTCTGACCTAGCTGTTGGGCTCTCTTCAATGGCTGACCTGCTGCTGCTGCTG 2309

QY 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162  
DB 2310 GTTTCATGTTTACTCTACCTGATGTATGTAAGCACCAGCAGCAGATTGACCAATAT 2369

QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
DB 2370 CTGGGACTGTGAGGACTCACATAATGCTGTTGTGGCAAGATTCCAGGCTAAATCCCA 2429

QY 183 GlyLeuLysArgLysAlaGlu 189  
DB 2430 GCGGCTAAGAGGACGCTGAG 2450

RESULT 50

US-10-205-219-94

; Sequence 94, Application US/10205219

; Publication No. US20030138803A1

; GENERAL INFORMATION:

; APPLICANT: Warner-Lambert Company

; APPLICANT: Lee, Kevin

; APPLICANT: Dixon, Allstair

; APPLICANT: Brooksbank, Robert

; APPLICANT: Pinnock, Robert

; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain

; FILE REFERENCE: WL-A-018200

; CURRENT APPLICATION NUMBER: US/10/205,219

; CURRENT FILING DATE: 2002-07-24

; PRIOR APPLICATION NUMBER: GB 0118354.0

; PRIOR FILING DATE: 2001-07-27

; NUMBER OF SEQ ID NOS: 197

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 94

; LENGTH: 1502

; TYPE: DNA

; ORGANISM: Rattus norvegicus

; FEATURE:

; OTHER INFORMATION: rS-Rex-s

US-10-205-219-94

Alignment Scores:

Pred. No.: 3,968-75 Length: 1502

Score: 681.00 Matches: 127

Percent Similarity: 85.03% Conservative: 32

Best Local Similarity: 67.91% Mismatches: 28

Query Match: 73.15% Indels: 0

DB: 15 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-205-219-94 (1-1502)

QY 3 ValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSerLeu 22  
DB 179 ATTGACCTGTTGTTATGGCGGACATCAAGCAGCGGATGTTGGAGTTCCTG 238

QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
DB 239 CTGCTGCTCTCTCCCTGACCCAGTTACGCGTGGGAGCGTCTGCTGACCTTACCTGCCCTG 298

QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
DB 299 GCTGCCCTCTCTGCCACCATCAGCTTCGCGCATCTACAAGTCCGTTCTACAAGCTGTGCAG 358

QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
DB 359 AAACAGATGAGGTCACCCCTTCAAGGCTTACCTGGAGCTGGAGATCACCTGTGCCAG 418

QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102  
DB 419 GAGCAGATTCAGAGTACAGCAGCTGCTGAGCTATACGTGAACAGCAGCATTGAAGGAG 478

QY 103 LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
DB 479 CTAGGAGGCTCTCTCTGTCAGGACCTGCTGGATTCCTTAAATTTGAGTCTGCTCATG 538

QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeu 142  
DB 539 TGGCTCTGACTAGTGGGCTCTCTCAATGGCTGACCTGCTGCTTATGGCTGTG 598

QY 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162  
DB 599 GTTTCGATGTTTACTCTACCTGCTGATATGTTAAGCACCAGCAGCAGTTGACCAATAT 658

QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182  
DB 659 CTGGGACTGTGAGGACTCACATAACACCCGTTGTGGCAAGATTCCAGGCTAAATCCCC 718

QY 183 GlyLeuLysArgLysAlaGlu 189  
DB 719 GCGGCTAAGAGGACGCTGAG 739

RESULT 51

US-10-267-502-215

; Sequence 215, Application US/10267502

; Publication No. US20040071700A1

; GENERAL INFORMATION:

; APPLICANT: Kim, Jaeseob

; APPLICANT: Galant, Ron

; TITLE OF INVENTION: Obesity Linked Genes

; FILE REFERENCE: LSD-07416

; CURRENT APPLICATION NUMBER: US/10/267,502

; CURRENT FILING DATE: 2003-01-27

; NUMBER OF SEQ ID NOS: 439

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 215

; LENGTH: 2343

; TYPE: DNA

; ORGANISM: Mus musculus

US-10-267-502-215

Alignment Scores:

Pred. No.: 8e-75 Length: 2343

Score: 681.00 Matches: 127

Percent Similarity: 85.03% Conservative: 32

Best Local Similarity: 67.91% Mismatches: 28

Query Match: 73.15% Indels: 0

DB: 18 Gaps: 0

US-09-830-972-29 COPY 990 1178 (1-189) x US-10-205-194-128 (1-1473)

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Qy 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62
Db 266 GCTGCCCTCTCGCCACCATCAGCTTCGCACTACAGTCCGTTACAGCTGTGCAG 325
Qy 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82
Db 326 AAAACAGATGAGGGTCAACCTTTCAAGGCTACCTGGAGCTGGAGATCACCCCTGTCCCAG 385
Qy 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102
Db 386 GAGCAGATCCAGAGTACAGACTGCTGCAGCTATACGTGAACAGACACTCTGAAGGAG 445
Qy 103 LeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMet 122
Db 446 CTACGAGGCTCTCTCTGTCACAGACCTAGTGGATTCCTAAATTTGACGCTCTCATG 505
Qy 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeu 142
Db 506 TGGCTCTGACCTAGCTGTTGGCGCACTCTTCAATGGCTGACCTGCTGCTATGGCTGTG 565
Qy 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162
Db 566 GTTTCGATGTTTACTCTACCTGTGTATATGTTAAGCACCGACGACAGCTTGACCAATAT 625
Qy 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePro 182
Db 626 CTGGGACTGTGAGGACTCACATAACACCGTGTGGCANAGATCCAGGCTAAATATCCCC 685
Qy 183 GlyLeuLysArgLysAlaGlu 189
Db 686 GCGCGC-AAGAGGCGATGCTGAG 705

RESULT 54
US-10-408-967-1
; Sequence 1, Application US/10408967
; Publication No. US20040063161A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn Company
; APPLICANT: Yan, Riqiang
; APPLICANT: Lu, Yifeng
; TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease
; FILE REFERENCE: 00925
; CURRENT APPLICATION NUMBER: US/10/408,967
; CURRENT FILING DATE: 2003-04-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-408-967-1

Alignment Scores:
Pred. No.: 1,646-68 Length: 711
Score: 624.50 Matches: 115
Percent Similarity: 81.05% Conservative: 39
Best Local Similarity: 60.53% Mismatches: 35
Query Match: 67.08% Indels: 1
DB: 18 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-408-967-1 (1-711)
Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
Db 139 GCGGTGCAGATCTGATTTCTCGAGAGATGTGAAGAAGACTGGGTTGTCTTTGGCACC 198
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 199 ACGTGTATCATGCTCTTCCCTGGCAGCTTTCAGTGTGCATGAGTGGTGTCTTACCTC 258
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
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Db 259 ATCTGGGCTCTTCTCTGTCCACCATCAGCTTCAGGATCTACAGAGTCGGTCCATCCAAAGCT 318
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 319 GTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCTACCTGGAGCTAGACATTACTCTG 378
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 379 TCCTCAGAAGCTTTTCCATAATTACATGAATGCTGCCATGCTGCACATCAACAGGGCCCTG 438
Qy 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 439 AAATCATATTATTCGCTCTCTTCTGTGAAGAAGATCTGTTGACTCTCCTTGAAGCTGGCTGC 498
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db 499 TTCATGTGGCTGATGACCTATGTTGGTGTCTGTTTTTAACGGAAATCACCTCTCTAATCTT 558
Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 559 GCTGAAGTGTCTATTTTCAGTGTCCGATTGTCTATGAGAAGTACAAGACCCAGATTGAT 618
Qy 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 619 CACTATGTTGGCATGCGCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAAGCAAAA 678
Qy 181 IleProGlyLeu--LysArgLysAlaGlu 189
Db 679 CTCCTGGAATGTCGCAAAAAAAGGACAGAA 708

RESULT 55
US-10-106-698-1945
; Sequence 1945, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 1945
; LENGTH: 1330
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-106-698-1945

Alignment Scores:
Pred. No.: 4,426-68 Length: 1330
Score: 624.50 Matches: 115
Percent Similarity: 81.05% Conservative: 39
Best Local Similarity: 60.53% Mismatches: 35
Query Match: 67.08% Indels: 1
DB: 15 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-106-698-1945 (1-1330)
Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
Db 297 GCGGTGCAGATCTGATTTCTCGAGAGATGTGAAGAAGACTGGGTTGTCTTTGGCACC 356
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 357 ACGTGTATCATGCTCTTCCCTGGCAGCTTTCAGTGTGCATGAGTGGTGTCTTACCTC 416
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
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Db 417 ATCTGGCTCTTCTCTGTGACCATCAGCTTCAGGATCTACAGTCCGTCATCCAGCT 476
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 477 GTACAGAAGTCAGAGAAGGCCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCTG 536
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 537 TCCTCAGAAGCTTTCATTAATTACATGAATGCTGCCATGCTGCACATCAACAGGGCCCTG 596
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 597 AAATCATATTATTCGTCTCTTCTGGTAGAAGATCTGTTGACTCCTTTGAAGCTGGCTGTC 656
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db 657 TTCATGTGGCTGATGACCTATGTTGGTGTGTTTAAACGGAATCACCCCTTCTAATTC 716
QY 141 AlaLeuLysSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 717 GCTGAACCTGCTCATTTTTCAGTGTCCCGATTGCTATGAGAAGTACCAAGACCCAGATTGAT 776
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 777 CACTATGTTGGCATCGCCGAGATCAGACCAAGTCAATTTGTTGAAGAATCCAAAGCAAAA 836
QY 181 IleProGlyLeu---LysArgLysAlaGlu 189
Db 837 CTCCTTGGATCGCCCAAAAAAAGGCAGAA 866
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## RESULT 56

US-09-729-674-19

; Sequence 19, Application US/09729674

; Patent No. US2001003935A1

; GENERAL INFORMATION:

; APPLICANT: Jacobs, Kenneth

; APPLICANT: McCoy, John M.

; APPLICANT: LaVallie, Edward R.

; APPLICANT: Collins-Racie, Lisa A.

; APPLICANT: Evans, Cheryl

; APPLICANT: Merberg, David

; APPLICANT: Treacy, Maurice

; APPLICANT: Agostino, Michael J.

; APPLICANT: Steininger II, Robert J.

; APPLICANT: Spaulding, Vikki

; APPLICANT: Wong, Gordon G.

; APPLICANT: Clark, Hilary

; APPLICANT: Fechtel, Kim

; APPLICANT: Genetics Institute, Inc.

; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

; FILE REFERENCE: 6055-64X

; CURRENT APPLICATION NUMBER: US/09/729,674

; PRIOR FILING DATE: 2000-12-04

; PRIOR APPLICATION NUMBER: 09/539,330

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 283

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 19

; LENGTH: 1656

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-729-674-19

## Alignment Scores:

Pred. No.:	6,26e-68	Length:	1656
Score:	624.50	Matches:	115
Percent Similarity:	81.05%	Conservative:	39
Best Local Similarity:	60.53%	Mismatches:	35
Query Match:	67.08%	Indels:	1
DB:	9	Gaps:	1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-729-674-19 (1-1656)

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QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
Db 165 GGGTGGCAGATCTGATTTCTGGAGAGATGTGAAGAGACTGGGTTTCTCTTGGCACC 224
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 225 AGCTGATCATCTGTTTCCCTGGCAGCTTTTCAGTGTCTCAGTGTCTCAGTGTGTTTCTTACCTC 284
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db 285 ATCTGGCTCTTCTCTGTGCACCATCAGCTTCAGATCTCAAGTCCGTCATCCAAAGCT 344
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 345 GTACAGAAGTCAGAGAAGGCCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCTG 404
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 405 TCCTCAGAAGCTTTCATTAATTACATGAATGCTGCCATGCTGCACATCAACAGGGCCCTG 464
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
Db 465 AAATCATATTATTCGTCTCTTCTGGTAGAAGATCTGTTGACTCCTTTGAAGCTGGCTGTC 524
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db 525 TTCATGTGGCTGATGACCTATGTTGGTGTGTTTAAACGGAATCACCCCTTCTAATTC 584
QY 141 AlaLeuLysSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 585 GCTGAACCTGCTCATTTTCAGTGTCCCGATTGCTATGAGAAGTACCAAGACCCAGATTGAT 644
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 645 CACTATGTTGGCATCGCCGAGATCAGACCAAGTCAATTTGTTGAAGAATCCAAAGCAAAA 704
QY 181 IleProGlyLeu---LysArgLysAlaGlu 189
Db 705 CTCCTTGGATCGCCCAAAAAAAGGCAGAA 734
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## RESULT 57

US-10-913-553-19

; Sequence 19, Application US/10913553

; Publication No. US20050003491A1

; GENERAL INFORMATION:

; APPLICANT: Jacobs, Kenneth

; APPLICANT: McCoy, John M.

; APPLICANT: LaVallie, Edward R.

; APPLICANT: Collins-Racie, Lisa A.

; APPLICANT: Evans, Cheryl

; APPLICANT: Merberg, David

; APPLICANT: Treacy, Maurice

; APPLICANT: Agostino, Michael J.

; APPLICANT: Steininger II, Robert J.

; APPLICANT: Spaulding, Vikki

; APPLICANT: Wong, Gordon G.

; APPLICANT: Clark, Hilary

; APPLICANT: Fechtel, Kim

; APPLICANT: Genetics Institute, Inc.

; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

; FILE REFERENCE: 6055-64X

; CURRENT APPLICATION NUMBER: US/10/913,553

; PRIOR FILING DATE: 2004-08-09

; PRIOR APPLICATION NUMBER: US/09/539,330

; NUMBER OF SEQ ID NOS: 283

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 19

; LENGTH: 1656

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-913-553-19

**Alignment Scores:**

Pred. No.: 624-50	Length: 1656
Score: 624.50	Matches: 115
Percent Similarity: 81.05%	Conservative: 39
Best Local Similarity: 60.53%	Mismatches: 35
Query Match: 67.08%	Indels: 1
DB: 9	Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-913-553-19 (1-1656)

Qy 1 SerValValAspLeuLeuSerLeuThrArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 165 GCGGTGCAGATCTGATTTCCTGGAGAGATGGAAGAAGACTGGGTTTCTTTGGCACC 224  
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerLeuThrAlaTyrlle 40  
Db 225 ACGTGATCATGCTGCTCCCTGGCAGCTTTCACTGTCATCAGTGTGGTTCTTTACCTC 284  
Qy 41 AlaLeuAlaLeuSerValThrIleSerPheAglileTyryLysGlyValIleGlnAla 60  
Db 285 ATCTGGCTCTTCTCTGTCCATCACCTTCCAGATCTACAGATCTACAGTCCGTCATCCAGCT 344  
Qy 61 IleGlnLysSerAspGluGlyHisProPheAglilaTyryLeuGluSerGluValAlaIle 80  
Db 345 GTACAGAAGTCAGAAGAGGCCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCTG 404  
Qy 81 SerGluGluLeuValGlnLysTyrsenSerAlaLeuGlyHisValasnCysThrIle 100  
Db 405 TCCTCAGAGCTTTCATTAATTACATGAATGCTGCCATGCTGCATCAACAGGCCCTG 464  
Qy 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 465 AAATCATTAATTCGTCCTCTTCTGGTAGAAGATCTGGTTGACTCTTGAAGCTGGCTGTC 524  
Qy 121 LeuMetTrpValPheThrTyrrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
Db 525 TTCAATGCTGCTGATGACCTATGTTGGTGTGTTTAAACGGAATCACCTCTTAATTCTT 584  
Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrgluArgHisGlnAlaGlnIleasp 160  
Db 585 GCTGAAGTCTCATTTTCAGTGTCCGATGCTGATGAGAGATGACAGACCCAGATTGAT 644  
Qy 161 HistyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlalys 180  
Db 645 CACTATGTTGGCATCCCGCAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAAA 704  
Qy 181 IleProGlyLeu---LysArgLysAlaGlu 189  
Db 705 CTCCTGGAAATGCCCAAAAAAAGGCAGAA 734

**RESULT 58**  
US-09-765-205-25  
; Sequence 25, Application US/09765205  
; Patent No. US20020034800A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Li  
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES  
; FILE REFERENCE: 1458.004/200130.449  
; CURRENT APPLICATION NUMBER: US/09/765,205  
; CURRENT FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: US/09/212,440  
; PRIOR FILING DATE: 1998-12-16  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25  
; LENGTH: 1668  
; TYPE: DNA  
; ORGANISM: human  
US-09-765-205-25

**Alignment Scores:**

Pred. No.: 624-50	Length: 1668
Score: 624.50	Matches: 115
Percent Similarity: 81.05%	Conservative: 39
Best Local Similarity: 60.53%	Mismatches: 35
Query Match: 67.08%	Indels: 1
DB: 21	Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-765-205-25 (1-1668)

Qy 1 SerValValAspLeuLeuSerLeuThrArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 237 GCGGTGCAGATCTGATTTCCTGGAGAGATGGAAGAAGACTGGGTTTCTTTGGCACC 296  
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrlle 40  
Db 297 ACGTGTATCATGCTGCTCCCTGGCAGCTTTCACTGTCATCAGTGTGGTTCTTTACCTC 356  
Qy 41 AlaLeuAlaLeuSerValThrIleSerPheAglileTyryLysGlyValIleGlnAla 60  
Db 357 ATCTGGCTCTTCTCTGTCCATCACCTTCCAGATCTACAGTCCGTCATCCAGCT 416  
Qy 61 IleGlnLysSerAspGluGlyHisProPheAglilaTyryLeuGluSerGluValAlaIle 80  
Db 417 GTACAGAAGTCAGAAGAGGCCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCTG 476  
Qy 81 SerGluGluLeuValGlnLysTyrsenSerAlaLeuGlyHisValasnCysThrIle 100  
Db 477 TCCTCAGAGCTTTCATTAATTACATGAATGCTGCCATGCTGCATCAACAGGCCCTG 536  
Qy 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 537 AAATCATTAATTCGTCCTCTTCTGGTAGAAGATCTGGTTGACTCTTGAAGCTGGCTGTC 596  
Qy 121 LeuMetTrpValPheThrTyrrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
Db 597 TTCATGTCGCTGATGACCTATGTTGGTGTGTTTAAACGGAATCACCTCTTAATTCTT 656  
Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrgluArgHisGlnAlaGlnIleasp 160  
Db 657 GCTGAAGTCTCATTTTCAGTGTCCGATGCTGATGAGAGATGACAGACCCAGATTGAT 716  
Qy 161 HistyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlalys 180  
Db 717 CACTATGTTGGCATCCCGCAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAAA 776  
Qy 181 IleProGlyLeu---LysArgLysAlaGlu 189  
Db 777 CTCCTGGAAATGCCCAAAAAAAGGCAGAA 806

**RESULT 59**  
US-10-347-669-25  
; Sequence 25, Application US/10347669  
; Publication No. US20050084850A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Li  
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES  
; FILE REFERENCE: 1458.004/200130.449  
; CURRENT APPLICATION NUMBER: US/10/347,669  
; CURRENT FILING DATE: 2003-01-16  
; PRIOR APPLICATION NUMBER: US/09/212,440  
; PRIOR FILING DATE: 1998-12-16  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25  
; LENGTH: 1668  
; TYPE: DNA  
; ORGANISM: human  
US-10-347-669-25

**Alignment Scores:**

Pred. No.: 624-50	Length: 1668
Score: 624.50	Matches: 115
Percent Similarity: 81.05%	Conservative: 39
Best Local Similarity: 60.53%	Mismatches: 35
Query Match: 67.08%	Indels: 1
DB: 21	Gaps: 1

US-09-765-205-25

Qy 1 SerValValAspLeuLeuSerLeuThrArgAspIleLysLysThrGlyValValPheGlyAla 20  
Db 165 GCGGTGCAGATCTGATTTCCTGGAGAGATGGAAGAAGACTGGGTTTCTTTGGCACC 224  
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerLeuThrAlaTyrlle 40  
Db 225 ACGTGATCATGCTGCTCCCTGGCAGCTTTCACTGTCATCAGTGTGGTTCTTTACCTC 284  
Qy 41 AlaLeuAlaLeuSerValThrIleSerPheAglileTyryLysGlyValIleGlnAla 60  
Db 285 ATCTGGCTCTTCTCTGTCCATCACCTTCCAGATCTACAGATCTACAGTCCGTCATCCAGCT 344  
Qy 61 IleGlnLysSerAspGluGlyHisProPheAglilaTyryLeuGluSerGluValAlaIle 80  
Db 345 GTACAGAAGTCAGAAGAGGCCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCTG 404  
Qy 81 SerGluGluLeuValGlnLysTyrsenSerAlaLeuGlyHisValasnCysThrIle 100  
Db 405 TCCTCAGAGCTTTCATTAATTACATGAATGCTGCCATGCTGCATCAACAGGCCCTG 464  
Qy 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120  
Db 465 AAATCATTAATTCGTCCTCTTCTGGTAGAAGATCTGGTTGACTCTTGAAGCTGGCTGTC 524  
Qy 121 LeuMetTrpValPheThrTyrrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140  
Db 525 TTCAATGCTGCTGATGACCTATGTTGGTGTGTTTAAACGGAATCACCTCTTAATTCTT 584  
Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrgluArgHisGlnAlaGlnIleasp 160  
Db 585 GCTGAAGTCTCATTTTCAGTGTCCGATGCTGATGAGAGATGACAGACCCAGATTGAT 644  
Qy 161 HistyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlalys 180  
Db 645 CACTATGTTGGCATCCCGCAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAAA 704  
Qy 181 IleProGlyLeu---LysArgLysAlaGlu 189  
Db 705 CTCCTGGAAATGCCCAAAAAAAGGCAGAA 734

**RESULT 58**  
US-09-765-205-25  
; Sequence 25, Application US/09765205  
; Patent No. US20020034800A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Li  
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES  
; FILE REFERENCE: 1458.004/200130.449  
; CURRENT APPLICATION NUMBER: US/09/765,205  
; CURRENT FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: US/09/212,440  
; PRIOR FILING DATE: 1998-12-16  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25  
; LENGTH: 1668  
; TYPE: DNA  
; ORGANISM: human  
US-09-765-205-25

**Alignment Scores:**

Pred. No.: 624-50	Length: 1668
Score: 624.50	Matches: 115
Percent Similarity:	





1	PRIOR APPLICATION NUMBER: 60/047,615
2	PRIOR FILING DATE: 1997-05-23
3	PRIOR APPLICATION NUMBER: 60/047,597
4	PRIOR FILING DATE: 1997-05-23
5	PRIOR APPLICATION NUMBER: 60/047,502
6	PRIOR FILING DATE: 1997-05-23
7	PRIOR APPLICATION NUMBER: 60/047,633
8	PRIOR FILING DATE: 1997-05-23
9	PRIOR APPLICATION NUMBER: 60/047,583
10	PRIOR FILING DATE: 1997-05-23
11	PRIOR APPLICATION NUMBER: 60/047,617
12	PRIOR FILING DATE: 1997-05-23
13	PRIOR APPLICATION NUMBER: 60/047,618
14	PRIOR FILING DATE: 1997-05-23
15	PRIOR APPLICATION NUMBER: 60/047,503
16	PRIOR FILING DATE: 1997-05-23
17	PRIOR APPLICATION NUMBER: 60/047,592
18	PRIOR FILING DATE: 1997-05-23
19	PRIOR APPLICATION NUMBER: 60/047,588
20	PRIOR FILING DATE: 1997-05-23
21	PRIOR APPLICATION NUMBER: 60/047,584
22	PRIOR FILING DATE: 1997-05-23
23	PRIOR APPLICATION NUMBER: 60/047,500
24	PRIOR FILING DATE: 1997-05-23
25	PRIOR APPLICATION NUMBER: 60/047,587
26	PRIOR FILING DATE: 1997-05-23
27	PRIOR APPLICATION NUMBER: 60/047,492
28	PRIOR FILING DATE: 1997-05-23
29	PRIOR APPLICATION NUMBER: 60/047,598
30	PRIOR FILING DATE: 1997-05-23
31	PRIOR APPLICATION NUMBER: 60/047,613
32	PRIOR FILING DATE: 1997-05-23
33	PRIOR APPLICATION NUMBER: 60/047,582
34	PRIOR FILING DATE: 1997-05-23
35	PRIOR APPLICATION NUMBER: 60/047,596
36	PRIOR FILING DATE: 1997-05-23
37	PRIOR APPLICATION NUMBER: 60/047,612
38	PRIOR FILING DATE: 1997-05-23
39	PRIOR APPLICATION NUMBER: 60/047,632
40	PRIOR FILING DATE: 1997-05-23
41	PRIOR APPLICATION NUMBER: 60/047,601
42	PRIOR FILING DATE: 1997-05-23
43	PRIOR APPLICATION NUMBER: 60/043,580
44	PRIOR FILING DATE: 1997-04-11
45	PRIOR APPLICATION NUMBER: 60/043,568
46	PRIOR FILING DATE: 1997-04-11
47	PRIOR APPLICATION NUMBER: 60/043,314
48	PRIOR FILING DATE: 1997-04-11
49	PRIOR APPLICATION NUMBER: 60/043,671
50	PRIOR FILING DATE: 1997-04-11
51	PRIOR APPLICATION NUMBER: 60/043,674
52	PRIOR FILING DATE: 1997-04-11
53	PRIOR APPLICATION NUMBER: 60/043,669
54	PRIOR FILING DATE: 1997-04-11
55	PRIOR APPLICATION NUMBER: 60/043,312
56	PRIOR FILING DATE: 1997-04-11
57	PRIOR APPLICATION NUMBER: 60/043,313
58	PRIOR FILING DATE: 1997-04-11
59	PRIOR APPLICATION NUMBER: 60/048,974
60	PRIOR FILING DATE: 1997-06-06
61	PRIOR APPLICATION NUMBER: 60/056,886
62	PRIOR FILING DATE: 1997-08-22
63	PRIOR APPLICATION NUMBER: 60/056,877
64	PRIOR FILING DATE: 1997-08-22
65	PRIOR APPLICATION NUMBER: 60/056,889

1	PRIOR FILING DATE: 1997-08-22	
2	PRIOR APPLICATION NUMBER: 60/056,893	
3	PRIOR FILING DATE: 1997-08-22	
4	PRIOR APPLICATION NUMBER: 60/056,630	
5	PRIOR FILING DATE: 1997-08-22	
6	PRIOR APPLICATION NUMBER: 60/056,878	
7	PRIOR FILING DATE: 1997-08-22	
8	PRIOR APPLICATION NUMBER: 60/056,662	
9	PRIOR FILING DATE: 1997-08-22	
10	PRIOR APPLICATION NUMBER: 60/056,872	
11	PRIOR FILING DATE: 1997-08-22	
12	PRIOR APPLICATION NUMBER: 60/056,882	
13	PRIOR FILING DATE: 1997-08-22	
14	PRIOR APPLICATION NUMBER: 60/056,637	
15	PRIOR FILING DATE: 1997-08-22	
16	PRIOR APPLICATION NUMBER: 60/056,903	
17	PRIOR FILING DATE: 1997-08-22	
18	PRIOR APPLICATION NUMBER: 60/056,888	
19	PRIOR FILING DATE: 1997-08-22	
20	PRIOR APPLICATION NUMBER: 60/056,879	
21	PRIOR FILING DATE: 1997-08-22	
22	PRIOR APPLICATION NUMBER: 60/056,880	
23	PRIOR FILING DATE: 1997-08-22	
24	PRIOR APPLICATION NUMBER: 60/056,894	
25	PRIOR FILING DATE: 1997-08-22	
26	PRIOR APPLICATION NUMBER: 60/056,911	
27	PRIOR FILING DATE: 1997-08-22	
28	PRIOR APPLICATION NUMBER: 60/056,636	
29	PRIOR FILING DATE: 1997-08-22	
30	PRIOR APPLICATION NUMBER: 60/056,874	
31	PRIOR FILING DATE: 1997-08-22	
32	PRIOR APPLICATION NUMBER: 60/056,910	
33	PRIOR FILING DATE: 1997-08-22	
34	PRIOR APPLICATION NUMBER: 60/056,864	
35	PRIOR FILING DATE: 1997-08-22	
36	PRIOR APPLICATION NUMBER: 60/056,892	
37	PRIOR FILING DATE: 1997-08-22	
38	PRIOR APPLICATION NUMBER: 60/057,761	
39	PRIOR FILING DATE: 1997-08-22	
40	PRIOR APPLICATION NUMBER: 60/047,595	
41	PRIOR FILING DATE: 1997-05-23	
42	PRIOR APPLICATION NUMBER: 60/047,599	
43	PRIOR FILING DATE: 1997-05-23	
44	PRIOR APPLICATION NUMBER: 60/047,588	
45	PRIOR FILING DATE: 1997-05-23	
46	PRIOR APPLICATION NUMBER: 60/047,585	
47	PRIOR FILING DATE: 1997-05-23	
48	PRIOR APPLICATION NUMBER: 60/047,586	
49	PRIOR FILING DATE: 1997-05-23	
50	PRIOR APPLICATION NUMBER: 60/047,590	
51	PRIOR FILING DATE: 1997-05-23	
52	PRIOR APPLICATION NUMBER: 60/047,594	
53	PRIOR FILING DATE: 1997-05-23	
54	PRIOR APPLICATION NUMBER: 60/047,589	
55	PRIOR FILING DATE: 1997-05-23	
56	PRIOR APPLICATION NUMBER: 60/047,593	
57	PRIOR FILING DATE: 1997-05-23	
58	PRIOR APPLICATION NUMBER: 60/047,614	
59	PRIOR FILING DATE: 1997-05-23	
60	PRIOR APPLICATION NUMBER: 60/043,578	
61	PRIOR FILING DATE: 1997-04-11	
62	PRIOR APPLICATION NUMBER: 60/043,576	
63	PRIOR FILING DATE: 1997-04-11	
64	PRIOR APPLICATION NUMBER: 60/047,501	
65	PRIOR FILING DATE: 1997-05-23	
66	PRIOR APPLICATION NUMBER: 60/043,670	
67	PRIOR FILING DATE: 1997-04-11	
68	PRIOR APPLICATION NUMBER: 60/056,632	
69	PRIOR FILING DATE: 1997-08-22	



## RESULT 63

US-10-276-774-980  
; Sequence 980, Application US/10276774  
; Publication No. US20040053245A1  
; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.  
; APPLICANT: Tang, Y, Tom et al  
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-030  
; CURRENT APPLICATION NUMBER: US/10/276,774

; PRIORITY FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/560,875  
; PRIORITY FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: 09/496,914  
; PRIORITY FILING DATE: 2000-02-03

; NUMBER OF SEQ ID NOS: 2700  
; SOFTWARE: Custom

; SEQ ID NO 980

; LENGTH: 1915

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-276-774-980

## Alignment Scores:

Pred. No.:	7,87e-68	Length:	1915
Score:	624.50	Matches:	115
Percent Similarity:	81.05%	Conservative:	39
Best Local Similarity:	60.53%	Mismatches:	35
Query Match:	67.08%	Indels:	1
DB:	18	Gaps:	1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-276-774-980 (1-1915)

Qy	1	SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla	20
Db	287	GGGTCGACGATCTGATTTCTGGAGAGATGTGAAGAAGACTGGGTTGTCTTTGGCACC	346
Qy	21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	347	ACGTCGATCATGCTCTTCCCTGGCAGCTTTTCAGTGTTCATGCTGTTCTTTACCTC	406
Qy	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
Db	407	ATCTGGGCTCTCTCTGTACCATCAGCTTCAGATCTACAGTCCGTATCCAGCT	466
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
Db	467	GTACAGAAGTCAGAAAGAGGCCATCCATTCAAAGCTTACCTGAGCTAGACATTACTCTG	526
Qy	81	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle	100
Db	527	TCCTCAGAAGCTTTCCATAAATTACATGAATGTGTCATGTGTCATCAACAGGCGCCCTG	586
Qy	101	LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal	120
Db	587	AAACTATTATTCGTCTCTTCTGGTGAAGATCTGGTTGATCTCTTGAAGCTGGCTGTC	646
Qy	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
Db	647	TTCATGTGGCTGATGACCTATGTTGTTGCTGTTTAAACGGAATCACCTTCTAATCTCT	706
Qy	141	AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp	160
Db	707	GCTGAACGTCTCATTTTCAGTCTCCGATTTGTCTATGAGAAGTACACAGCCAGATTGAT	766
Qy	161	HisTyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLys	180
Db	767	CACATGTTGGTCATGCCGAGATCAGACCAAGTCAATTTGTTGAAAAGATCAACAGCAAA	826
Qy	181	IleProGlyLeu---LysArgLysAlaGlu	189
Db	827	CTCCCTGGATCGCCANAAAAAAGGAGNA	856

## RESULT 64

US-09-809-391-255

; Sequence 255, Application US/09809391

; Publication No. US20030049618A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: 186 Human Secreted proteins

; FILE REFERENCE: P2002P2

; CURRENT APPLICATION NUMBER: US/09/809,391

; CURRENT FILING DATE: 2001-03-16

; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 761

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 255

; LENGTH: 2664

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (2623)

; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: SITE

; LOCATION: (2640)

; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: SITE

; LOCATION: (2652)

; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: SITE

; LOCATION: (2662)

; OTHER INFORMATION: n equals a,t,g, or c

US-09-809-391-255

## Alignment Scores:

Pred. No.:	1,33e-67	Length:	2664
Score:	624.50	Matches:	115
Percent Similarity:	81.05%	Conservative:	39
Best Local Similarity:	60.53%	Mismatches:	35
Query Match:	67.08%	Indels:	1
DB:	10	Gaps:	1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-809-391-255 (1-2664)

Qy	1	SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla	20
Db	262	CGGTGCACGATCTGATTTCTGGAGAGATGTGAAGAAGACTGGGTTGTCTTTGGCACC	321
Qy	21	SerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle	40
Db	322	ACGTCGATCATGCTGCTTCCCTGGCAGCTTTTCAGTGTTCATGCTGTTCTTTACCTC	381
Qy	41	AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla	60
Db	382	ATCTGGGCTCTCTCTGTCCATCAGCTTCAGGATCTACAAAGTCCGTATCCAGCT	441
Qy	61	IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle	80
Db	442	GTACAGAAGTCAGAAAGAGGCCATCCATTAAAGCTTACCTGGAGCTAGACATTACTCTG	501
Qy	81	SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle	100
Db	502	TCCTCAGAAGCTTCCATAAATTACATGAATGCTGCCATGTCATCAACAGGCGCCCTG	561
Qy	101	LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal	120
Db	562	AAACTATTATTCGTCTCTTCTGTAGAGATCTGGTTGACTCTCTTGAAGCTGGCTGTC	621
Qy	121	LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu	140
Db	622	TTCAATGGCTGATGACCTATGTTGGTGTCTTTTAAACGGAATCACCTTCTTAATCTT	681
Qy	141	AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp	160

Db 682 GCTGAAGTCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGATTGAT 741  
Qy 161 HistyleuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 742 CACTATGTTGGCATCCCGAGATCAGACCAAGTCAATTGTTGAAAGATCCAAGCAAAA 801  
Qy 181 IleProGlyLeu--LysArgLysAlaGlu 189  
Db 802 CTCCTTGGATCCCAAAAAAAGGCAGAA 831

RESULT 65  
US-09-882-171-255  
; Sequence 255, Application US/09882171  
; Publication No. US20030175858A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P2  
; CURRENT APPLICATION NUMBER: US/09/882,171  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 09/809,391  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 09/149,476  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: PCT/US98/04493  
; PRIOR FILING DATE: 1998-03-06  
; PRIOR APPLICATION NUMBER: 60/040,162  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,333  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/038,621  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,626  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,334  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,336  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,163  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/047,600  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,615  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,597  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,502  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,633  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,583  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,617  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,618  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,503  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,592  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,581  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,584  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,500  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,587  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,492  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,598  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,613

; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,582  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,596  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,612  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,632  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,601  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/043,580  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,568  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,314  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,569  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,311  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,671  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,674  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,669  
; PRIOR FILING DATE: 1997-04-11  
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; PRIOR APPLICATION NUMBER: 60/043,313  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,672  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,315  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/048,974  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/056,886  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,877  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,889  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,893  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,630  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,878  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,662  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,872  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,882  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,637  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,903  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,888  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,879  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,880  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,894  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,911  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,636  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,874  
; PRIOR FILING DATE: 1997-08-22

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; PRIOR APPLICATION NUMBER: 60/056,910
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,864
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,631
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,845
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,892
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,761
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/047,595
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,599
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,588
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,585
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,586
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,590
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,594
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,589
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,593
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,614
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,578
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/047,501
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,670
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/056,632
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,876
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,881
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,909
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,875
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05

Alignment Scores:
Pred. No.: 1,338-67 Length: 2664
Score: 624.50 Matches: 115
Percent Similarity: 81.0% Conservative: 39
Best Local Similarity: 60.53% Mismatches: 35
Query Match: 67.08% Indels: 1

DB: 10 Gaps: 1
US-09-830-972-29_COPY_990_1178 (1-189) x US-09-882-171-255 (1-2664)
Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleIysThrGlyValValPheGlyAla 20
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
262 GCGGTGCACGATCTGATTTCTGGAGAGATGTGAAGAGACTGGGTTTGTCTTTGGCACC 321
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
322 ACGCTGATCATGCTGCTTCCCTGGACGCTTCAGTGTCACTGAGTGTGGTTCCTTACCTC 381
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAla 60
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
382 ATCTGGCTCTTCTCTGTCACCATCAGCTTCAGGATCTACAGTCCGTCATCCAGCT 441
Qy 61 IleGlnIysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
442 GTACAGAAGTCAGAAGAGGCCATCCATTCAAAGCTACCTGGACGTAGACATTACTCTG 501
Qy 81 SerGluGluLeuValGlnIysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
502 TCCTCAGAAGCTTCCATATAATACATGAATGCTGCATGGTGACATCAACAGGGCCCTG 561
Qy 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuIysPheAlaVal 120
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
562 AAACCTATTATTCGTCCTCTTCGTAGAAGATCTGGTTGACTCTCTTGAAGCTGGCTGTC 621
Qy 121 LeuMetTrpValPheThrTyrValIleGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
622 TTCATGTGGCTGATGACCTATGTTGGTCTGCTTTTAAACGGAATCACCCCTTCTAATTCTT 681
Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
682 GCTGAACCTGCTCATTTTTCAGTGTCCCGATTCTCTATGAGAAGTACAGACCCAGATTGAT 741
Qy 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
742 CACTATGTGGCATCGCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAGCAAAA 801
Qy 181 IleProGlyLeu---LysArgLysAlaGlu 189
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
802 CTCCTCGAATCGCCAAAAGGCGAGAA 831

RESULT 66
US-10-184-861-255
; Sequence 255, Application US/10164861
; Publication No. US20030225248A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/10/164,861
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 255
; LENGTH: 2664
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2623)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2640)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
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; NAME/KEY: SITE
; LOCATION: (2652)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2662)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-164-861-255

Alignment Scores:
Pred. No.: 1,336-67 Length: 2664
Score: 624.50 Matches: 115
Percent Similarity: 81.05% Conservative: 39
Best Local Similarity: 60.53% Mismatches: 35
Query Match: 67.08% Indels: 1
DB: 17 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-164-861-255 (1-2664)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysGlyThrGlyValValPheGlyAla 20
Db 262 GCGGTGCAGCATCTGATTTCTGGAGAGATGTGAAGAGACTGGGGTTCTCTTTGGCACC 321
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 322 ACCTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTCTACAGTGTGGTTCTTACCTC 381
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60
Db 382 ATCTGGCTCTTCTCTGTCCACCATCAGCTTCAGGATCTACAGTCCGTCATCCAACT 441
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleGluSerGluValAlaIle 80
Db 442 GTACAGAAGTCAGAAGAGCCATCCATTCAAAGCCCTACCTGGACGCTAGACATTACTCTG 501
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 502 TCTCAGAGCTTCTCATTAATACATGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 561
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 562 AAATCATATTATTCGCTCTCTTCTGTTAGAGATCTGTTGACTCTCTTGAAGCTGGCTGC 621
QY 121 LeuMetTrpValPheThrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 622 TTATGCTGGCTGATGACCTATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 681
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 682 GCTGAAGTCTCATTTCTAGTGTCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 741
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 742 CACTATGTTGGCATCGCCCGAGATCAGCAAGTCAATGTTGTTGAAAGATCCCAAGCAAAA 801
QY 181 IleProGlyLeu---LysArgLysAlaGlu 189
Db 802 CTCCTCGGAATCGCCCAAAAAGAGGAGAA 831

RESULT 67
US-10-723-860-6867
; Sequence 6867, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739

; NAME/KEY: SITE
; LOCATION: (2652)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2662)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-164-861-255

Alignment Scores:
Pred. No.: 1,336-67 Length: 2664
Score: 624.50 Matches: 115
Percent Similarity: 81.05% Conservative: 39
Best Local Similarity: 60.53% Mismatches: 35
Query Match: 67.08% Indels: 1
DB: 17 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-164-861-255 (1-2664)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysGlyThrGlyValValPheGlyAla 20
Db 262 GCGGTGCAGCATCTGATTTCTGGAGAGATGTGAAGAGACTGGGGTTCTCTTTGGCACC 321
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 322 ACCTGATCATGCTGCTTCCCTGGCAGCTTTCAGTGTCTACAGTGTGGTTCTTACCTC 381
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60
Db 382 ATCTGGCTCTTCTCTGTCCACCATCAGCTTCAGGATCTACAGTCCGTCATCCAACT 441
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrIleGluSerGluValAlaIle 80
Db 442 GTACAGAAGTCAGAAGAGCCATCCATTCAAAGCCCTACCTGGACGCTAGACATTACTCTG 501
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db 502 TCTCAGAGCTTCTCATTAATACATGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 561
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db 562 AAATCATATTATTCGCTCTCTTCTGTTAGAGATCTGTTGACTCTCTTGAAGCTGGCTGC 621
QY 121 LeuMetTrpValPheThrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db 622 TTATGCTGGCTGATGACCTATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 681
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db 682 GCTGAAGTCTCATTTCTAGTGTCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 741
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db 742 CACTATGTTGGCATCGCCCGAGATCAGCAAGTCAATGTTGTTGAAAGATCCCAAGCAAAA 801
QY 181 IleProGlyLeu---LysArgLysAlaGlu 189
Db 802 CTCCTCGGAATCGCCCAAAAAGAGGAGAA 831

RESULT 68
US-10-723-860-449
; Sequence 449, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
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; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.11  
; SEQ ID NO 449  
; LENGTH: 3637  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-108-260A-449

Alignment Scores:  
Pred. No.: 9,3e-67 Length: 3637  
Score: 619.50 Matches: 115  
Percent Similarity: 80.53% Conservative: 38  
Best Local Similarity: 60.53% Mismatches: 36  
Query Match: 66.54% Indels: 1  
DB: 17 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-108-260A-449 (1-3637)

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Db 1379 TCAGTGCAGCATCTGATTTCTCGAGAGATGGAAGAAGACTGGGTTGTCTTTGGCACC 1438
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1439 ACGCTGATCATGCTGCTTTCCCTGCGCAGCTTTCAGTGTGCAGTGTGGTTTCTTACCTC 1498
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1499 ATCTGGCTCTCTCTGTCCACCATCAGCTTCAGAGTCTACAGTCCGTTCATCCAGCT 1558
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1559 GTACAGAAGTCAGAGAAGAGCCATTTCATTCAAAGCCTACCTGGAGCTAGACATTACTCTG 1618
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1619 TCCTCAGAAGCTTTCCATAATTACATGAATGCTGCATGTGTCATCAACAGAGGCCCTG 1678
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 101 LysGluLeuArgGluPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1679 AACTCATATTTCGTCTCTTCTGTGAGAAGATCTGGTTGACTCTCTGAAGCTGGCTGTC 1738
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1739 TTCAATGGCTGATGACCTATGTTGCTGCTGTTTTTAACGGAATCACCTTCTTAATCTT 1798
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Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1799 GCTGAACCTGCTCATTTTCAGTGTCCCGATTGCTATGAGAAGTACAAGACCAGATTGAT 1858
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Qy 161 HistyLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1859 CACTATGTTGGCATCGCCCGAGATCAGACCAGTCAATGTTGAAAAGATCAAGCAAAA 1918
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 181 IleProGlyLeu---LysArgLysAlaGlu 189
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1919 CTCCTCGAATCGCCCAAAAAGAGGCAGAA 1948
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## RESULT 69

US-10-159-563-443  
; Sequence 443, Application US/10159563  
; Publication No. US20040009154A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus  
; APPLICANT: Peterson, Carsten  
; APPLICANT: Meltzer, Paul  
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR  
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS  
; FILE REFERENCE: 11613.56US11  
; CURRENT APPLICATION NUMBER: US/10/159,563  
; CURRENT FILING DATE: 2002-12-09  
; PRIOR APPLICATION NUMBER: US 10/133,937

; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 444  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 443  
; LENGTH: 3637  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-159-563-443

Alignment Scores:  
Pred. No.: 9,3e-67 Length: 3637  
Score: 619.50 Matches: 115  
Percent Similarity: 80.53% Conservative: 38  
Best Local Similarity: 60.53% Mismatches: 36  
Query Match: 66.54% Indels: 1  
DB: 17 Gaps: 1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-159-563-443 (1-3637)

```
Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
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Db 1379 TCAGTGCAGCATCTGATTTCTCGAGAGATGGAAGAAGACTGGGTTGTCTTTGGCACC 1438
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1439 ACGCTGATCATGCTGCTTTCCCTGCGCAGCTTTCAGTGTGCAGTGTGGTTTCTTACCTC 1498
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1499 ATCTGGCTCTCTCTGTCCACCATCAGCTTCAGAGTCTACAGTCCGTTCATCCAGCT 1558
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1559 GTACAGAAGTCAGAGAAGAGCCATTTCATTCAAAGCCTACCTGGAGCTAGACATTACTCTG 1618
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1619 TCCTCAGAAGCTTTCCATAATTACATGAATGCTGCATGTGTCATCAACAGAGGCCCTG 1678
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 101 LysGluLeuArgGluPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1679 AACTCATATTTCGTCTCTTCTGTGAGAAGATCTGGTTGACTCTCTGAAGCTGGCTGTC 1738
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1739 TTCAATGGCTGATGACCTATGTTGCTGCTGTTTTTAACGGAATCACCTTCTTAATCTT 1798
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1799 GCTGAACCTGCTCATTTTCAGTGTCCCGATTGCTATGAGAAGTACAAGACCAGATTGAT 1858
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 161 HistyLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1859 CACTATGTTGGCATCGCCCGAGATCAGACCAGTCAATGTTGAAAAGATCAAGCAAAA 1918
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 181 IleProGlyLeu---LysArgLysAlaGlu 189
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1919 CTCCTCGAATCGCCCAAAAAGAGGCAGAA 1948
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

## RESULT 70

US-09-823-245A-510  
; Sequence 510, Application US/09823245A  
; Publication No. US20020039760A1  
; GENERAL INFORMATION:  
; APPLICANT: Wong, Gordon G.  
; APPLICANT: Clark, Hilary  
; APPLICANT: Fichtel, Kim  
; APPLICANT: Agostino, Michael J.  
; APPLICANT: Howes, Steven H.  
; APPLICANT: Resnick, Richard J.  
; APPLICANT: Gulukota, Kamalakari  
; APPLICANT: Graham, James R.  
; APPLICANT: Genetics Institute, Inc.

```
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6401
; CURRENT APPLICATION NUMBER: US/09/823,245A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/194,941
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 510
; LENGTH: 1636
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-823-245A-510

Alignment Scores:
Pred. No.: 1,576-64 Length: 1636
Score: 597.50 Matches: 114
Percent Similarity: 80.53% Conservative: 39
Best Local Similarity: 60.00% Mismatches: 36
Query Match: 64.18% Indels: 2
DB: Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-823-245A-510 (1-1636)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
248 GCGGTCACGATCTGATTTCTGGAGAGATGTGAAGAACCTGGGTTCTCTTGGCACC 307
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
308 AGCTGATCATGCTGCTTTC-CTGGCAGCTTTCAGTGTATCATGTTGGTGTCTTACCTC 366
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
367 ATCTGGCTCTTCTCTGTGCACCATCAGCTTCAGGATCTACAACTGCGTCACTCAAGCT 426
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
427 GTACAGAAGTCAGAAGAGGCCATCCATTCAAAGCCCTACCTGGACGTAGACATTACTCTG 486
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
487 TCCTCAGAGCTTTCATTAATACATGAATGCTGCCATCGTGCAATCAACAGGCCCTG 546
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
547 AAACCTCATTATCTCTCTTCTGTTAGAGATCTGGTTGACTCTCTTGAAGCTGGCTGC 606
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
607 TTCATGTGGCTGATGACCTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 666
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
667 GCTGAAGCTCTCATTTCTAGTGTCCCGATTGTCTATGAGAAGTACAGACCCAGATTGAT 726
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
727 CACTATGTTGGCATCCCGCAGATCAGACCAAGTCAATTGTTGAAAAGATCCCAAGCAAAA 786
QY 181 IleProGlyLeu--LysArgLysAlaGlu 189
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
787 CTCCTCGGAATCCCAAAAAAAGGCGAGAA 816

RESULT 71
US-09-960-352-5154
; Sequence 5154, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 9092
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 39-LIB3058-023-Q1-K1-B4
US-09-960-352-9092

Alignment Scores:
Pred. No.: 3,056-62 Length: 423
Score: 572.00 Matches: 115
Percent Similarity: 100.00% Conservative: 1
```

```
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 5154
; LENGTH: 389
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 22-LIB34-043-Q1-E1-P5
US-09-960-352-5154

Alignment Scores:
Pred. No.: 28-62 Length: 389
Score: 573.00 Matches: 117
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.15% Mismatches: 0
Query Match: 61.55% Indels: 0
DB: Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-960-352-5154 (1-389)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 GTGTGTGACCTCCTCTACTGGAGAGACATTAAGAACACTGGAGTGGTGTGGTGGCCAGC 93
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
94 TTGTTCTCTGCTCTCGCTGACAGTATTACAGATTGTGAGTGTAAAGGCTGTATCCAGGCTATC 153
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
154 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAGGATCTGAAGTTCGTATATCT 213
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
214 CAGAATCTGATGAAGGCCACCCATTCAGGCAATATTTGGATCTGAAGTTCGTATATCT 273
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
274 GAGGAGTTGGTTTCAGAAAGTACAGCAATCTGCTCTTGGTCACTGTTAACTGCACATAAAA 333
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAla 119
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
334 GAACCTCAGACGCTCTCTTCTAGTATGATTAGTTGATTTCTCTGAAGTTTGA 387

RESULT 72
US-09-960-352-9092
; Sequence 9092, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 9092
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 39-LIB3058-023-Q1-K1-B4
US-09-960-352-9092

Alignment Scores:
Pred. No.: 3,056-62 Length: 423
Score: 572.00 Matches: 115
Percent Similarity: 100.00% Conservative: 1
```



```
Best Local Similarity: 99.14% Mismatches: 0
Query Match: 61.44% Indels: 0
DB: 9 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-960-352-9092 (1-423)

QY 74 LeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTy+SerAsnSerAlaLeu 93
DB 3 TTGGAATCTGAAGTTGCTATATCTGATGAGTTGGTTCAGAACTACAGCAATTCCTCTT 62
QY 94 GlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspSerLeuVal 113
DB 63 GGTCTGTTAACTGCACATAAAGAACTCAGACGCTCTCTTAGTTGATGATTTAGTT 122
QY 114 AspSerLeuLysPheAlaValLeuMetTrpValPheThrTy+ValGlyAlaLeuPheAsn 133
DB 123 GATTCCTGAGTTTGCAGTGTTGATGGGTATTTACCTATGTTGGTCTTGTTCAT 182
QY 134 GlyLeuThrLeuLeuLeuAlaLeuIleSerLeuPheSerValProValIleTy+Glu 153
DB 183 GGTCTGACACTACTAATTTTGGCTCTGATTTTCACTTTCAGTGTTCTCTTATTTATGAA 242
QY 154 ArgHisGlnAlaGlnIleAspHisTy+LeuGlyLeuAlaAsnLysValLysAspAla 173
DB 243 CGGCATCAGCGCAATAGATCATTTCTGGGACTTGCATAAATAAGAAATGTTAAAGATGCT 302
QY 174 MetAlaLysIleGlnAlaLysIleProGlyLeuLysArgLysAlaGlu 189
DB 303 ATGGCTAAATCCAGCAAAAATCCCTGGATTGAAAGCGTAAAGCTGAA 350

RESULT 73
US-10-302-172-111
; Sequence 111, Application US/10302172
; Publication No. US20040053250A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20040053250A1 Arginine-rich Protein-like Nucleic Acids an
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803.1CNCP
; CURRENT APPLICATION NUMBER: US/10/302,172
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/225,251
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT US02/05095
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 950
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 111
; LENGTH: 3517
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (196)..(654)
US-10-302-172-111

Alignment Scores:
Pred. No.: 4e-57 Length: 3517
Score: 543.00 Matches: 104
Percent Similarity: 69.46% Conservative: 37
Best Local Similarity: 51.23% Mismatches: 34
Query Match: 58.32% Indels: 28
DB: 18 Gaps: 2

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-302-172-111 (1-3517)

QY 2 ValValAspLeuLysTy+TrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
DB 2906 GTGCAGATCTGATTTCTTCTGGAGAGATGTGAAGAAGATGGGTTTGTCTTTGGCACCAGC 2965
```

```
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTy+IleAla 41
DB 2966 CTGATCATGCTGCTTTCCCTGGACGCTTTCAGTGTGATCAGTGGTGTTCITTAACCTCATC 3025
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTy+LysGlyValIleGlnAlaIle 61
DB 3036 CTGGCTCTTCTCTGTCCACCATCAGCTTCAAGATCTCAAGTCCGTTCATCCAGCTGTA 3085
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTy+LeuGluSerGluValAlaIleSer 81
DB 3086 CAGAAGTCAGAAGAAGGCCCATCCATTCAAGCCCTACCTGGACGTAGACATTAATCTGTCTC 3145
QY 82 GluGluLeuValGlnLysTy+SerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
DB 3146 TCAGAAAGCTTTCATATTAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3205
QY 102 GluLeuArgArgLeuPheLeuValAspSerLeuValAspSerLeuLysPheAlaValLeu 121
DB 3206 CTCATTAATCTGCTCTTCTGTTAGAGATCTGGTGTGACTCTCTTGAAGCTGGCTGCTTTC 3265
QY 122 MetTrpValPheThrTy+ValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
DB 3266 ATGTGGCTGATGACCTATGTTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3325
QY 142 LeuIleSerLeuPheSerValProValIleTy+GluArgHisGln---AlaGlnIle--- 159
DB 3326 GAATGCTCATTTTTCAGTGTCCGATTTGCTATGAGAAGTACAGGATGACGTGTGCTA 3385
QY 159 ----- 159
DB 3386 GCGCTGACGAGCAAGAGTCCACACTGAAGTATCAGAGAAGCTCCAGGGCAAAAAGCAA 3445
QY 160 -----AspHisTy+LeuGlyLeuAlaAsnLysValLysAspAla 173
DB 3446 GAGGCACCAGACCAGATGATCACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATT 3505
QY 174 MetAlaLys 176
DB 3506 GTTGAAGAAG 3514

RESULT 74
US-10-660-946-4
; Sequence 4, Application US/10660946
; Publication No. US20040063131A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/660,946
; FILING DATE: 12-Sep-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/228,213A
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/700,607
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1095 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: THPINOB01
; CLONE: 31870
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-660-946-4
Alignment Scores:
Pred. No.: 7,63e-56 Length: 1095
Score: 526.50 Matches: 104
Percent Similarity: 72.77% Conservative: 35
Best Local Similarity: 54.45% Mismatches: 30
Query Match: 56.55% Indels: 22
DB: 18 Gaps: 2
US-09-830-972-29_COPY_990_1178 (1-189) x US-10-660-946-4 (1-1095)
QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
329 GCGGTGCAGATCTGAATTTMTGGAGAGATGTGAAGAAGACTGGGTGTCTTTGGCACC 388
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
389 ACCTGATCATGCTGCTTCCCTGGCAGCTTCAGTGTCTATCATGCTGGTTCCTACCTC 448
QY 41 AlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
449 ATCCTGGCTCTTCTCTGTGCACCATCAGCTTCAGGATCTACAACTCCGTCATCCAACT 508
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
509 GTACAGAAGTCAGAAAGGCCATCCATTCAAAGCCCTACCTGGACGTAGACATTAATCTG 568
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
569 TCCTCAGAGCTTCCATAATACATGAATGCTGCCATGCTGCACATCAACAGGCCCTG 628
QY 101 LysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
629 AAACCTCATTTCTCTCTCTGTTAGAGATCTGGTTGACTCCTTTGAAGCTGGCTGTC 688
QY 121 LeuMetTrpValPheThrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
689 TTCATGCTGGCTGATGACCTATGTGTGCTGTTTAAACGGAATCAACCTTCTAAATCTT 748
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
749 GCTGAACCTGCTCATTTNAGTGTCCCGATGTGTATNAGAGTAC----- 793
QY 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAla 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
794 -----AAGGTTCACAGCAA 808
QY 180 sIleProGlyLeu---LysArgLysAlaGlu 189
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
809 ACTCCCTGGAATCGCCAAAAAAGGCGAA 839
RESULT 75
US-10-267-502-211
; Sequence 211, Application US/10267502
; Publication No. US20040071700A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 211
; LENGTH: 669
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-10-267-502-211
Alignment Scores:
Pred. No.: 2,31e-55 Length: 669
Score: 520.00 Matches: 96
Percent Similarity: 73.40% Conservative: 42
Best Local Similarity: 51.06% Mismatches: 50
Query Match: 55.85% Indels: 0
DB: 18 Gaps: 0
US-09-830-972-29_COPY_990_1178 (1-189) x US-10-267-502-211 (1-669)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
76 GTGGAATCCCTTATCTACTGCGCGCATGTGAAGAAATCGGCATTTGCTTCGCGCTGCG 135
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
136 CTGATCACACTGGCGCCATCTCCAGCTTCTCGGTGATCAGCGTGTTCGCCCTACTTGTG 195
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
196 CTCCTCAACCTCTCTCGGCACCGCTGCCCTTCAGAACTCAACAATCTGTGACACAGGCG 255
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
256 CAAAAGACAAACAGGCGTCAACCCCTTTAAGGATTACCTGGAGCTGGATCTGACGCTGTC 315
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
316 CACGAAAGGTACAGAACATTCGCGCGTGGCTGTGGCACATATCAATGCTTCACTCTCC 375
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
376 GAGCTGAGCGCTGTTCTTCTGTGGAGATATCATCGATTCGATCAAGTTGCGCGTCAIT 435
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
436 CTGTGGGTCTTCACCTACGTGGGTGCTGCTGTTCAATGGCATGACTCTGGTCACTTTGG 495
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
496 TTTGCTCTGCTGTTTACCTTGCCCAAGGTCTACGAGAACACAAAGCAATCGATCGACT 555
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
556 CACTTGGATCTGGTGGCGAGCAAAATTCACAGAAATCACCAGCAAGATCCGAGTGGCCATC 615
QY 182 ProGlyLeuLysArgLysAlaGlu 189
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
616 CCCATTGGCAACAAGAACGCCGAG 639
RESULT 76
US-09-809-391-102
; Sequence 102, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
```

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; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 794
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-809-391-102

Alignment Scores:
Pred. No.:      8.58e-54      Length:      794
Score:          508.50      Matches:     102
Percent Similarity: 76.37%      Conservative: 37
Best Local Similarity: 56.04%      Mismatches:  41
Query Match:      54.62%      Indels:       3
DB:              10      Gaps:         0

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-809-391-102 (1-794)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleValSerThrGlyValValPheGlyAla 20
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
254 CGGTGACGATCGATTTCTGGAGATGTGAAGAGACTGGGTTGTCTTTGGAC-- 311

Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerVal-ThrAlaTyrIl 40
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
312 ACGTGATCATGCTGCTTCCTGGCAGCTTCAGTGTCACTGTGGGTTCTTAMCT 371

Qy 40 eAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrIleValIleGlnAl 60
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
372 CATCTGGCTCTCTCTCTGTCACCATCTTCAGGATCTACCAAGTCGTCATCCAAGC 431

Qy 60 alleGlnIleSerAspGluGlyHisProPhe-ArgAlaTyrLeuGluSerGluValAlaI 80
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
432 TGTWAGAAATCAGAAAGGCCATCCCAAGCCCTACCTGGACGTAGACATTACTC 491

Qy 80 leSerGluGluLeuValGlnIleTyrSerAsnSerAlaLeuGlyHisValAsnCystrI 100
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
492 TGTCTCAGAGCTTTCATATATACATGATGTCGATGTCATCACTCAACAGGCCCC 551

Qy 100 leIysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuIleValPheAlav 120
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
552 TGAACATCATATTCTCTCTCTCTGTTAGAGATCTGTTGACTCTCTTGAAGCTGGCTG 611

Qy 120 alLeuMetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLe 140
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
612 TCCTCATGTGCTGATGATGATGCTGTTGCTGTTTAAACGGAATCACCTTCTAATTC 671

Qy 140 euAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleA 160
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
672 TTGCTGAAGTCTCATTTTCTAGTGTCCGATGCTATGAGAGTACAGACCCAGATTG 731

Qy 160 spHisTyrLeuGlyLeuAlaLeuAsnIleValSerValIleValMetAlaIleGlnAla 180
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
732 ATCACTATGTTGGCATGCCCGGAGATCAGACCAAGTCAATTGTTTGAAGAAGTCCAAGCA 791

Qy 180 ys 180
Db :|||
792 AA 793

RESULT 77
US-09-882-171-102
; Sequence 102, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,583
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,617
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,618
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,503
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,592
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,581
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,584
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,500
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,587
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,492
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,598
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,613
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,582
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,596
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,612
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,632
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,580
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,568
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,314
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,569
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,311
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,671
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Qy		1	SerValValAspLeuLeuSerLeuThrValPheSerIleValSerVal-ThrAlaTyrIle	40
Dy				
Db		254	GCGGTGACGATGATTCTTGAGAGATGGAGAAGACTGGGTGTCTTTGGAC--	311
Qy		21	SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerVal-ThrAlaTyrIle	40
Dy				
Db		312	ACGCTGATCATGTGCTTTCCCTGGCAGCTTTCAGTGTTCATCACTGGTTCCTTAMCT	371
Qy		40	eAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnal	60
Dy				
Db		372	CATCTTGGCTCTTCTCTGTGCACCATCACTTCAGGATCACAAAGTCGTCATCCAAGC	431
Qy		60	allcGlnLysSerAspGluGlyHisProPhe-ArgAlaTyrIleuGlusGrGluValAlaI	80
Dy				
Db		432	TGTCAGGAARTCAGAAAGAAGGCCATCCAAAGCCCTACTCGACGTAGACATTACTTC	491
Qy		80	leSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrI	100

Db 492 TGCTCTCAGAGCTTTCCATAATTACATGAATGCTGCCATGTCACATCAACAGGGCCC 551  
 Qy 100 leLysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlav 120  
 Db 552 TGAAGCTCATATTTCGTCTCTTTCTGGTAGAAGATCTGGTGACTCCTTGAAGCTGGCTG 611  
 Qy 120 alLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeL 140  
 Db 612 TCTTCATGTGGCTGATGACCTATGTTGGTGCTGTTTAAACGGAATCACCCCTTCTAATTC 671  
 Qy 140 euAlaLeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleA 160  
 Db 672 TTGCTGAAGCTGCTCATTTTTCAGTGCTCCGATGTTCTATGAGAAGTACAAAGACCCAGATTG 731  
 Qy 160 spHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaL 180  
 Db 732 ATCACTATGTTGGCATCGCCGAGATCAGACCAAGTCAATTGTTGAAAGAAGATCCCAAGCA 791  
 Qy 180 Ys 180  
 Db 792 AA 793

## RESULT 78

US-10-164-861-102

; Sequence 102, Application US/10164861

; Publication No. US20030225248A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 186 Human Secreted proteins

; FILE REFERENCE: P2002P1

; CURRENT APPLICATION NUMBER: US/10/164,861

; CURRENT FILING DATE: 2002-06-10

; PRIOR APPLICATION NUMBER: US/09/149,476

; PRIOR FILING DATE: 1998-09-08

; PRIOR APPLICATION NUMBER: PCT/US98/04493

; PRIOR FILING DATE: 1998-03-06

; NUMBER OF SEQ ID NOS: 757

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 102

; LENGTH: 794

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-164-861-102

## Alignment Scores:

Pred. No.:	8,58e-54	Length:	794
Score:	508.50	Matches:	102
Percent Similarity:	76.37%	Conservative:	37
Best Local Similarity:	56.04%	Mismatches:	41
Query Match:	54.62%	Indels:	3
DB:	17	Gaps:	0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-164-861-102 (1-794)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20  
 Db 254 CGGCTGCAGATCTGATTTCTGGAGAGATGTGAGAGAGATGGGTTGTCTTTGGAC-- 311  
 Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerVal-ThrAlaTyrIle 40  
 Db 312 ACGCTGATCATGCTGCTTTCCCTGGCAGCTTTTCAGTGTTCATGTCGTGGGTTCTTAMCT 371  
 Qy 40 eAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAl 60  
 Db 372 CATCTGCTCTCTCTCTGTGCACCATCARCTTTCAGGATCTCAACAGTCCGTCATCCAAAGC 431  
 Qy 60 atleGlnLysSerAspGluGlyHisProPhe-ArgAlaTyrIleLeuSerGluValAlaI 80  
 Db 432 TGTWCAGARTCAAGARAGGCCATCCATTCGAAGCCCTACTGAGCATGAGCATATTCTC 491  
 Qy 80 leSerGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrI 100  
 Db 492 TGCTCTCAGAGCTTTCCATAATTACATGAATGCTGCCATGTCGTCACATCAACAGGGCCC 551

Qy 100 leLysGluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlav 120  
 Db 552 TGAAGCTCATATTTCGTCTCTTTCTGGTAGAAGATCTGGTGACTCCTTGAAGCTGGCTG 611  
 Qy 120 alLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeL 140  
 Db 612 TCTTCATGTGGCTGATGACCTATGTTGGTGCTGTTTAAACGGAATCACCCCTTCTAATTC 671  
 Qy 140 euAlaLeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleA 160  
 Db 672 TTGCTGAAGCTGCTCATTTTTCAGTGCTCCGATGTTCTATGAGAAGTACAAAGACCCAGATTG 731  
 Qy 160 spHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaL 180  
 Db 732 ATCACTATGTTGGCATCGCCGAGATCAGACCAAGTCAATTGTTGAAAGAAGATCCCAAGCA 791  
 Qy 180 Ys 180  
 Db 792 AA 793

## RESULT 79

US-10-424-599-57998

; Sequence 57998, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 57998

; LENGTH: 878

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_23384C.1

US-10-424-599-57998

## Alignment Scores:

Pred. No.:	1.01e-53	Length:	878
Score:	508.50	Matches:	96
Percent Similarity:	74.47%	Conservative:	44
Best Local Similarity:	51.06%	Mismatches:	47
Query Match:	54.62%	Indels:	1
DB:	18	Gaps:	1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-424-599-57998 (1-878)

Qy 2 ValValaLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 Db 152 GTGGAGAGCCCTGATCTACTGCGCGGATTCGAGAAATCCGGTCCAGTGTTCGGAGAGTA 211  
 Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 212 CTCGTGCTTCTACTCGCTCTTACATATTTCTCTTAATCAGTGTGTAGCTTACCGTTTCA 271  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 272 CTCATCACCCCTGGCATAAATTTAGCGTTTGAATTTACAAAGATTTGTTACAAAGCAT 331  
 Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 332 CAAAAGACTGCGGATGGACATCCATTCGAAGATATCTGGAACTCGATGTGTCTCTACCC 391  
 Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 392 CAAGAAAAGTTAAACAAATCACAGAAGTGGCGGTTGCACACATCAATGCCCGCTATTGTG 451



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Db 114 ATGCTGCTTCCCTGCGACGCTTTTCAGTGTGCATCAGTGTGGTTTCTTACCTCATCTGGCT 173
Qy 44 LeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLys 63
Db 174 CTCTCTCTGTCACCATCAGCTTCAGGATCTAAGATCCGTCATCCAGCTGTACAGAAG 233
Qy 64 SerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGlu 83
Db 234 TCAGAAGAAGGCGCATCCATTCAAGCGCTACCTGGAGCTAGACATTAATCTGTCTCTCAGAA 293
Qy 84 LeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeu 103
Db 294 GCTTTCCATAATTAATGATGAATCCGTCATGCGGTCATCAACAGGCGCCCTGAAGACTCAT 353
Qy 104 ArgAlaGluLeuPheValAspLeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 123
Db 354 ATTCGTCTCTTCTGGTAGAAGATCTGTTGACTCTCTGAACTGGCTGTCTTCAATGGG 413
Qy 124 ValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIle 143
Db 414 CTGATGACCTATGTTGGTGTCTGTTTAAACGGAATCACCCCTCTTAATCTTGTGCTGAAC 473
Qy 144 SerLeuPheSerVal 148
Db 474 CTCATTTTCAGRGTC 488

RESULT 82
US-10-242-535A-17576
; Sequence 17576, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17576
; LENGTH: 566
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-17576

Alignment Scores:
Pred. No.: 1.45e-51 Length: 566
Score: 489.00 Matches: 102
Percent Similarity: 99.04% Conservative: 1
Best Local Similarity: 98.08% Mismatches: 1
Query Match: 52.52% Indels: 1
DB: 17 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-242-535A-17576 (1-566)
Qy 86 GlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgArg 105
Db 1 CAGAAGCACAGTAATTCGTCTTGG-CATGTGAACCTGCACGATTAAGAACTCAGGCGC 59
Qy 106 LeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPhe 125
Db 60 CTCCTCTTAGTTGATTTAGTTGATTTCTCTGAAGTTTGCAGTATTGATGTGGGTATTT 119
Qy 126 ThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeu 145
Db 120 ACCTATGTGTGGTGCCTTGTGTTAAATGGTGTGACACTACTGATTTTGGCTCTCATTTCACTC 179
Qy 146 PheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeu 165
Db 180 TTCAGTGTCTCTGTTATTTATGAACGGCAGTCAGGACAGATAGATCATTTCTAGACTT 239
Qy 166 AlabaenLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 185
Db 240 GCAAAATGAAGATGTTAAAGATGCTATGCTTAATCCAAGCAAAATCCCTGGATTGAAG 299
Qy 186 ArgLysAlaGlu 189
Db 300 CGCAAGCTGAA 311
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Db 120 ACCTATGTGTGGTGCCTTGTGTTAAATGGTGTGACACTACTGATTTTGGCTCTCATTTCACTC 179
Qy 146 PheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeu 165
Db 180 TTCAGTGTCTCTGTTATTTATGAACGGCAGTCAGGACAGATAGATCATTTCTAGACTT 239
Qy 166 AlabaenLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 185
Db 240 GCAAAATGAAGATGTTAAAGATGCTATGCTTAATCCAAGCAAAATCCCTGGATTGAAG 299
Qy 186 ArgLysAlaGlu 189
Db 300 CGCAAGCTGAA 311

RESULT 83
US-10-085-783A-17576
; Sequence 17576, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17576
; LENGTH: 566
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-17576

Alignment Scores:
Pred. No.: 1.45e-51 Length: 566
Score: 489.00 Matches: 102
Percent Similarity: 99.04% Conservative: 1
Best Local Similarity: 98.08% Mismatches: 1
Query Match: 52.52% Indels: 1
DB: 18 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-085-783A-17576 (1-566)
Qy 86 GlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgArg 105
Db 1 CAGAAGCACAGTAATTCGTCTTGG-CATGTGAACCTGCACGATTAAGAACTCAGGCGC 59
Qy 106 LeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPhe 125
Db 60 CTCCTCTTAGTTGATTTAGTTGATTTCTCTGAAGTTTGCAGTATTGATGTGGGTATTT 119
Qy 126 ThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeu 145
Db 120 ACCTATGTGTGGTGCCTTGTGTTAAATGGTGTGACACTACTGATTTTGGCTCTCATTTCACTC 179
Qy 146 PheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeu 165
Db 180 TTCAGTGTCTCTGTTATTTATGAACGGCAGTCAGGACAGATAGATCATTTCTAGACTT 239
Qy 166 AlabaenLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLys 185
Db 240 GCAAAATGAAGATGTTAAAGATGCTATGCTTAATCCAAGCAAAATCCCTGGATTGAAG 299
Qy 186 ArgLysAlaGlu 189
Db 300 CGCAAGCTGAA 311
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Db 1074 CTGTGCTGCTCGCGCACCATCTCTCTCAGGGTTTACCGCAAGTGTCTCGAGCCGCTG 1133
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 1134 CACCGGGGGATGGAGCCAAACCTTTTCCAGGCTTACCTGGATGTGGACCTCACCTGACT 1193
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db 1194 CGGAGCAGACGAGAGCTTTGTCCACCATGATCACCTCCGCGTGGTCTCGCGGCCACG 1253
Qy 102 GluLeuArgGluPheLeuValAspLeuValAspLeuValAspLeuValAspLeuValLeu 121
Db 1254 CAGCTGCGGCACCTTCTTCCTGTAGAACCTCTCGTGGATTCCTCAAGCTGGCCCTCCTC 1313
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
Db 1314 TTCTACATCTTCCACCTTCTGCGGTGGTCCATCTTCAATGGTGTGACTCTTCTCAATCTGGA 1373
Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 1374 GTGATTGGTCTATTACCATCCCTCTGTGACCGCAGCACCAGCTCAGATCCACCAA 1433
Qy 162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 1434 TATGTGGGGTTGGTGACCAATCAGTTGAGCCACATCAAAAGCTTAAGATCCGAGCTAAATC 1493
Qy 182 ProGlyLeu-----LysArgLysAla 188
Db 1494 CAGGAGCGGAGCCCTGCTCTCGACGCGCAGTCTCCGGATCCAAAGCCAAAGCC 1553
Qy 189 Glu 189
Db 1554 GAA 1556

RESULT 86
US-10-723-860-3043
; Sequence 3043, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05982.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3043
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-3043

Alignment Scores:
Pred. No.: 1,128-48 Length: 2190
Score: 473.50 Matches: 95
Percent Similarity: 65.67% Conservative: 37
Best Local Similarity: 47.26% Mismatches: 56
Query Match: 50.86% Indels: 13
DB: 20 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-723-860-3043 (1-2190)
Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 1162 GTGGCGGACCTGCTGCTACTGGAAGACACGAGGAGCTCAGGAGTGGTCTTACAGGCTG 1221
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 1162 GTGGCGGACCTGCTGCTACTGGAAGACACGAGGAGCTCAGGAGTGGTCTTACAGGCTG 1221
```

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Db 1222 ATGCTCTCCCTCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTCTGCT 1281
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 1282 CTGTGCTGCTCTCTGCGCACCATCTCTCTCAGGGTTTACCGCAAGTGTCTCGAGCCGCTG 1341
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 1342 CACCGGGGGATGGAGCCAAACCTTTTCCAGGCTTACCTGGATGTGGACCTCACCTGACT 1401
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db 1402 CGGAGCAGACGAGAGCTTTGTCCACCATGATCACCTCCGCGTGGTCTCGCGGCCACG 1461
Qy 102 GluLeuArgGluPheLeuValAspLeuValAspLeuValAspLeuValAspLeuValLeu 121
Db 1462 CAGCTGCGGCACCTTCTTCTGTTAGAACCTCTCGTGGATTCCTCAAGCTGGCCCTCCTC 1521
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
Db 1522 TTCTACATCTTCCACCTTCTGCGGTGGTCCATCTTCAATGGTGTGACTCTTCTCATCTGGA 1581
Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 1582 GTGATTGGTCTATTACCATCCCTCTGTGACCGCAGCACCAGCTCAGATCCACCAA 1641
Qy 162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 1642 TATGTGGGGTTGGTGACCAATCAGTTGAGCCACATCAAAAGCTTAAGATCCGAGCTAAATC 1701
Qy 182 ProGlyLeu-----LysArgLysAla 188
Db 1702 CCAGGAGCGGAGCCCTGCTCTGACGCGCAGTCTCCGGATCCAAAGCCAAAGCC 1761
Qy 189 Glu 189
Db 1762 GAA 1764

RESULT 87
US-10-723-860-7073
; Sequence 7073, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05982.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7073
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-7073

Alignment Scores:
Pred. No.: 1,89e-48 Length: 3044
Score: 473.50 Matches: 95
Percent Similarity: 65.67% Conservative: 37
Best Local Similarity: 47.26% Mismatches: 56
Query Match: 50.86% Indels: 13
DB: 20 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-723-860-7073 (1-3044)
Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 1162 GTGGCGGACCTGCTGCTACTGGAAGACACGAGGAGCTCAGGAGTGGTCTTACAGGCTG 1221
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Db 872 GTGGCGGACCTGCTACTGGAAGACACAGGAGCTCAGGAGTGTCTTCACAGCCCTG 931
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 932 ATGGTCTCCTCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 991
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 61
Db 992 CTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1051
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 1052 CACCGGGGGATGGAGCCAACTTTCCAGGCTTCTGAGTGTGAGTGTGAGTGTGAGT 1111
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db 1112 CGSGAGCAGACGGAAGCTTTGCTCCACAGATCACCTCCGCGTGTCTCGGCGGCCAG 1171
Qy 102 GluLeuArgLeuPheLeuValAspLeuValAspLeuValAspLeuValAspLeuVal 121
Db 1172 CAGCTCGGCGACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1231
Qy 122 MetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
Db 1232 TTCTACATCTTGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1291
Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 1292 GTGATTGGTCTATTACCATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1351
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 181
Db 1352 TATGCGGGTGTGTGACCAATCATGTTGAGCCACATCAAAAGCTAAAGTCCGAGTAA 1411
Qy 182 ProGlyLeu-----LysArgLysAla 188
Db 1412 CCAGGACCGGACCTGCGCTCTGCAGCAGCGCAGTCTCCGATCCAAAGCAAGCC 1471
Qy 189 Glu 189
Db 1472 GAA 1474

RESULT 88
US-09-960-352-2205
; Sequence 2205, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 2205
; LENGTH: 431
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (309)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 10-LiB3058-011-Q1-K1-C5
US-09-960-352-2205

Alignment Scores:
Pred. No.: 4,73e-44 Length: 431
Score: 428.00 Matches: 89
Percent Similarity: 98.89% Conservative: 0
Best Local Similarity: 98.89% Mismatches: 1
```

```
Query Match: 45.97% Indels: 0
DB: Gaps: 0
US-09-830-972-29_COPY_990_1178 (1-189) x US-09-960-352-2205 (1-431)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 161 GTTGTGTGACCTCTCTACTGGAGACATTAAGAGACTGGAGTGTGTGTGGCCAGC 220
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 221 TTGTTCTCTGCTCTCTGCTGACAGTATTTCACCAATGTGAGTGTAAACGCGCTTACATTGCC 280
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 61
Db 281 TTGGCCCTGCTCTCTGTGACTATCAGCTNTAGGATATATAAGGTTGTGATCCAGGCTATC 340
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 341 CAGAAATCTGATGAAGGCCACCCATTTCAGGCGATATTTCGAATCTGAAGTTGCTATATCT 400
Qy 82 GluGluLeuValGlnLysTyrSerAsnSer 91
Db 401 GAGGAGTTGTTTCAGAAAGTACAGCAATCTCT 430

RESULT 89
US-10-052-283-137
; Sequence 137, Application US/10052283
; Publication No. US20030064379A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Goddard, Audrey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND METHOD OF USE THEREOF
; FILE REFERENCE: P2751R1C1
; CURRENT APPLICATION NUMBER: US/10/052,283
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: PCT/US00/20006
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/145,701
; PRIOR FILING DATE: 1999-07-26
; NUMBER OF SEQ ID NOS: 564
; SEQ ID NO 137
; LENGTH: 598
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-052-283-137

Alignment Scores:
Pred. No.: 8.7e-40 Length: 598
Score: 396.00 Matches: 74
Percent Similarity: 80.83% Conservative: 23
Best Local Similarity: 61.67% Mismatches: 0
Query Match: 42.53% Indels: 0
DB: Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-052-283-137 (1-598)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
Db 234 CGGTGTCACGATCTGATTTCTTGGAGAGATGTGAAGAGACTGGGTTTGTCTTTGGCACC 293
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db 294 ACGCTGATCATGCTGCTTCTCCCTGCGCAGCTTTTCAGTGTCTCAGTGTGTTTCTTACCCTC 353
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60
Db 354 ATCTTGGCTCTTCTCTCTGTCCACCATCAGCTTCAGGATCTACAAGTCCGCTCATCCAGCT 413
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db 414 GTACAGAGCTCAGAAAGGCCCATTCATTCAAAGCCTACCTGGACGCTAGACATTACTCTG 473
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US-10-050-704-93
; Sequence 93, Application US/10050704
; Publication No. US20030050442A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/10/050,704
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 09/684,524
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2317)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-050-704-93

Alignment Scores:
Pred. No.: 1.84e-34 Length: 2454
Score: 361.50 Matches: 67
Percent Similarity: 77.50% Conservative: 26
Best Local Similarity: 55.83% Mismatches: 26
Query Match: 38.83% Indels: 1
DB: 14 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-050-704-93 (1-2454)
QY 71 ArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsn 90
Db 59 AGAGCCTACCTGACGTAGACATTACTCTGCTCAGAAAGCTTCCATAATTACATGAAT 118
QY 91 SerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAsp 110
Db 119 GCTGCCATGCTGCACATCAACAGGCGCCCTGAACCTATTATTCTCTCTCTCTGTAGAA 178
QY 111 AspLeuValAspSerLeuLysPheAlaValLeuMetTyrValPheThrTyrValGlyAla 130
Db 179 GATCTGGTTGACTCTCTGAAGCTGGCTGCTTCATGCTGCTGATGACCTATGTTGGTGCT 238
QY 131 LeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValProVal 150
Db 239 GTTTTAAACGAATCAACCTCTTAATTCTTGTGAACTCTGCTGCTGCTGCTGCTGCTGCT 298
QY 151 IleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaLeuAsnLysAsnVal 170
Db 299 GTCTATGAGAAGTACAAAGACCCAGATTGATCACTATGTTGGCATCGCCGAGATCAGACC 358
QY 171 LysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeu---LysArgLysAlaGlu 189
Db 359 AAGTCAATTGTTGAAAGATCAAGCAAACTCCCTGGAACTCCCTGGAACTCCCAAAAAAGGCGAA 418

RESULT 93
US-10-798-512-93
; Sequence 93, Application US/10798512
; Publication No. US20040152164A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/10/798,512
; CURRENT FILING DATE: 2004-03-12
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; PRIOR APPLICATION NUMBER: US/09/684,524
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2317)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-798-512-93

Alignment Scores:
Pred. No.: 1.84e-34 Length: 2454
Score: 361.50 Matches: 67
Percent Similarity: 77.50% Conservative: 26
Best Local Similarity: 55.83% Mismatches: 26
Query Match: 38.83% Indels: 1
DB: 19 Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x US-10-798-512-93 (1-2454)
QY 71 ArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsn 90
Db 59 AGAGCCTACCTGACGTAGACATTACTCTGCTCAGAAAGCTTCCATAATTACATGAAT 118
QY 91 SerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAsp 110
Db 119 GCTGCCATGCTGCACATCAACAGGCGCCCTGAACCTATTATTCTCTCTCTCTGTAGAA 178
QY 111 AspLeuValAspSerLeuLysPheAlaValLeuMetTyrValPheThrTyrValGlyAla 130
Db 179 GATCTGGTTGACTCTCTGAAGCTGGCTGCTTCATGCTGCTGATGACCTATGTTGGTGCT 238
QY 131 LeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValProVal 150
Db 239 GTTTTAAACGAATCAACCTCTTAATTCTTGTGAACTCTGCTGCTGCTGCTGCTGCTGCT 298
QY 151 IleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaLeuAsnLysAsnVal 170
Db 299 GTCTATGAGAAGTACAAAGACCCAGATTGATCACTATGTTGGCATCGCCGAGATCAGACC 358
QY 171 LysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeu---LysArgLysAlaGlu 189
Db 359 AAGTCAATTGTTGAAAGATCAAGCAAACTCCCTGGAACTCCCTGGAACTCCCAAAAAAGGCGAA 418

RESULT 94
US-09-880-107-3484
; Sequence 3484, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
```

SEQ ID NO 3484

LENGTH: 639  
TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Genbank Accession No. US20020142981A1 W27023

NAME/KEY: unsure

LOCATION: (1)..(639)

OTHER INFORMATION: n = a or c or g or t

US-09-880-107-3484

Alignment Scores:

Pred. No.: 1.11e-33 Length: 639  
Score: 348.00 Matches: 83  
Percent Similarity: 81.73% Conservative: 2  
Best Local Similarity: 79.81% Mismatches: 12  
Query Match: 37.38% Indels: 8  
DB: 9 Gaps: 2

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-09-880-107-3484 (1-639)

Qy 2 ValValAspLeuLeuTyTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 233 GTTGTGACCTCTCTGAGAGACATTAAAGAGACTGGAGTGTGTTGGTCCAGC 292  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyRileAla 41  
Db 293 CTATTCCTGCTGCTTTCATTGACGATTTAGCATTTGAGCTTAACAGCTACATTGCC 352  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyLysGlyValIleGlnAlaIle 61  
Db 353 TTGNCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 412  
Qy 62 GlnLysSer-AspGluGlyHisPropheArgAlaTyRileuGluSerGluValAlaIle-- 80  
Db 413 CAGAAATCAAGATGAAGGCCACCCATTGAGGCATATCTGAGGCATATCTGAAGTGNTATTCT 472  
Qy 81 ---SerGluGluLeuValGlnLysTy-SerAsnSerAlaLeuGlyHisValAsnCyth 99  
Db 473 TAGGAGTGGTCANAGTCAGATCTGTCT-----GGCGANGTGAAGTGAAC 519  
Qy 99 rIleLysGlu 102  
Db 520 GATAAAGGAC 529

RESULT 95

US-10-633-423-9

Sequence 9, Application US/10633423

Publication No. US20040191240A1

GENERAL INFORMATION:

APPLICANT: Tohyama, Masaya

APPLICANT: Yamashita, Toshinide

TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION

FILE REFERENCE: 59150-8023.US800

CURRENT APPLICATION NUMBER: US/10/633,423

CURRENT FILING DATE: 2003-07-11

PRIOR APPLICATION NUMBER: US 10/427,741

PRIOR FILING DATE: 2003-04-30

PRIOR APPLICATION NUMBER: JP 2003-92923

PRIOR FILING DATE: 2003-03-28

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn version 3.1

SEQ ID NO 9

LENGTH: 60615

TYPE: DNA

ORGANISM: Mus musculus

US-10-633-423-9

Alignment Scores:

Pred. No.: 1.14e-29 Length: 60615  
Score: 341.00 Matches: 70  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 36.63%

DB: 19 Indels: 0  
Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-633-423-9 (1-60615)

Qy 2 ValValAspLeuLeuTyTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21

Db 45956 GTTGTGACCTCTCTGAGAGACATTAAAGAGACTGGAGTGTGTTGGTCCAGC 46015

Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyRileAla 41

Db 46016 TTATTCCTGCTGCTCTCTGACAGTGTTCAGCATTTGAGTGAACGCCCTACATTGCC 46075

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyLysGlyValIleGlnAlaIle 61

Db 46076 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGCTATC 46135

Qy 62 GlnLysSerAspGluGlyHisPropheArg 71

Db 46136 CAGAAATCAGATGAAGGCCACCCATTTCAGG 46165

RESULT 96

US-10-427-741-9

Sequence 9, Application US/10427741

Publication No. US20040191291A1

GENERAL INFORMATION:

APPLICANT: Tohyama, Masaya

APPLICANT: Yamashita, Toshinide

TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION

FILE REFERENCE: 59150-8023

CURRENT APPLICATION NUMBER: US/10/427,741

CURRENT FILING DATE: 2003-04-30

PRIOR APPLICATION NUMBER: JP 2003-92923

PRIOR FILING DATE: 2003-03-28

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PatentIn version 3.1

SEQ ID NO 9

LENGTH: 60615

TYPE: DNA

ORGANISM: Mus musculus

US-10-427-741-9

Alignment Scores:

Pred. No.: 1.14e-29 Length: 60615  
Score: 341.00 Matches: 70  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 36.63% Indels: 0  
DB: 19 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x US-10-427-741-9 (1-60615)

Qy 2 ValValAspLeuLeuTyTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21

Db 45956 GTTGTGACCTCTCTGAGAGACATTAAAGAGACTGGAGTGTGTTGGTCCAGC 46015

Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyRileAla 41

Db 46016 TTATTCCTGCTGCTCTCTGACAGTGTTCAGCATTTGAGTGAACGCCCTACATTGCC 46075

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyLysGlyValIleGlnAlaIle 61

Db 46076 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGCTATC 46135

Qy 62 GlnLysSerAspGluGlyHisPropheArg 71

Db 46136 CAGAAATCAGATGAAGGCCACCCATTTCAGG 46165

RESULT 97

US-09-758-140-19

Sequence 19, Application US/09758140

Patent No. US20020012965A1

GENERAL INFORMATION:

```
; APPLICANT: Strittmatter, Stephen M.
; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth
; FILE REFERENCE: 44574-5073-US
; CURRENT APPLICATION NUMBER: US/09/758,140
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/175,707
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,378
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 198
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(198)
; OTHER INFORMATION: Full receptor binding region of No. US20020012965A1o gene
US-09-758-140-19

Alignment Scores:
Pred. No.: 2,42e-32 Length: 198
Score: 331.00 Matches: 66
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 35.55% Indels: 0
DB: Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-758-140-19 (1-198)

QY 51 PheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPhe 70
Db 1 TTTAGGATATACAAAGGTTGATCCAAAGCTATCCAGAAATCAGATCAAGGCCACCATTC 60

QY 71 ArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsn 90
Db 61 AGGGCATATCTGGAATCTGAAATCTGATATCTGAGAGTTGGTTCAGAAAGTACAGTAAT 120

QY 91 SerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgGluLeuPheLeuValAsp 110
Db 121 TCTGCTCTTGGTCATGTGAATGTCAGCATAAAGAACTCAGGCGCTCTTCTTAGTTGAT 180

QY 111 AspLeuValAspSerLeu 116
Db 181 GATTAGTTGATTTCTGTG 198

RESULT 98
US-09-972-599A-19
; Sequence 19, Application US/09972599A
; Patent No. US20020077295A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
; FILE REFERENCE: C077 CIP US
; CURRENT APPLICATION NUMBER: US/09/972,599A
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/236,378
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 198

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(497)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-5532

~Alignment Scores:
Pred. No.: 1,2e-31 Length: 497
Score: 330.50 Matches: 61
Percent Similarity: 81.55% Conservative: 23
Best Local Similarity: 59.22% Mismatches: 18
Query Match: 35.50% Indels: 1
DB: Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-918-995-5532 (1-497)

QY 88 TyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgGluLeuPhe 107
Db 57 TACATGAATGCTGCCATGGGCACATCAACAGTCCCTGAAACTCATATTATTCCTCTCTT 116
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; APPLICANT: Strittmatter, Stephen M.
; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth
; FILE REFERENCE: 44574-5073-US
; CURRENT APPLICATION NUMBER: US/09/758,140
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/175,707
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,378
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 198
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(198)
; OTHER INFORMATION: Full receptor binding region of No. US20020012965A1o gene
US-09-758-140-19

Alignment Scores:
Pred. No.: 2,42e-32 Length: 198
Score: 331.00 Matches: 66
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 35.55% Indels: 0
DB: Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-758-140-19 (1-198)

QY 51 PheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPhe 70
Db 1 TTTAGGATATACAAAGGTTGATCCAAAGCTATCCAGAAATCAGATCAAGGCCACCATTC 60

QY 71 ArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsn 90
Db 61 AGGGCATATCTGGAATCTGAAATCTGATATCTGAGAGTTGGTTCAGAAAGTACAGTAAT 120

QY 91 SerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgGluLeuPheLeuValAsp 110
Db 121 TCTGCTCTTGGTCATGTGAATGTCAGCATAAAGAACTCAGGCGCTCTTCTTAGTTGAT 180

QY 111 AspLeuValAspSerLeu 116
Db 181 GATTAGTTGATTTCTGTG 198

RESULT 98
US-09-972-599A-19
; Sequence 19, Application US/09972599A
; Patent No. US20020077295A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
; FILE REFERENCE: C077 CIP US
; CURRENT APPLICATION NUMBER: US/09/972,599A
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/236,378
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 198

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(497)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-5532

~Alignment Scores:
Pred. No.: 1,2e-31 Length: 497
Score: 330.50 Matches: 61
Percent Similarity: 81.55% Conservative: 23
Best Local Similarity: 59.22% Mismatches: 18
Query Match: 35.50% Indels: 1
DB: Gaps: 1

US-09-830-972-29_COPY_990_1178 (1-189) x US-09-918-995-5532 (1-497)

QY 88 TyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgGluLeuPhe 107
Db 57 TACATGAATGCTGCCATGGGCACATCAACAGTCCCTGAAACTCATATTATTCCTCTCTT 116
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Qy		
117	CTGTGAAGATCTGGTTGACTCCCTGAAGTCGGCTGCTCTTCATGTGGCTGATGACCTAT	176
Db		
128	ValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSer	147
Qy		
177	GTTGGTGTGTTTTTAACGGAATCACCCCTTCTAATCTTGCTGAACGTCTCATTTTCAGT	236
Db		
148	ValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsn	167
Qy		
237	GTCCCGATTGTCTATGAGAAGTACAAAGACCCAGATTGATCACTATTGTTGGCATCGCCGGA	296
Db		
168	LysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeu--LysArg	186
Qy		
297	GATCAGACCAAGTCAATTGTTGAAAGAATCCAGCAAAACTCCCTGGAAATGCCCAAAA	356
Db		
187	LysAlaGlu	189
Qy		
357	AAGGCAGAA	365
Db		

RESULT 100

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US-09-372-599A-21
; Sequence 21, Application US/09972599A
; Patent No. US20020077295A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
; FILE REFERENCE: C077 CIP US
; CURRENT APPLICATION NUMBER: US/09/972,599A
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/236,378
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 198
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence encoding amino acids 1055-1111
; OTHER INFORMATION: of human No. US20020077295A10A
; US-09-372-599A-21

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Alignment Scores:	
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Best Local Similarity:	100.00%
Query Match:	35.45%
DB:	9
Length:	198
Matches:	66
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-830-972-29 COPY 990 1178 (1-189) x US-09-972-599A-21 (1-198)

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Db	1	A	G	G	A	T	A	C	A	A	G	G	T	G	T	G	A	T	C	C	A	G	T	A	T	C	A	G	A	A	T	C	A	G	A	A	T	C	A	G	A	A	T	C	A	G	60							
Qy	72	A	l	a	T	r	L	e	u	S	e	r	G	L	u	V	a	L	a	l	a	r	e	S	e	r	G	L	u	L	e	u	V	a	L	u	S	e	r	G	L	n	L	y	S	r	S	e	r	91				
Db	61	G	C	A	T	A	T	C	G	A	A	T	T	G	C	T	A	T	A	T	C	T	G	A	G	A	G	T	T	G	T	T	C	A	A	G	T	A	C	A	G	T	A	A	T	T	120							
Qy	92	A	l	a	L	e	u	G	L	y	H	i	s	V	a	L	a	S	e	r	C	y	e	T	h	r	i	L	e	y	S	G	L	u	L	e	u	A	r	g	L	e	u	P	h	e	u	V	a	L	a	S	p	111
Db	121	G	C	T	T	G	G	T	C	A	T	G	T	G	A	A	C	T	G	C	A	C	A	T	A	A	A	G	A	A	C	T	C	A	G	G	C	G	C	T	T	C	T	T	A	G	T	T	C	A	T	180		

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 19, 2005, 06:25:42 ; Search time 2558 Seconds  
(without alignments)  
2812.411 Million cell updates/sec

Title: US-09-830-972-29\_COPY\_990\_1178

Perfect score: 931

Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQKIPGLKRAE 189

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum Match 100%

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/Cgm2\_1/USPTO\_spool\_p/US09830972/runat\_16062005\_153945\_19031/app\_query.fasta\_1.654  
-DB=EST -QFMT=fastcap -SUFFIX=est -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45  
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-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-NO\_WMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gse1:\*  
9: gb\_gse2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	927	99.6	598	7	CF118424 fs543.z1
2	927	99.6	600	9	AY404970 Homo sapi
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4	927	99.6	667	7	CN429712 170006000
5	927	99.6	672	7	CK977984 4109431 B
6	927	99.6	682	6	CB162885 K-EST0223
7	927	99.6	712	7	CK971318 4087182 B
8	927	99.6	743	6	CD102817 AGENCOURT
9	927	99.6	758	4	BG697436 602660623

10	927	99.6	788	1	AL533461
11	927	99.6	843	4	BG570231
12	927	99.6	849	7	CR765672
13	927	99.6	875	1	AL573494
14	927	99.6	1540	3	CR611869
15	927	99.6	1785	3	AF077050
16	924	99.2	730	1	AU297347
17	921	98.9	634	6	CB067821
18	921	98.9	670	7	CV030029
19	921	98.9	960	7	CN646472
20	921	98.9	983	7	CN803408
21	921	98.9	1031	7	CN647521
22	915	98.3	805	7	CO735185
23	915	98.3	958	4	BM801698
24	914	98.2	757	4	BG715173
25	913	98.1	1042	5	BU845601
26	913	98.1	1042	7	CN805577
27	912	98.0	592	7	CN482802
28	912	98.0	871	6	CD110203
29	911	97.9	600	9	AY404972
30	911	97.9	679	4	BI149602
31	911	97.9	708	4	BI157842
32	908	97.5	779	7	CO401465
33	908	97.5	1013	7	CO048918
34	908	97.5	1018	7	CN801888
35	905	97.2	794	1	AU080127
36	905	97.2	799	1	AU080133
37	904	97.1	695	7	CV077130
38	904	97.1	758	4	BG740561
39	904	97.1	791	7	CF977898
40	904	97.1	1081	7	CN641703
41	902	96.9	747	4	BG623462
42	900	96.7	585	7	CO259245
43	899	96.6	742	4	BT838242
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45	894	96.0	781	4	BI079496

ALIGNMENTS

RESULT 1

CF118424

LOCUS

DEFINITION

fs543.z1 fs 103-105d fetal sheep skin library Ovis aries

sequence.

CF118424

VERSION

CF118424.1

KEYWORDS

EST.

SOURCE

ORGANISM

Ovis aries (sheep)

Ovis aries

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Caprinae; Ovis.

REFERENCE

1 (bases 1 to 598)

ADELSON, D.L., Cam, G.R., Desilva, U. and Franklin, I.R.

Gene expression in sheep skin and wool (hair)

Genomics 83 (1), 95-105 (2003)

Contact: Adelson, David L.

CSIRO Livestock Industries

306 Carmody Road, St Lucia QLD 4067, Australia

Tel: +61 7 3214 2700

Fax: +61 7 3214 2900

Email: li-enquiries@csiro.au.

Location/Qualifiers

1..598

/organism="Ovis aries"

/mol\_type="mRNA"

/strain="Merino"

/db\_xref="taxon:9940"

/sex="male"

/dev\_stage="103-105d pc fetus"

/lab\_host="BM25.8"

/clone\_lib="fs 103-105d fetal sheep skin library"

598 bp mRNA linear EST 23-JUL-2003

/note="Organ: midflank skin; Vector: pTriplex; Site\_1: EcoRI; Site\_2: XbaI; Arrayed library filters screened by hybridization with labeled dinucleotide repeats. first strand synthesis XbaI-(dT)15 primed, EcoRI adaptors were ligated to cDNA before cloning. EcoRI- NotI- SalI adaptor sequence; 5'-AATTCGGCGCGGTGAC GCGCGCGCGAGTGG-P04-5', 5' sequencing primer 5' TCCGAGATCTGGCAGGC 3' 3', sequencing primer 5' TAATACGACTCACTATAGG 3' submitted sequences in excess of 50 bp after vector and quality clipping(phred 13) submitted to GenBank."

## ORIGIN

Alignment Scores: 2.74e-104 Length: 598  
 Pred. No.: 927.00 Matches: 188  
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 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.57% Indels: 0  
 DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CF118424 (1-598)

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 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
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 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 152 TTGGCCCTCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 211  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 212 CAGAAATCTGATGAGGACACCCATTTCAGGCATATTTCGAAATCTGAAATTCGTATATCT 271  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 272 GAGGAGTTGGTTGAGAGTACAGTAATTCGTCTTGGTCAATGATGAGTGCACAAATAAA 331  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
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## RESULT 2

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 VERSION AY404970.1 GI:39760944  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE  
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.  
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 /gene="RTN4"  
 /locus\_tag="HCM2068"

## FEATURES

source

gene

## ORIGIN

Alignment Scores: 2.75e-104 Length: 600  
 Pred. No.: 927.00 Matches: 188  
 Score: 927.00  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.57% Indels: 0  
 DB: 9 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AY404970 (1-600)

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 Db 34 GTTGTGACCTCTCTCTGAGAGACATTAGAGACTGGAGTGGTGGTGGCCAGC 93  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 94 CTATTCTCTGCTCTTTCATTCAGCATTTTCAGCATTTGAGCGTAAACAGCTACATTGCC 153  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 154 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 213  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 214 CAGAAATCAGATGAGGCCACCCATTTCAGGCATATCTGGAATCTGAAGTTGCTATATCT 273  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 274 GAGGAGTTGGTTTCAGAAAGTACAGTAATTCCTCTTGGTTCATGTGAACCTGCACGATAAG 333  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 334 GAATCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAAGTTTCAGGTGTG 393  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
 Db 394 ATGTGGGTATTTACCTATGTTGGTGGCTTGTTCATGTTCTGCACACTACTGATTTGGCT 453  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 454 CTCAATTCACCTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 513  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 600)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

Science 302 (5652), 1960-1963 (2003)

14671302

2 (bases 1 to 600)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers

1..600

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

<1..>600

/gene="RTN4"

/locus\_tag="HCM2068"

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Db      514 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAGCAAAATC 573
Qy      182 ProGlyLeuValArgLysAlaGlu 189
Db      574 CCTGGATTGAAGCGCAAAAGCTGAA 597

RESULT 3
LOCUS   CB215381
DEFINITION NISC_np05d12.y1 NICHHD_HS_Ut1 Homo sapiens cDNA clone IMAGE:5937070
5', mRNA sequence.
ACCESSION CB215381
VERSION   CB215381.1 GI:28263573
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 650)
AUTHORS  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE    Tumor Gene Index
JOURNAL  Unpublished (1997)
COMMENT  Contact: Robert Strausberg, Ph.D.
        Email: cgapbs-re@mail.nih.gov
        CDNA Library Preparation:
        CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
        DNA Sequencing by: National Institutes of Health Intramural
        Sequencing Center (NISC)
        Clone distribution: NCI-CGAP clone distribution information can be
        found through the I.M.A.G.E. Consortium/LLNL at:
        info@image.llnl.gov
        Plate: LLNL13163 row: G column: 23
        Seq primer: M13R1 reverse primer (ABI).
        Location/Qualifiers
            1..650
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:5937070"
                /sex="female"
                /tissue_type="normal endometrium, late proliferative
                phase, cycle day 13"
                /lab_host="DH10B (T1-resistant)"
                /clone_lib="NICHHD_HS_Ut1"
                /note="Organ: uterus; Vector: pCMV-SPORT6.1.cdbb (ResGen,
                Invitrogen Corporation); Site 1: Not1; Site 2: EcoRV;
                Cloned unidirectionally from microquantity amounts of mRNA
                from normal endometrial tissue (late proliferative phase,
                cycle day 13). Average insert size 1.9 kb. Library
                constructed by ResGen (Invitrogen Corporation)."
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## ORIGIN

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Alignment Scores:
Pred. No.:      3 09e-104      Length:      650
Score:          927.00      Matches:      188
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     99.57%      Indels:      0
DB:              6      Gaps:          0
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US-09-830-972-29_COPY_990_1178 (1-189) x CB215381 (1-650)
```

```

Qy      2 ValValAspLeuLeuTyrTrpArgAspIleTysThrGlyValValPheGlyAlaSer 21
Db      19 GTTGTGACCTCCTCTACTGAGACATTAAAGACTGGAGTGGTGGTGGCCAGC 78
Qy      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db      79 CTATTCTCTGCTCTTTCATGATGATTTACGATTTGTGAGCATTTGAGCGTAAACGCTACATTGCC 138
Qy      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
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```

Db      139 TTGGCCCTGCTCTCTGTGCACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 198
Qy      62 GlnIysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db      199 CAGAAATCAGATGAAGGCCACCCCATTCAGGGCATATCTGGAAATCTGGAAGTTGCTATATCT 258
Qy      82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db      259 GAGGAGTTGGTTCAGAGTACAGTAATTTCTGCTCTTGGTCACTGTGAACTGCACGATAAAG 318
Qy      102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db      319 GAACCTCAGGCGCCTCTCTCTTAGTTGATGATTAGTTAGTTCTCTGAAGTTTCAGTGTG 378
Qy      122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
Db      379 ATGTGGGTATTTACCTATGTTGGTGCCCTGTTTAAATGCTGTGACACTACTGATTTGGCT 438
Qy      142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db      439 CTCAATTCACCTTCAGTGTTCCCTGTTATTTATGACGGCATCAGGCACAGATAGTATCAT 498
Qy      162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      499 TATCTAGGACTTGCAATTAAGAATGTTAAAGATGCTATGGCTAAATCCAGCAAAATC 558
Qy      182 ProGlyLeuLysArgLysAlaGlu 189
Db      559 CCTGGATTGAAGCGCAAAAGCTGAA 582

RESULT 4
LOCUS   CN429712
DEFINITION 667 bp mRNA linear EST 16-MAY-2004
ACCESSION 17000600059220 GRN_PRENEU Homo sapiens cDNA 5', mRNA sequence.
VERSION   CN429712
KEYWORDS  CN429712.1 GI:47417306
SOURCE    EST.
ORGANISM  Homo sapiens (human)
REFERENCE 1 (bases 1 to 667)
AUTHORS   Li Y., Xu C., Fang R., Guegler, K., Rao, M.S., Mandalam, R.,
        Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fiek, G.J.,
        Lebkowski, J. and Stanton, L.W.
        Transcriptional characterization elucidates signaling networks that
        control human ES cell growth and differentiation
        Nat. Biotechnol. 22 (6), 707-716 (2004)
        Contact: Brandenberger R
        Regenerative Medicine
        Geron Corporation
        230 Constitution Drive, Menlo Park, CA 94025, USA
        Tel: 650 473 8658
        Fax: 650 473 7760
        Email: rbrandenberger@geron.com
        Insert Length: 667 Std Error: 0.00.
        Location/Qualifiers
            1..667
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /tissue_type="embryonic stem cell, retinoic acid and
                mitogen-treated hES cell line H7"
                /clone_lib="GRN_PRENEU"
                /note="oligo dt primed, full-length enriched cDNA library
                from hES cell line H7 (p29) maintained in feeder-free
                conditions. Embryoid bodies were generated in the presence
                of all-trans retinoic acid and mitogens."
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## ORIGIN

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Alignment Scores:
Pred. No.:      3.2e-104      Length:      667
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Db      645  CCTGGATTGAACGCTAAAGCTGAA 668
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RESULT 6
CB162885
LOCUS      682 bp mRNA linear EST 30-JAN-2003
DEFINITION K-EST0223580 L18POOLin1 Homo sapiens cDNA clone L18POOLin1-41-F04
5', mRNA sequence.
ACCESSION CB162885
VERSION   CB162885.1 GI:28149011
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 682)
AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE     21C Frontier Korean EST Project 2001
JOURNAL   Unpublished (2002)
COMMENT   Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel.: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 41, row: F column: 04
High quality sequence stop: 682.
Location/Qualifiers
1..682
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L18POOLin1-41-F04"
/cell_line="SNU-354+Cho-CK+Choi-CK+HLK-3"
/lab_host="Top10P"
/clone_lib="L18POOLin1"
/note="Organ: Liver; Vector: p77T3-Pac; Site 1: EcoRI;
Site 2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
culture."
ORIGIN
Alignment Scores:
Pred. No.: 3,316-104 Length: 682
Score: 927.00 Matches: 188
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.57% Indels: 0
DB: 6 Gaps: 0
US-09-830-972-29_copy_990_1178 (1-189) x CB162885 (1-682)
Qy      2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
|||||
Db      115 GTTGTGACCTCTCTACTGGAGACACATTAGAAGACTGGAGTGGTGTGGTCCAGC 174
|||||
Qy      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
|||||
Db      175 CTATTCTCTGCTCTTTCATTGACAGTATTACAGATTGTGAGCGTAAAGCCTACATTGCC 234
|||||
Qy      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
|||||
Db      235 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAGCTATC 294
|||||
Qy      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
|||||
Db      295 CAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTCTGGAATCTGCTATATCT 354
|||||
Qy      82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCyseThrIleLys 101
|||||
Db      355 GAGGAGTTGGTTCAAGAGTACAGTAATTTCTGCTCTTGGTTCATGTGAACCTGCACGATAAG 414
|||||
Qy      102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
|||||
Db      415 GAATCTCAGGCCCTCTTCTTAGTTGATGATTAGTTAGTTCTCTGAAGTTTGCAGCTGTG 474
|||||
Qy      122 MetTrpValPheThrTyrValGlyValAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
|||||
Db      475 ATGTGGGTATTACCTAATGTGGTGGCTTTGTTAATGTCTGACACTACTGATTTGGCT 534
|||||
Qy      142 LeuLeSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
|||||
Db      535 CTCATTTCACTCTTCAGTGTTCCTGTTATTATGAACGGCATCAGGCACAGATAGATCAT 594
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Qy      162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
|||||
Db      595 TATCTAGGACTTGCATAATAAGAAATGTTAAAGATGCTATGGCTAAATAATCCAGCAAAATC 654
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Qy      182 ProGlyLeuLysArgLysAlaGlu 189
|||||
Db      655 CTGGATTGAAGCGCAAGCTGAA 678
|||||
RESULT 7
CBK971318
LOCUS      712 bp mRNA linear EST 16-MAR-2004
DEFINITION 4087182 BARC 9BOV Bos taurus cDNA clone 9BOV3_J07 5', mRNA
sequence.
ACCESSION CBK971318
VERSION   CBK971318.1 GI:45489292
KEYWORDS  EST.
SOURCE    Bos taurus (cow)
ORGANISM  Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 712)
AUTHORS   Sonstegard, T.S., Van Taseell, C.P., Matukumalli, L.K., Harhay,
G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
TITLE     Production of EST from cDNA libraries derived from immunologically
activated bovine gut
JOURNAL   Unpublished (2004)
COMMENT   Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
Tel: 3015048416
Fax: 3015048414
Email: tads@nri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt "-trim.fasta. Vector identified
by cross_match using options -minmatch 12 -minscore 12
Plate: 3 row: J column: 07
Seq primer: CCCAGTCACGACGTTGTAAACCG
High quality sequence stop: 712.
Location/Qualifiers
1..712
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone="9BOV3_J07"
/sex="Male"
/tissue_type="pooled"
/dev_stage="Multiple"
/lab_host="DH10B T1 phage resistant"
/clone_lib="BARC 9BOV"
/note="Organ: Abomasum; Vector: pagen-1; Site 1: EcoRV;
Site 2: NotI; Equimolar amounts of mRNA extracted from
fundic and pyloric abomasums of 18 and 21 week old steers.
Exposure to Osteragia osteragi was initiated at 15 weeks
of age. fundic and pyloric abomasum"

```

## ORIGIN

## Alignment Scores:

Pred. No.: 3,528-104 Length: 712  
 Score: 927.00 Matches: 188  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.57% Indels: 0  
 DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CK971318 (1-712)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 DB 18 GTTGTGACCTCTCTACTGGAGAGACATTAAGAGACTGGAGTGGTGTGGTGCACG 77  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 DB 78 TTGTTCTCTGCTCTCGCTGACAGTATTCAGCATTTGAGTGTAAAGGCTACATTGCC 137  
 QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAlaIle 61  
 DB 138 TTGGCCCTGCTCTCTGACTATCAGCTTTAGCATATATAAGGCTGTGATCCAGGCTATC 197  
 QY 62 GlnLysSerAspGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 198 CAGAAATCTGATGAAGCCACCCATTCAGGGCATATTTGGAAATCTGAAGTTGCTATATCT 257  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 DB 258 GAGGAGTTGGTCAGAGTACAGCAATTCCTCTTGGTCATGTTAACTGCACATATAA 317  
 QY 102 GluLeuArgGluPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 DB 318 GAACTCAGACGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAGTTTGCAGTGTG 377  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 DB 378 ATGTGGGTATTTACCTATGTTGGTGTCTTGTCAATGGTGTGACATCTACTAATTTGGCT 437  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 DB 438 CTGATTTCACTCTCTAGTGTCTCTGTTATTTATGAACGGCATCAGCGCAATAGATCAT 497  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 DB 498 TATCTGGACTTGCAAAATGAAGATGTTAAGATGCTATGGCTAAATCCAAAGCAAAATC 557  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 DB 558 CCTGGATTGAAGCGTAAAGCTGAA 581

## RESULT 8

CD102817

LOCUS

CD102817 743 bp mRNA linear EST 15-MAY-2003

DEFINITION

AGENCOURT 14009211 NIH\_MGC\_186 Homo sapiens cdna clone

ACCESSION

CD102817

VERSION

CD102817.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 743)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC Clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDCM166 row: m column: 24

High quality sequence stop: 617.

## FEATURES

source

1..743

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:30373271"

/lab\_host="DH10B (T1 phage-resistant)"

/note="Organ: Pooled-Skin; Vector: pDMR-LIB; Site 1: Sfil  
 (ggcattatggcc); Site 2: Sfil (ggcgcctggcc); Library is  
 oligo-dT primed and directionally cloned. cDNA was  
 prepared from a pooled samples of tissues from Skin,  
 meninges, duramatter, pia matter and choroid plexus. 5'  
 and 3' adaptors were used in cloning as follows: 5'  
 adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor  
 sequence: 5'-ATTCTAGAGCGCGGCGGCATG-DT(30)BN-3',  
 (where B = A, C, or G and N = A, C, G, or T). Average  
 insert size 1.47 kb (range 0.50-4.0 kb). 15/15 colonies  
 contained inserts by PCR. This library was enriched for  
 full-length clones and was constructed by Clontech  
 Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC  
 Library"

## ORIGIN

## Alignment Scores:

Pred. No.: 3,748-104 Length: 743  
 Score: 927.00 Matches: 188  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.57% Indels: 0  
 DB: 6 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CD102817 (1-743)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 DB 151 GTTGTGACCTCTCTACTGGAGAGACATTAAGAGACTGGAGTGGTGTGGTGCACG 210  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 DB 211 CTATTCCTGCTCTTTCATTCAGATTAATTCAGCAATTCAGGCGTAAACAGCTACATTCG 270  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 DB 271 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCAAGCTATC 330  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 331 CAGAAATCAGATGAAGCCACCCATTCAGGCGCATATCTGGAATCTGAAGTTGCTATATCT 390  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 DB 391 GAGGAGTTGGTTTCAGAAATACAGTAAATTCCTCTTGGTTCATGTGAACCTGCACGATAAAG 450  
 QY 102 GluLeuArgGluPheLeuValAspPheLeuValAspSerLeuLysPheAlaValLeu 121  
 DB 451 GAACTCAGGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 510  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 DB 511 ATGTGGGTATTTACCTATGTTGGTGGCTTTGTTTAAATGTTCTGCACACTACTGATTTGGCT 570  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 DB 571 CTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 630  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

```

|||||
631 TATCTAGGACTTGCAGAAATGTTAAAGATGCTGTGGCTAAATCCAAAGCAAAATC 690
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QY 182 ProGlyLeuValArgLeuAlaGlu 189
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Db 691 CCTGGAATTAAGCGCAAGCTGAA 714
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RESULT 9
LOCUS BG697436 758 bp mRNA linear EST 07-MAY-2001
DEFINITION 602660823F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4804012 5',
mRNA sequence.
ACCESSION BG697436
VERSION BG697436.1 GI:13963656
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 758)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLA10700 row: m column: 05
High quality sequence stop: 756.
Location/Qualifiers
1..758
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4804012"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Skn3"
/note="Organ: skin; Vector: pCMV-SPORT6; Site:1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Alignment Scores:
Pred. No.: 3.85e-104 Length: 758
Score: 927.00 Matches: 188
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.57% Indels: 0
DB: 4 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x BG697436 (1-758)

QY 2 ValValAspLeuLeuTyrTrpArgAspLeuLysThrGlyValValPheGlyAlaSer 21
|||||
Db 132 GTTGTGACCTCTCTACTGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGGCCAGC 191
|||||
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
|||||
Db 192 CTATTCTGCTGCTTTCATTGACAGTATTTCAGCATTTGAGCGTAAACGCCCTACATTGCC 251
|||||
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
|||||
Db 252 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGATATACAGGGTGTGATCCAAAGCTATC 311
|||||
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
|||||
Db 312 CAGAAATCAGATGAAGGCCCAACCCATTCAGGGCATATCTGGAATCTGAAGTTCCTATATCT 371
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QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
|||||
Db 372 GAGGAGTTGGTTTCAGAGTACAGTAATCTCTGCTCTTGGTCATGTGAACTGCACGATAAG 431
|||||
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
|||||
Db 432 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 491
|||||
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheGlnGlyLeuThrLeuLeuIleLeuAla 141
|||||
Db 492 ATGTGGGTATTACCTATGTGTGGTCCCTGTGTTTAAATGCTCTGACACTACTGATTTGGCT 551
|||||
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
|||||
Db 552 CTCAATTCACCTCTTCAGTGTTCCTGTTATTATGAACGGCATCAGGCACAGATAGATCAT 611
|||||
QY 162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
|||||
Db 612 TATCTAGGACTTGCAGAAATGAAATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAATC 671
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QY 182 ProGlyLeuLysArgLysAlaGlu 189
|||||
Db 672 CCTGGATTGAAGCGCAAGCTGAA 695
|||||

RESULT 10
LOCUS ALS533461 788 bp mRNA linear EST 24-MAR-2004
DEFINITION ALS533461 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
CSODN004YU08 5-PRIME, mRNA sequence.
ACCESSION ALS533461
VERSION ALS533461.3 GI:45708351
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 788)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 13, 2001 this sequence version replaced gi:31260542.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 1423.r.
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODN004DE04QPI&c=1423.r.
FEATURES
Location/Qualifiers
1..788
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODN004YU08"
/tissue_type="ADULT BRAIN"
/dev_stage="adult"
/clone_lib="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN
Alignment Scores:
Pred. No.: 4.07e-104 Length: 788
Score: 927.00 Matches: 188

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Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.57% Indels: 0  
 DB: 1 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AL5333461 (1-788)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLeuThrGlyValValPheGlyAlaSer 21  
 Db 156 GTTGTGACCTCTGCTACTGGAGAGACATTAAAGAGCTGGAGTGGTGTGGTGCAGC 215

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValLeuAla 41  
 Db 216 CTATTCCTGCTGCTTTTCATGACAGTATTGAGCAATGTGAGCGTAAACGCTACATTGCC 275

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 276 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGTTGTGATCCAGCTATC 335

QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 336 CAGAAATCAGATGAAGGCCACCCATTTCAGGCGATATCTGGAATCTCGAAGTTGCTATATCT 395

QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 396 GAGGAGTTGTTTCTGAGAGTACAGTAATCTGCTCTTGGTCATGTGAACGCGACGATAAG 455

QY 102 GluLeuArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 456 GAACTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATCTCTGAAGTTGCGAGTTG 515

QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 516 ATGTGGGTATTTACCTATGTTGGTGGCTTTGTTTAATGGTCTGCACACTACTGATTTGGCT 575

QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 576 CTCAITTCACCTCTTCAGTGTCTCTGTTATTATGAACGGCATCAGGACAGATAGATCAT 635

QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 636 TATCTAGGACTTGCAATTAAGATGTTAAAGATGCTATGGCTAAATCCACAGCAAAATC 695

QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 Db 696 CCTGGATTGAAGCGCAAAAGCTGAA 719

RESULT 11  
 BG570231  
 LOCUS 602590632F1 NIH\_MGC\_77 Homo sapiens cdna clone IMAGE:4717662 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BG570231  
 VERSION BG570231.1 GI:13577884  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 843)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-r@mail.nih.gov  
 Tissue Procurement: CLONTECH Laboratories, Inc.  
 CDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLCM1567 row: 0 column: 07

High quality sequence stop: 801.  
 Location/Qualifiers  
 1. .843  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4717662"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NIH MGC 77"  
 /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:  
 sf11 (ggccctcgcc); Site 2: sf11 (ggccattggcc); 5' and  
 3' adaptors were used in cloning as follows: 5' adaptor  
 sequence: 5'-CACGCCCATTAAGCC-3' and 3' adaptor sequence:  
 5'-ATTCTAGAGCGCGCGCCGATG-df(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size 1.9  
 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA). Note: this is a NIH\_MGC Library."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 4,48e-104 Length: 843  
 Score: 927.00 Matches: 188  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.57% Indels: 0  
 DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BG570231 (1-843)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 2 GTTGTGACCTCTCTACTGGAGAGACATTAAAGAGCTGGAGTGGTGTGGTGCAGC 61

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValLeuAla 41  
 Db 62 CTATTCCTGCTCTCTTCATGACGATTTACAGATTTGAGCGTAAACGCTACATGTC 121

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 122 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGTTGTGATCCAGCTATC 181

QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 182 CAGAAATCAGATGAAGGCCACCCATTTCAGGCGATATCTGGAATCTCGAAGTTGCTATATCT 241

QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 242 GAGGAGTTGGTTTCAGAGTACAGTAATCTGCTCTTGGTCATGTGAACGCGATGAAG 301

QY 102 GluLeuArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 302 GAACTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAAGTTGCGAGTTG 361

QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuLeuAla 141  
 Db 362 ATGTGGGTATTTACCTATGTTGGTGGCTTGTTTTAATGGTCTGCACACTACTGATTTGGCT 421

QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 422 CTCATTTCACTCTTCAGTGTCTCTGTTATTATGAACGGCATCAGGACAGATAGATCAT 481

QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 482 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCACAGCAAAATC 541

QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 Db 542 CCTGGATTGAAGCGCAAAAGCTGAA 565

RESULT 12  
 CR765672



LOCUS CR765672 849 bp mRNA linear EST 23-SEP-2004  
 DEFINITION DKFZp469C2134 r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone  
 ACCESSION CR765672  
 VERSION CR765672.1 GI:52605968  
 KEYWORDS EST.  
 SOURCE Pongo pygmaeus (orangutan)  
 ORGANISM Pongo pygmaeus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.  
 REFERENCE 1 (bases 1 to 849)  
 AUTHORS Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Schaipp,A.,  
 Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and  
 Wiemann,S.  
 TITLE Pongo pygmaeus mRNA (Ottenwaelder,B., Obermaier,B.,  
 Deutschenbaur,S., et al.)  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: MIPS  
 MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
 This is the 5' sequence of the clone insert. Clone from S. Wiemann,  
 Molecular Genome Analysis, German Cancer Research Center (DKFZ);  
 Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix  
 (Martinsried/Germany) within the cDNA sequencing consortium of the  
 German Genome Project. This clone (DKFZp469C2134) is available at  
 the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in  
 Berlin, Germany. Please contact RZPD for ordering:  
 http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469C2134  
 Further information about the clone and the sequencing project is  
 available at http://mips.gsf.de/projects/cdna/  
 FEATURES  
 Location/Qualifiers  
 1..849  
 /organism="Pongo pygmaeus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="DKFZp469C2134"  
 /tissue type="kidney"  
 /dev stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="469 (synonym: pkid1)"  
 /note="Vector: pSport1\_Sfi; Site\_1: SfiI; Site\_2: SfiIb"  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 4,52e-104 Length: 849  
 Score: 927.00 Matches: 188  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.57% Indels: 0  
 DB: 7 Gaps: 0  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x CR765672 (1-849)  
 Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 Db 150 GTTGTGACCTCTCTACTCGAGAGACATTAAAGACTGGAGTGGTGTGGTGGCAGC 209  
 Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 210 CTATTCTCTGCTGCTTTCATTGACAGTATTGACGATTTGAGCTGTGAACACGCTACATTGCC 269  
 Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaTle 61  
 Db 270 TTGGCCCTGCTTCTCTGACCATCATCAGCTTTAGGATATACAGGGTGTGATCAAGCTATC 329  
 Qy 62 GlnLysSerAspGluGlyYhiProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 330 CAGAAATCAGATGAGGCCACCCATTTCAGGCATATCTGGAATCTGGAAGTTGCTATATCT 389  
 Qy 82 GluGluLeuValGlnLysTyrSerAnsSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 390 GAGGAGTGGTTTCAGAGTACAGTAATTTCTGCTCTTGTGTCATGTGTAACACTGACGATAAG 449

Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 450 GAACTCAGCGCCCTCTTCTTAGTTGATGATTTAGTTAGTTCTCTGAAGTTTGCAGTGTG 509  
 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAnsGlyLeuThrLeuLeuIleLeuAla 141  
 Db 510 ATGTGGGTATTACCTATGTTGTGTCCTTGTATTAATGCTCTGACGCTACTGATTTGGCT 569  
 Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 570 CTCAATTCACCTCTTCAGTGTTCCTGTTTATTATGACGGCATCAGGCACAGATAGATCAT 629  
 Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 630 TATCTAGGACTTGCAATTAAGAATGTTAAAGATCTATGGCTAAATCCAAGCGCAAAATC 689  
 Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
 Db 690 CCTGGATTGAAGCGCAAAAGCTGAA 713  
 RESULT 13  
 AL573494/c  
 LOCUS AL573494 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
 DEFINITION Clone CSODI051YB11 3-PRIME, mRNA sequence.  
 ACCESSION AL573494  
 VERSION AL573494.3 GI:46246666  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 875)  
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT On Feb 16, 2001 this sequence version replaced gi:31294840.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 1423.r  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdna?s=CSODI051CA06NFI&c=1423.r.  
 FEATURES  
 Location/Qualifiers  
 1..875  
 /organism="Homo sapiens"  
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 /db\_xref="taxon:9606"  
 /clone="CSODI051YB11"  
 /tissue type="PLACENTA COT 25-NORMALIZED"  
 /clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 4,72e-104 Length: 875  
 Score: 927.00 Matches: 188  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.57% Indels: 0  
 DB: 1 Gaps: 0  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x AL573494 (1-875)

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QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 875 GTGTGTGACCTCTGTACTGGAGAGACATTAAGAACACTGGAGTGGTGTGGTCCACG 816
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 815 CTATTCTCTGCTCTTCATACAGTATTCAGCATTTGTGAGCGGTAAACAGCTTACATTGCC 756
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 755 TTGGCCCTGCTCTCTGTACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAAGCTATC 696
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 695 CAGAAATCAGATGAAGCCACCCATTCAGGGCATATCTGGAATCTGAACTTGTCTATATCT 636
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCystrIleLys 101
Db 635 GAGGAGTTGGTCAGAGTACAGTAATCTGCTTGGTCATGTGACTGACAGTAAG 576
QY 102 GluLeuArgGluLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 575 GAACTCAGCGGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAGGTTTGCAGTGTG 516
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
Db 515 ATGTGGGTATTTACCTATGTTGGTGGCTTTGTTAATGGTCTGACACTACTGATTTGGCT 456
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 455 CTCATTTCTACTCTCAGTGTCTCTGTTATTTAAGACGCATCAGCACAGATAGATCAT 396
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 395 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAATC 336
QY 182 ProGlyLeuLysArgLysAlaGlu 189
Db 335 CCTGGATTGAAGCGCAAGCTGAA 312

RESULT 14
CR611869
LOCUS full-length cDNA clone CS0DN004YJ08 of Adult brain of Homo sapiens
DEFINITION (human).
ACCESSION CR611869
VERSION 1 GI:50492676
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
REMARK Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
REFERENCE 2 (bases 1 to 1540)
Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
COMMENT - Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source Location/Qualifiers
1..1540
/organism="Homo sapiens"

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DN004YJ08"
/tissue_type="Adult brain"
/plasmid="pCMVSPORT_6"

ALIGNMENT SCORES:
Pred. No.: 1.06e-103 Length: 1540
Score: 927.00 Matches: 188
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.57% Indels: 0
DB: 3 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x CR611869 (1-1540)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 156 GTGTGTGACCTCTGTACTGGAGAGACATTAAGAACACTGGAGTGGTGTGGTCCACG 215
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 216 CTATTCTCTGCTCTTCATTCAGCATTTTCAGCATTTGTGAGCGGTAAACAGCTTACATTGCC 275
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 276 TTGGCCCTGCTCTCTGTACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAAGCTATC 335
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 336 CAGAAATCAGATGAAGCGCCACCCATTCAGGGCATATCTGGAATCTGAACTTGTCTATATCT 395
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCystrIleLys 101
Db 396 GAGGAGTTGGTCAGAGTACAGTAATCTGCTTGGTCATGTGACTGACAGTAAG 455
QY 102 GluLeuArgGluLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 456 GAACTCAGCGGCTCTCTTAGTTGATGATTTAGTTGATTTCTGAGGTTTGCAGTGTG 515
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
Db 516 ATGTGGGTATTTACCTATGTTGGTGGCTTTGTTAATGGTCTGACACTACTGATTTGGCT 575
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 576 CTCATTTCTACTCTCAGTGTCTCTGTTATTTAAGACGCATCAGCACAGATAGATCAT 635
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 636 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAATC 695
QY 182 ProGlyLeuLysArgLysAlaGlu 189
Db 696 CCTGGATTGAAGCGCAAGCTGAA 719

RESULT 15
AF077050
LOCUS Homo sapiens neuroendocrine-specific protein C homolog mRNA,
DEFINITION complete cds.
ACCESSION AF077050
VERSION AF077050.1 GI:4689147
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE Song, H., Peng, Y., Zhou, J., Huang, Q., Dai, M., Mao, Y., Yu, Y., Xu, X.,
Luo, B., Hu, R. and Chen, J.
Human neuroendocrine-specific protein C (NSP) homolog gene

```

JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1785)  
AUTHORS Song, H.  
TITLE Direct Submission  
JOURNAL Submitted (10-JUN-1998) Rui-Jin Hospital, Shanghai Institute of  
Endocrinology, Molecular Medical Center, 197 Rui-Jin Road II,  
Shanghai 200025, P.R. China  
FEATURES Location/Qualifiers  
source 1..1785  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/tissue\_type="pituitary"  
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/codon\_start=1  
/product="neuroendocrine-specific protein C homolog"  
/protein\_id="AAD27783.1"  
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/translation="MDGQKQWKDVLDLYWRDIKKTGVVFGASFLILLSLTVFSIV  
SVTVIALALLSVTSFRIYKGVIOAIQKSDGHPFRAYLESEVAISELVOKYSNSA  
LGHVNCTIKELRLPLVDLDVSLKFAVLMVFTVVGALFNGLLTLLILALISLSPVP  
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## ORIGIN

Alignment Scores:  
Pred. No.: 1.31e-103 Length: 1785  
Score: 927.00 Matches: 188  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.57% Indels: 0  
DB: 3 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AF077050 (1-1785)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 247 GTTGTGACCTCCTCTGTGACCATCAGCTTAGAAGACTTGAAGAGCTGGAGTGGTGTGGTCCAGC 306  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 307 CTATTCTCGCTCTTTCATTTGACAGTATTCAGCATTTGAGCGTAAACAGCTTACATTCGCC 366  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 367 TTGGCCCTGCTCTCTGTGACCATCAGCTTAGAATATACAGGGTGTGATCCAGCTATC 426  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 427 CAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGAATCTGGAATCTGCTATATCT 486  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
DB 487 GAGGAGTGGTTCAGAAGTACAGTAATCTCTGCTTTGGTTCATGTAAGCTGCACGATAAG 546  
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
DB 547 GAACCTCAGCGCTCTCTTAGTTCATGATTTAGTTGATCTCTGAAAGTTGCAGTGTG 606  
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
DB 607 ATGTGGGTATTTACCTATGTTGGTCTGTTTAAATGGTCTGACACTACTGATTTGGCT 666  
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
DB 667 CTCATTTCACTCTCAGTGTTCCTGTATTTATGAACGGCATCAGGCGCAGATAGATCAT 726  
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
DB 727 TATCTAGGACTTGCAAAATAGAAATGTTAAAGATGCTATGGCTAAATCCAGCAAAATC 786  
QY 182 ProGlyLeuLysArgLysAlaGlu 189  
DB 787 CTGTGATTGAAGCGCAAGCTGAA 810

## RESULT 16

AU297347  
LOCUS AU297347 730 bp mRNA linear EST 08-MAY-2003  
DEFINITION AU297347 female adult cerebrum, full-length enriched chimpanzee  
cDNA library Pan troglodytes verus cDNA clone PorA0834 5' similar  
to human RefSeq mRNA NM\_007008, mRNA sequence.  
ACCESSION AU297347  
VERSION AU297347.1 GI:29531646  
KEYWORDS EST.  
SOURCE Pan troglodytes verus  
ORGANISM Pan troglodytes verus  
REFERENCE 1 (bases 1 to 730)  
AUTHORS Sakate,R., Osada,N., Hida,M., Sugano,S., Hayasaka,I., Shimohira,N.,  
Yanagi,S., Suto,Y., Hashimoto,K. and Hirai,M.  
TITLE Analysis of 5'-end sequences of chimpanzee cDNAs  
JOURNAL Genome Res. 13 (5), 1022-1026 (2003)  
MEDLINE 22612989  
PUBMED 12727913  
COMMENT Contact: Momoki Hirai  
Department of Integrated Biosciences  
The University of Tokyo, Graduate School of Frontier Sciences  
5-1-5 Kashiwanoha, Kashiwa, Chiba 277-8562, Japan  
Tel: 81-4-7136-3688  
Fax: 81-4-7136-3687  
Email: mhirai@k.u-tokyo.ac.jp.  
Location/Qualifiers  
source 1..730  
/organism="Pan troglodytes verus"  
/mol\_type="mRNA"  
/sub\_species="verus"  
/db\_xref="taxon:37012"  
/clone="PorA0834"  
/sex="female"  
/tissue\_type="cerebrum"  
/dev\_stage="adult"  
/clone\_lib="female adult cerebrum, full-length enriched  
chimpanzee cDNA library"

## ORIGIN

Alignment Scores:  
Pred. No.: 8.59e-104 Length: 730  
Score: 924.00 Matches: 187  
Percent Similarity: 100.00% Conservatives: 1  
Best Local Similarity: 99.47% Mismatches: 0  
Query Match: 99.25% Indels: 0  
DB: 1 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AU297347 (1-730)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
DB 162 GTTGTGACCTCCTCTGTGACCATCAGCTTAGAAGACTTGAAGAGCTGGAGTGGTGTGGTCCAGC 221  
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
DB 222 CTATTCTCGCTCTTTCATTTGACAGTATTCAGCATTTGAGTGTAAACAGCTTACATTCGCC 281  
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
DB 282 TTGGCCCTGCTCTCTGTGACCATCAGCTTAGGATATACAGGGTGTGATCCAGCTATC 341  
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
DB 342 CAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGGAATCTGGAATCTGCTATATCT 401  
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
DB 402 GAGGAGTGGTTCAGAAGTACAGTAATTTCTCTTGTGTCATGTAAGCTGCACGATAAG 461  
QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121

```

Db      462 GAACCTCAGCGGCTCTCTTAGTTGATGATTTAGTTGATCTCTGAAGTTTCAGGTG 521
QY      122 MetTrrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
Db      522 ATGTGGTATTACCTATGTTGGTGGCTTTGTTTAAATGGTCTGACACTACTGATTTGGCT 581
QY      142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db      582 CTCATTTCACCTCTCAGTGTCTCTGTTATTATTAAGCGGCATCAGGCACAGATAGATCAT 641
QY      162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      642 TATCTAGGACTTGCAAAATAGAAATGTTAAAGATGCTATGGCTAAATCAAGCGAAATC 701
QY      182 ProGlyLeuLysArgLysAlaGlu 189
Db      702 CCTGGATTGAGCGCAAACTGNA 725

```

RESULT 17  
CB067821  
LOCUS  
DEFINITION  
iQ38a06\_v1 HR85 islet Homo sapiens cDNA clone IMAGE: 5' similar to  
TR:09Y293 Q9Y293 FOOCEN-S. [1] ; mRNA sequence.

ACCESSION  
CB067821  
VERSION  
CB067821.1 GI:27812341  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
REFERENCE  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 634)  
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,  
Lemishka, I., Secor, M., Brestelli, J., Gradwohl, G., Clifton, S.,  
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,  
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,  
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, R.,  
Williams, T., Jackson, Y., and Bowers, Y.  
Endocrine Pancreas Consortium  
Unpublished (2000)

Other ESTs: iQ38a06.x1  
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
Endocrine Pancreas Consortium  
Harvard University, Howard Hughes Medical Institute  
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
MA 02138  
Tel: 617-495-1812  
Fax: 617-495-8557  
Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:  
Washington University Genome Sequencing Center For information on  
obtaining a clone please contact: Dr. Hiroshi Inoue  
(hinoue@im.wustl.edu)  
Seq primer: -40UP from Gibco  
High quality sequence stop: 460.  
Location/Qualifiers  
1. .634

FEATURES  
source  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:"  
/tissue\_type="Purified pancreatic islet"  
/lab\_host="HR85 islet"

Notes="Organ: Pancreas; Vector: pBluescript SK(-); Site\_1:  
NotI; Site\_2: XhoI; cDNA made by oligo-dT priming.  
Size: selected on agarose gel. Average insert size ~1kb. 5'  
XhoI site was destroyed after directional cloning.  
Amplified once. Contact information: Hiroshi Inoue, MD,  
Metabolism Div. (Alan Permutt Lab), Washington University  
School of Medicine, Box 8127, 660 South Euclid Ave., St.  
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:  
314-362-1916, Fax: 314-747-2692."

## ORIGIN

Alignment Scores:  
Pred. No.: 1.65e-103 Length: 634  
Score: 921.00 Matches: 187  
Percent Similarity: 99.47% Conservative: 0  
Best Local Similarity: 99.47% Mismatches: 1  
Query Match: 98.93% Indels: 0  
DB: 6 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CB067821 (1-634)

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QY      2 ValValAspLeuLeuTyrTrrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db      71 GTTGTGTACCTCTCTACTGAGAGACATTAAAGAGACTGGAGTGGTGTGGTGGCCAGC 130
QY      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db      131 CTATTCTCTGCTCTTTCATTGACATTTTCAGATTGTGAGCGGTACAGCCCTACATTGCC 190
QY      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db      191 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAAGCTATC 250
QY      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db      251 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGGAAGTTGCTATATCT 310
QY      82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCystrIleLys 101
Db      311 GAGGAGTTGGTTTCAGAGTACAGTAATCTGCTCTTGGTCATGTGACTGCAGATAAG 370
QY      102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db      371 GAACCTCAGCGGCTCTCTTCTAGTGTGATTTAGTTGATCTCTGAAGTTTCAGGTGTTG 430
QY      122 MetTrrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
Db      431 ATGTGGGTATTTACCTATGTTGGTGGCTGTTTAAATGGTCTGACACTACTGATTTGGCT 490
QY      142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db      491 CTCATTTTCATCTTTCAGTGTCTCTGTTATTATGAAGCATCAGGCACAGATAGATCAT 550
QY      162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      551 TATCTAGGACTTGCAAAATAGAAATGTTAAAGATGCTATGGCTAAATCAAGCAAAATC 610
QY      182 ProGlyLeuLysArgLysAlaGlu 189
Db      611 CCTGGATTGAGCGCAAAAGCTGAA 634

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## RESULT 18

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

CV030029 670 bp mRNA linear EST 20-AUG-2004  
9024 Full length cDNA from the Mammalian Gene Collection Homo  
sapiens cDNA 5' similar to BC014366, mRNA sequence.

CV030029  
CV030029.1 GI:51488245

EST.  
CV030029.1

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 670)

Rual, J.F., Hirozane-Kishikawa, T., Hao, T., Bertin, N., Li, S.,  
Dricot, A., Li, N., Rosenberg, J., Lamesch, P., Vidalain, P.O.,  
Clingingsmith, T.R., Hartley, J.L., Esposito, D., Cheo, D., Moore, T.,  
Simmons, B., Sequerra, R., Bosak, S., Doucette-Stamm, L., Ie, Feuch, C.,  
Vandenhaute, J., Cusick, M.E., Albaladejo, J., Hill, D.E. and Vidal, M.  
Human ORFeome Version 1.1: a Platform for Reverse Proteomics  
Genome Res. (2004) In press  
Contact: Vidal M

Marc Vidal Laboratory  
Dana Farber Cancer Institute  
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA  
Tel: 617 632 5180  
Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu

ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF results from a PCR reaction using an MGC full-length cDNA as template DNA and ORF specific primers

PCR Primers

FORWARD: ATGGACGGTCAGAGAAAATGG

BACKWARD: CATTACGCTTGGCTTCAATC

Insert Length: 670 Std Error: 66.00

Plate: 11045 row: 02 column: B

Seq primer: ACTGGCGCTGCTTTTACACGTCGTGACTGGGMAAAC

High quality sequence start: 101

High quality sequence stop: 669

POLYA=No.

#### FEATURES

Location/Qualifiers

1..670

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/tissue type="mixed"

/clone lib="Full Length cDNA from the Mammalian Gene Collection"

/note="Vector: mixed; The ORFs were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway cloning into pDONR223 Donor vector. Reference: MGC (Mammalian Gene Collection) Program Team, Generation and Initial Analysis of more than 15,000 Full-Length Human and Mouse cDNA Sequences. PNAS, 2002, 99(26), 16899-16903"

#### ORIGIN

##### Alignment Scores:

Pred. No.: 1..79e-103 Length: 670  
Score: 921.00 Matches: 187  
Percent Similarity: 99.47% Conservative: 0  
Best Local Similarity: 99.47% Mismatches: 1  
Query Match: 98.93% Indels: 0  
DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CV030029 (1-670)

Qy 2 ValValAspLeuLeuTyTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 34 GTTGTGACCTCCTCTACTGGAGAGACATTAAAGACTGGAGTGGTGTGTTGGTGCCAGC 93  
Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrlleAla 41  
Db 94 CTATTCTCGCTCTTTCATTGACAGATTTCAGCATTTGGAGCGTAACAGCCTACATTGCC 153  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrlLysGlyValIleGlnAlaIle 61  
Db 154 TTGGCCCTGCTCTGTGACCATCAGCTTAGGATATACAGGGTGTGATCCAGCTATC 213  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrlLeuGluSerGluValAlaIleSer 81  
Db 214 CAGAAATCAGATGAAGGCCACCCATTACGGGCATATCTGGAATCTGGAAGTTGCTATATCT 273  
Qy 82 GluGluLeuValGlnLysTyTrpSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 274 GAGGAGTTGGTTTCAGAGTACAGTAATTTCTGCTCTGTGTCATGTGAATCGCACGATAAG 333  
Qy 102 GluLeuArgGluLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 334 GNACTCAGCGCGCTCTTCTAGTTCATGATTAGTTGATTCTCTGAAAGTTGCAGTGTG 393  
Qy 122 MetTrpValPheThrTyTrpValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
Db 394 ATGTGGGTATTACCTATGTTGGTCCCTGTTTAATGCTCTGACACTACTGATTTGGCT 453

Qy 142 LeuIleSerLeuPheSerValProValIleTyTrpGluArgHisGlnAlaGlnIleAspHis 161  
Db 454 CTCATTTCACTCTTCAGTGTTCCTGTTATTATGAACGGCATCAGGCACAGATAGATCAT 513  
Qy 162 TyrlLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 514 TATCTAGACTTGCATAATAAGATGTTAAAGATGCTATGGCTAAATCCAAGCAAAATC 573  
Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 574 CTTGGATTGAAGCGCANAGCTGAA 597  
RESULT 19  
LOCUS CN646472 960 bp mRNA linear EST 13-MAY-2004  
DEFINITION ILLUMIGEN MCQ 26335 Katze\_MMR Macaca mulatta cDNA clone IBIUM-8548  
5' similar to Bases 129 to 958 highly similar to human RTN4  
(Hs.436349), mRNA sequence.  
ACCESSION CN646472  
VERSION CN646472.1 GI:47159915  
KEYWORDS EST.  
SOURCE Macaca mulatta (rhesus monkey)  
ORGANISM Macaca mulatta  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
Cercopitheciinae; Macaca.  
REFERENCE 1 (bases 1 to 960)  
AUTHORS Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magnus,C.L.  
TITLE Large-scale Rhesus Macaque cDNA Sequencing  
JOURNAL Unpublished (2003)  
COMMENT Contact: C. Magnus  
Illumigen Biosciences Inc.  
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA  
Tel: 2063780400  
Fax: 2063780408  
Email: cmagnus@illumigen.com  
Sequenced on 2004.03.09. 743 Q20 bases.  
PCR Primers  
FORWARD: CCCTCACTAAAGGGAACAAA  
BACKWARD: CACTATAGGCGGATTTGGTA  
Insert Length: 960 Std Error: 0.00  
Plate: CL000173 row: H column: 11  
Seq primer: CCCTCACTAAAGGGAACAAA  
POLYA=No.  
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Location/Qualifiers  
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/dev stage="adult"  
/lab host="E. coli SOLR"  
/clone lib="Katze\_MMR"  
/note="Organ: brain; Vector: Uni-ZAP XR; Site 1: Ecor I;  
Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis  
kit (catalog #200400) and ZAP-cDNA Gigapack III Gold  
Cloning Kit (Catalog #200450)"  
ORIGIN  
Alignment Scores:  
Pred. No.: 2.99e-103 Length: 960  
Score: 921.00 Matches: 186  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 98.94% Mismatches: 0  
Query Match: 98.93% Indels: 0  
DB: 7 Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x CN646472 (1-960)  
Qy 2 ValValAspLeuLeuTyTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
Db 34 GTTGTGACCTCCTCTACTGGAGAGACATTAAAGACTGGAGTGGTGTGTTGGTGCCAGC 93

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Db 129 GTTGTGACCTCTCTACTGAGAGACATGAGAGACTGGAGTGGTGTGGTGGCCAGC 188
Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 189 CTATTCCTGCTGCTTTTCATTCAGACGATTTACGACATTTGAGTGTAAACAGCCTACATGGC 248
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAlaIle 61
Db 249 TTGGCCCTGCTCTCTGTGACCATCTTGTAGATATACAGGGGTGTGATCCAGCTATC 308
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 309 CAGAAATCAGATGAGAGCCACCCATTCAGGCATATCTGGAATCTGAAGTTGGATATCT 368
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db 369 GAGGAGTTGGTTTTCAGAAATACAGTAATCTCTGCTTGTGTCATGTGAACGACGATAAAG 428
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 429 GAACTCAGGCGCCTCTCTTAGTTGATGATTTAGTTGATTTCTGAAGTTTGCAGTGTG 488
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
Db 489 ATGTGGGTATTTACCTATGTTGGTGGCTTGTGTTTAAATGGTCTGACGCTACTGATTTGGCT 548
Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 549 CTCAATTCATCTCTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 608
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 609 TATCTAGGACTTGCAAATAGAAATGTTAAAGATGCTATGGCTAAATAATCCAGCGAAATC 668
Qy 182 ProGlyLeuLysArgLysAlaGlu 189
Db 669 CCTGGATTGAGCGCAAGCTGAA 692

RESULT 20
CN803408 983 bp mRNA linear EST 26-MAY-2004
ILLUMIGEN MCQ 32945 Katze MMR Macaca mulatta cDNA clone
IBIUW:11396 57 similar to Bases 136 to 983 highly similar to human
RTN4 (Hs.436349), mRNA sequence.
CN803408
CN803408.1 GI:47699384
Macaca mulatta (rhesus monkey)
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
Cercopitheinae; Macaca.
REFERENCE
1 (bases 1 to 983)
Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)
Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.04.03. 731 Q20 bases.
PCR Primers
FORWARD: CCTCTACTAAGGGAACAAAA
BACKWARD: CACTATAGGCGCAATTGGTA
Insert Length: 983 Std Error: 0.00
Plate: CL000275 Row: C Column: 03
Seq primer: CCTCTACTAAGGGAACAAAA
POLYA=No. Location/Qualifiers
1. .983
/organism="Macaca mulatta"
FEATURES
source
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/mol_type="mRNA"
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/dev_stage="adult"
/lab_host="E. coli SOLR"
/clone_lib="Katze MMR"
/note="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;
Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis
kit (catalog #200400) and ZAP-cDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"

ORIGIN
Alignment Scores: 3.09e-103 Length: 983
Pred. No.: 921.00 Matches: 186
Score: 921.00 Conservative: 2
Percent Similarity: 100.00%
Best Local Similarity: 98.94% Mismatches: 0
Query Match: 98.93% Indels: 0
DB: 7 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x CN803408 (1-983)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 136 GTTGTGACCTCTCTTCTTCTGAGAGACATGAGAGACTGGAGTGGTGTGGTGGCCAGC 195
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 196 CTATTCCTGCTGCTTTCATTCAGATGATTTACAGCTTGTGAGTGTAAACAGCCTACATGGC 255
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 256 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCTATC 315
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 316 CAGAAATCAGATGAGAGCGCCCATTCAGGCATATCTGGAATCTGAAGTTTGCAGTGTG 375
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db 376 GAGGAGTTGGTTTTCAGAAATACAGTAATCTCTGCTTGTGTCATGTGAACGACGATAAAG 435
Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 436 GAACTCAGGCGCCTCTCTTCTAGTGTGATTTAGTTGATTTCTGAAGTTTGCAGTGTG 495
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
Db 496 ATGTGGGTATTTACCTATGTTGGTGGCTTGTGTTTAAATGGTCTGACGCTACTGATTTGGCT 555
Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 556 CTCAATTCATCTCTCTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 615
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 616 TATCTAGGACTTGCAAATAGAAATGTTAAAGATGCTATGGCTAAATAATCCAGCGAAATC 675
Qy 182 ProGlyLeuLysArgLysAlaGlu 189
Db 676 CCTGGATTGAGCGCAAGCTGAA 699

RESULT 21
CN647521 1031 bp mRNA linear EST 13-MAY-2004
ILLUMIGEN MCQ 28658 Katze MMR Macaca mulatta cDNA clone IBIUW:7529
5' similar to Bases 129 to 1018 highly similar to human RTN4
(Hs.436349), mRNA sequence.
CN647521
CN647521.1 GI:47160964
EST.
KEYWORDS
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SOURCE Macaca mulatta (rhesus monkey)  
 ORGANISM Macaca mulatta  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 Cercopithecinae; Macaca.

REFERENCE 1 (bases 1 to 1031)  
 AUTHORS Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magnus, C.L.  
 TITLE Large-scale Rhesus Macaque cDNA Sequencing  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: C. Magnus  
 Illumigen Biosciences Inc.  
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA  
 Tel: 2063780400  
 Fax: 2063780408  
 Email: cmagnus@illumigen.com  
 Sequenced on 2004.03.24. 773 Q20 bases.  
 PCR Primers  
 FORWARD: CCTCACTAAGGGGACAAAA  
 BACKWARD: CACTATAGGCGGAATTGGTA  
 Insert Length: 1031 Std Error: 0.00  
 Plate: CL00187 row: G column: 05  
 Seq primer: CCTCACTAAGGGGACAAAA  
 POLYA=No.

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 1..1031  
 Location/Qualifiers  
 /organism="Macaca mulatta"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:9544"  
 /clone="IBI:W:7529"  
 /sex="female"  
 /dev\_stage="adult"  
 /lab\_host="E. coli SOLR"  
 /clone\_lib="Katze\_MMRB"  
 /note="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;  
 Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis  
 kit (Catalog #200400) and ZAP-cDNA Gigapack III Gold  
 Cloning Kit (Catalog #200450)"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 3.31e-103 Length: 1031  
 Score: 921.00 Matches: 186  
 Percent Similarity: 100.00% Conservative: 2  
 Best Local Similarity: 98.94% Mismatches: 0  
 Query Match: 98.93% Indels: 0  
 DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CN647521 (1-1031)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 DB 129 GTTGTGGACCTCCTCTACTGGAGACATGAAGAGACTGGAGTGTGTTGGTGCCAGC 188  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 DB 189 CTATTCTCGTCTTTCATTGACAGTATTGACATTGTGAGTGTGAACAGCTACATTGCC 248  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 DB 249 TTGGCCCTGCTCTCTGTGACCATCATGCTTTAGGATATACAGGGGTGTGATCAAGCTATC 308  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 309 CAGAAATCAGATGAAGGCCACCCATTCAGGCGATATCTGGAATCTGAAGTTGCCATATCT 368  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCythrIleLys 101  
 DB 369 GAGGAGTTGGTTTCAGAGTACAGTAATCTTCTCTTGTGTCATGTGAACTGCACGATAAG 428  
 QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 DB 429 GAACTCAGCGCGCTCTCTTAGTTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 488

QY 122 MetTrpValPheThrTyrValGlyValAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 DB 489 ATGTGGGTATTACTATGTTGGTGGCTTTGTTTAAATGCTGACCTACTGATTTGGCT 548  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 DB 549 CTCATTTTCACCTCTTCAGTGTTCCTGTTATTATTATGAACGGCATCAGGCACAGATGATCAT 608  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysPheAlaMetAlaLysIleGlnAlaLysIle 181  
 DB 609 TATCTAGGACTTGCATAATAAGAAATGTTAAAGATGCTATGGCTAAATAATCAAGCGAAATC 668  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 DB 669 CCTGATTGAAGCCCAAGACTGAA 692

RESULT 22  
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 LOCUS  
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 CDNA clone 10012 5', mRNA sequence.  
 ACCESSION CO735185  
 VERSION CO735185.1 GI:50822455  
 KEYWORDS EST.  
 SOURCE Spermophilus lateralis (golden-mantled ground squirrel)  
 ORGANISM Spermophilus lateralis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;  
 Spermophilus.

REFERENCE 1 (bases 1 to 805)  
 AUTHORS Williams, D.R., Gracey, A.Y., Martin, S.L., Hughes, M.A., Li, W.,  
 Rogers, J. and Cossins, A.R.  
 TITLE Microarray analysis of transcriptional changes during hibernation  
 JOURNAL in the golden mantled ground squirrel, Spermophilus lateralis  
 COMMENT Unpublished (2004)  
 CONTACT: Andrew R. Cossins  
 Laboratory for Environmental Gene Regulation  
 School of Biological Sciences, The Biosciences Building, Crown  
 Street, Liverpool, United Kingdom, L69 7ZB  
 Tel: +44(0)151-795-4510  
 Fax: +44(0)151-795-4431  
 Email: cossins@liv.ac.uk  
 Vector has been trimmed from this EST.  
 Plate: 10 row: 0 column: 12  
 Seq primer: pf1c T7 (5'-AATACGACTCATATAGGG-3')  
 High quality sequence stop: 805.  
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 /db\_xref="taxon:76772"  
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 /lab\_host="E.coli Electromax DH10B"  
 /clone\_lib="squirrel embryo library 1"  
 /note="Vector: pFLC; Site 1: SalI GTCGAG; Site 2: BamHI  
 GGATCC; Normalized and subtracted cDNA library prepared  
 from embryos"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 1.29e-102 Length: 805  
 Score: 915.00 Matches: 185  
 Percent Similarity: 99.47% Conservative: 2  
 Best Local Similarity: 98.40% Mismatches: 1  
 Query Match: 98.28% Indels: 0  
 DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CO735185 (1-805)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
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 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 240 TTATTCCTGCTGCTTTCATGACAGTATTCAGCATTTGAGTGTAAACACCTACATTCGC 299  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 300 TTGGCCCTGCTCTCTGACTATCAGCTTTAGATATATAAGGTGTGATCCAGCTATC 359  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 360 CAGAAATCAGATCAGAGCCACCCATTCAGGGCTTATTTGGAATCTGATCTGCTATATCT 419  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 420 GAGGAATTGATTACAGAAATACAGTAATCTGCTTTGGTCATGTGAACCTGCACGATAAAA 479  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 480 GAACCTAGACGCTCTCTCTAGTATGATGATTTAGTTGATTTCTAAAGTTTGCAGTATG 539  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuAla 141  
 Db 540 ATGTGGGTATTTACCTATGTTGGTCTGTTGTTCAATGGTCTGACACTACTGATTTTGGCT 599  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 600 CTGATTTCACTCTTCAGTGTCTCTGTTATTTAGAACGGCATCAGCACAAATAGATCAC 659  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 660 TATCTAGGACTTGATATAGAAATGTTAAAGATGCTATGCTAAATCCAGCAAAAT 719  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 Db 720 CCTGGATTGAAGCGCAAGCTGAA 743

RESULT 23  
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 LOCUS AGENCOURT\_6458941 NIH\_MGC\_88 Homo sapiens cDNA clone IMAGE:5558493  
 5', mRNA sequence.  
 ACCESSION BM801698  
 VERSION BM801698.1 GI:19118521  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 958)  
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
 Tissue procurement: ATCC  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM12281 row: i column: 22  
 High quality sequence start: 25  
 High quality sequence stop: 579.  
 Location/Qualifiers  
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FEATURES  
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/db\_xref="taxon:9606"  
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 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_88"  
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 Technologies. Note: this is a NIH\_MGC Library."

ORIGIN

Alignment Scores:  
 Pred. No.: 1.65e-102 Length: 958  
 Score: 915.00 Matches: 186  
 Percent Similarity: 98.94% Conservative: 0  
 Best Local Similarity: 98.94% Mismatches: 2  
 Query Match: 98.28% Indels: 0  
 DB: 4 Gaps: 0

US-09-830-972-29\_copy\_990\_1178 (1-189) x BM801698 (1-958)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 66 GTTGTGACCTCTCTACTCGAGACATTAAGAGACTGGAGTAGTGTGGTGCACG 125  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 126 CTATTCCTGCTCTCTTTCATGACAGTATTCAGCAATTTGTGAGCGTAAACAGCTACATTCGC 185  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 186 TTGGCCCTGCTCTCTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 245  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 246 CAGAAATCAGATCAGAGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 305  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 306 GAGGAGTTGGTTTCAGAAAGTACAGTAATCTGCTCTTGGTCTATGTGAACCTGCACGATAAAG 365  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 366 GAACCTAGACGCTCTCTCTAGTATGATTTAGTGTGATTTCTGAAAGTTGCGAGTGTG 425  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuAla 141  
 Db 426 ATGTGGGTATTTACCTATGTTGGTGGCTTGTATTAATGGTCTGACACTACTGATTTGGCT 485  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 486 CTCAATTCACCTCTCAGTGTCTCTGTTATTTATGAACGCATCAGCACACATAGATCAT 545  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 546 TATCTACGACTTGCAAATAAGAAATCTAAAGATGCTATGGCTTAAATCCAGCAAAATC 605  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 Db 606 CCTGGATTGAAGCGCAAGCTGAA 629

RESULT 24

LOCUS BG715173  
 DEFINITION 602675631P1 NIH\_MGC\_96 Homo sapiens cDNA clone IMAGE:4798279 5',  
 mRNA sequence.  
 ACCESSION BG715173  
 VERSION BG715173.1 GI:13994106  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;





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Db 244 GTTGTGACCTCTGTACTGGAGACATTAAGAACCTGGAGTGGTGTGGTGGCCAGC 303
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValrileAla 41
Db 304 CTATTCTCTGCTGCTTCAATGACAGTATTCAGCATTTGAGCGTAACAGCCTACATGGC 363
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAlaIle 61
Db 364 TTGGCCCTGCTCTCTGTGACCATTCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 423
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 424 CAGAAATCAGATGAAGCCACCCATTCAGGCATATCTGGATCTGAAGTTCATATCT 483
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db 484 GAGGAGTGTGTTTACCTATGTTGGTCTGTTTAAATGGTCTGACACTACTGATTTGGCT 563
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 664 CTCATTTCATCTTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 723
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 724 TATCTAGGACTTGCATAATAGATGTTNAAGATGCTATGGCTAANATCCAAAGCAAAATC 783
QY 182 ProGlyLeuLysArgLysAlaGlu 189
Db 784 CTTGGGATGAGCGCAAAAGCTGNA 807

CN805577 1042 bp mRNA linear EST 26-MAY-2004
ILLUMIGEN MCQ 36873 Katze MMR Macaca mulatta cDNA clone
IBIUW:12670 57 similar to Bases 138 to 1022 highly similar to human
RN4 (Hs.436349), mRNA sequence.
CN805577 GI:47701553
EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
Cercopitheinae; Macaca.
1 (bases 1 to 1042)
Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magnus, C.L.
Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)
Contact: C. Magnus
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagnus@illumigen.com
Sequenced on 2004.05.12. 633 Q20 bases.
PCR Primers
FORWARD: CCTCTACTAAAGGGAACAAA
BACKWARD: CACTATAGCGGAATTGGTA
Insert Length: 1042 Std Error: 0.00
Plate: CL000243 row: C column: 03
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POLYA=Yes.
Location/Qualifiers
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/organism="Macaca mulatta"

FEATURES
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/clone_lib="Katze_MMR"
/notes="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;
Site 2: Xho I; Created from Stratagene ZAP-cDNA synthesis
kit (catalog #200400) and ZAP-CDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"

ORIGIN
Alignment Scores:
Pred. No.: 3.3e-102 Length: 1042
Score: 913.00 Matches: 185
Percent Similarity: 99.47% Conservative: 2
Best Local Similarity: 98.40% Mismatches: 1
Query Match: 98.07% Indels: 0
DB: 7 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x CN805577 (1-1042)

QY 2 ValValAspLeuLeuTyrTrrArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 138 GTTGTGACCTCTCTTACTGGAGACATGAAGAAGACTGGAGTGGTGTGGTGGCCAGC 197
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValrileAla 41
Db 198 CTATTCTCTGCTGCTTTCATTGACAGTATTCAGCATTTGAGTGTGAACAGCCTACATGGC 257
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 258 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 317
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 318 CAGAAATCAGATGAAGCGCCACCATTCAGGGCATATCTGGAATCTGAAGTTCGATATCT 377
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db 378 GAGGAGTGTGTTTACAGAGTACAGTAACTCTGCTCTTGGTCACTGAGTGCACGATAAG 437
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 438 GAACTCAGCGCGCTCTCTTCTAGTATGATTTAGTGTGATTTCTCTGAAAGTTTCAGTGTG 497
QY 122 MetTrrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
Db 498 ATGTGGGTATTTTACCTATGTTGGTGGCTTGTATTATGGTCTGACGCTACTGATTTGGCT 557
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 558 CTCATTTCATCTTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 617
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 618 TATCTAGGACTTGCATAATAGAAATGTTAAAGATGCTATGGCTAAAAATCCAAAGCAAAATC 677
QY 182 ProGlyLeuLysArgLysAlaGlu 189
Db 678 CTTGGATTTGAAGCGCATAGCTGAA 701

RESULT 27
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LOCUS
DEFINITION Homo sapiens cDNA clone hw24hl2 5', mRNA sequence. Unamplified (hw)
ACCESSION CN482802
VERSION CN482802.1 GI:46564306
KEYWORDS EST.
SOURCE Homo sapiens (human)
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eumalia; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 592)

AUTHORS Tsai, J.Y. and Wistow, G.

TITLE Expressed sequence tag analysis of cultured primary human ocular pericytes

JOURNAL Unpublished (2004)

COMMENT Contact: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: graeme@helix.nih.gov  
Plate: 24 row: h column: 12  
Seq primer: M13RPI reverse primer (ABI).  
Location/Qualifiers  
1..592  
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/mol\_type="mRNA"  
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/cell\_type="pericytes"  
/dev\_stage="Adult"  
/lab\_host="EMDH10B"  
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Unamplified (hw)  
/note="Organ: Eye; Vector: pSport1; RNA was extracted from primary human pericytes in culture. A directionally cloned cDNA library in the pSPORT1 vector (Invitrogen) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual  
(http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adaptor  
[5'-pGACTAGTTCGATCGAGCGCCGCC(T)15-3']. cDNA was cloned in Not I/Sal I sites. EST analysis was performed at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Alignment Scores:  
Pred. No.: 1.96e-102 Length: 592  
Score: 912.00 Matches: 185  
Percent Similarity: 99.46% Conservative: 0  
Best Local Similarity: 99.46% Mismatches: 1  
Query Match: 97.96% Indels: 0  
DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CN482802 (1-592)

Qy 1 SerValValAspLeuLeuTyrTrpArgAspLeuLysLysThrGlyValValPheGlyAla 20  
Db 35 TCAGTGGTTCACCTCTCTGACGACATTAAGAAGACTGGAGTGGTGGTGCC 94  
Qy 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40  
Db 95 AGCCTATTCTCTGCTCTTCATGTGACAGATTTCAGCATTTGAGCGTAACAGCCTACATT 154  
Qy 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAla 60  
Db 155 GCCTTGGCCCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCT 214  
Qy 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80  
Db 215 ATCCAGAAATCAGATGAAGGCCACCATTCAGGGCATATCTGGAATCTGAAGTTGCTATA 274  
Qy 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100  
Db 275 TCTGAGGAGTTGGTTTCAGAAAGTACAGTAATCTCTCTGTGGTCATGTGAACCTGCACGATA 334  
Qy 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120

Db 335 AAGAACTCAGCGCGCTCTCTTAGTTGATGATTAGTTGATTTCTCTGAAGTTTCAGTG 394  
Qy 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140  
Db 395 TTGATGTGGGTATTTACCTATGTGGTGCCCTGTGTTAAATGGTCTGACACTACTGATTTG 454  
Qy 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160  
Db 455 GCTCTCTATTCACCTCTTCAGTGTTCCTGTTATTATGAACGCATCAGGCACAGATAGAT 514  
Qy 161 HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180  
Db 515 CATTATCTAGGACTTGCAATGAAGATGTTAAAGATGCTATGGCTAAATAATCCAGCAAT 574  
Qy 181 IleProGlyLeuLysArg 186  
Db 575 ATCCCTGATTGAAGCGC 592

RESULT 28  
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ACCESSION CD110203  
VERSION CD110203.1 GI:30754412  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 871)  
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Dr. Stefan Hansson  
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help and advice from Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: NDA347 row: p column: 18  
High quality sequence stop: 630.  
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/clone\_lib="NIH\_MGC 148"  
/note="Organ: placenta; Vector: pBluescriptR; Site 1:  
ali-xhol; Site 2: BamH; Library is oligo-dT primed and  
directionally cloned using primer  
5'-TTTTTTTTTTTTTNN-3', size-selected for average insert  
size 2.3 kb and normalized to ROT 5. This is a primary  
library enriched for full-length clones and constructed  
using the Cap-trapper method (Carninci, in preparation).  
Library constructed by M. Brownstein (NIH/NHGRI,  
National Institutes of Health). Note: this is a NIH\_MGC  
Library."

ORIGIN

Alignment Scores:  
Pred. No.: 3.4e-102 Length: 871  
Score: 912.00 Matches: 187  
Percent Similarity: 99.47% Conservative: 1  
Best Local Similarity: 98.94% Mismatches: 0

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Query Match: 97.96% Indels: 1
DB: 6 Gaps: 0
US-09-830-972-29_COPY_990_1178 (1-189) x CD110203 (1-871)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
DB 187 GTTGTGACCTCTGCTACTGGAGAGACATTAAGAACACTGGAGTGGTGTGGTGGCCAGC 246
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValrleAla 41
DB 247 CTATTCCTGCTGCTTTCATTCAGCATTTAGCATTTGAGCGTACACGCTACATTCGTC 306
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 307 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGCTGTGATCCAAGCTATC 366
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 367 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTCGAAGTTGCTATPATCT 426
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
DB 427 GAGGAGTTGGTTCAGAACTACAGTAATTTCTGCTTTGGTCACTGTGACGATGAAG 486
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 487 GAACTCAGCGGCTCTCTCTAGTTGATGATTTAGTTGATTTCTGAAATCTCGAAGTTG 546
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
DB 547 ATGTGGGATTAATACCTATGTTGGTGCCTGTTTAAATGGTCTGACATCTACTGATTTGGCT 606
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
DB 607 CTCAATTCATCTTCTAGTGTCTCTGTTATTAAGAACGCGCATCAGGCACAGATGATCAT 666
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
DB 667 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCNAATC 726
QY 182 ProGlyLeu-LysArgLysAlaGlu 189
DB 727 CCTGGAATGAAGCGCAAGGCTGAA 751

RESULT 29
AY404972 600 bp DNA linear GSS 16-DEC-2003
LOCUS Mus musculus RTN4 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY404972
VERSION AY404972.1 GI:39760946
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 600)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrier,S., Wang,G., Zheng,X.H., White,T.J., Sainsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
2 (bases 1 to 600)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrier,S., Wang,G., Zheng,X.H., White,T.J., Sainsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
```

```
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Source
1..600
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>600
/gene="RTN4"
/locus_tag="HCM2068"
ORIGIN
Alignment Scores: 2.65e-102 Length: 600
Pred. No.: 911.00 Matches: 185
Score: 99.47% Conservative: 2
Percent Similarity: 98.40% Mismatches: 1
Best Local Similarity: 97.85% Indels: 0
Query Match: 97.85% Gaps: 0
DB: 9
US-09-830-972-29_COPY_990_1178 (1-189) x AY404972 (1-600)
QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
DB 34 GTTGTGACCTCTCTGCTACTGGAGAGACATTAAGAACACTGGAGTGGTGTGGTGGCCAGC 93
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaValrleAla 41
DB 94 TTATTCCTGCTGCTCTCTGACAGTGTTCAGCATTTGAGGATATTAAGGCTGATCCAAGCTATC 153
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 154 TTGGCCCTGCTCTCTGTGACATCAGCTTTAGGATATTAAGGCTGATCCAAGCTATC 213
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 214 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGGAAGTTGCCATATCA 273
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
DB 274 GAGGAATGGTTCAGAAATATAGTAATTTCTGCTTCTGGTCACTGTGAACAGCAATAAAA 333
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 334 GAAATTGAGCGGCTCTCTCTTAGTGATGATTTAGTTGATTCCTGAAAGTTTCAGTGTTCG 393
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
DB 394 ATGTGGGATTTACTTACGTTGGTGCCTTGTTCATGTTGACACTACTGATTTTAGCC 453
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
DB 454 CTGATCTCATCTTTCAGTATTTCTGTTATATATGAACGCGCATCAGGCGCAGATGATCAT 513
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
DB 514 TATCTAGGACTTGCAAAACAAAGACGTTAAGGATGCGATGGCCAAATCCAAAGCAAAATC 573
QY 182 ProGlyLeuLysArgLysAlaGlu 189
DB 574 CCTGGAATGAAGCGCAAGGCTGAA 597
RESULT 30
B1149602
LOCUS B1149602
DEFINITION mRNA sequence.
ACCESSION B1149602
VERSION B1149602.1 GI:14609603
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NIH-MGC <http://mgi.nci.nih.gov/> National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-romail.nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLAM1062 row: c column: 04  
High quality sequence stop: 679.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source

1..679  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="CZECH II"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5011899"  
/tissue\_type="spontaneous tumor, metastatic to mammary."  
Stem cell origin.  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Lu29"  
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

ORIGIN

Alignment Scores:  
Pred. No.: 3.17e-102 Length: 679  
Score: 911.00 Matches: 185  
Percent Similarity: 99.47% Conservative: 2  
Best Local Similarity: 98.40% Mismatches: 1  
Query Match: 97.85% Indels: 0  
DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x B1149602 (1-679)

Qy 2 ValValAspLeuLeuTyrrArgAspIleValysThrGlyValValPheGlyAlaSer 21  
Db 37 GTTGTGACCTCTCTGTGACTATGAGACATTAAGAGACTGGAGTGTGTTGGTGCCAGC 96  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrrileAla 41  
Db 97 TTATTCCTGCTGCTCTGACAGTGTTCAGCATTTGCTGTAACGGCTTACATTGCC 156  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrrLysGlyValIleGlnAlaIle 61  
Db 157 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCAAGCTATC 216  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrrLeuGluSerGluValAlaIleSer 81  
Db 217 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGGAATGTCCTATCA 276  
Qy 82 GluGluLeuValGlnLysTyrrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 277 GAGGAATTTGTTTCAGAAATATAGTAATTTCTGCTCTTGTGTCATGTGAACAGCACATAAAA 336  
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 337 GAATGAGCGCTCTCTTCTAGTCATGATTTAGTTGATTCCTCAAGTTTGCAGTGTG 396  
Qy 122 MetTrpValPheThrTyrrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
Db 397 ATGTGGGTATTTACTTACGTGGTGCCCTGTTCAATGTTGTTGACACTACTGATTTAGCC 456  
Qy 142 LeuIleSerLeuPheSerValProValIleTyrrGluArgHisGlnAlaGlnIleAspHis 161

Db 457 CTGATCTCCTCTTCTCAGTATTCCTGTTATATATGAACGGCATCAGCGCCAGATGATCAT 516  
Qy 162 TyrrLeuGlyLeuAlaAsnLysAsnValysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 517 TATCTAGGACTTGCAACAAGAGTGTTAAGGATGCCATGGCCAAATCCAAAGCAAAATC 576  
Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 577 CCTGATTTGAAGCGCAAGACGAA 600  
RESULT 31  
B1157842  
LOCUS  
DEFINITION  
602923001F1 NCI CGAP Mam3 Mus musculus cDNA clone IMAGE:5062944 5', mRNA sequence.  
B1157842  
VERSION  
B1157842.1 GI:14617843  
KEYWORDS  
EST.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NIH-MGC <http://mgi.nci.nih.gov/> National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-romail.nih.gov  
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLAM1170 row: b column: 01  
High quality sequence stop: 708.  
Location/Qualifiers  
1..708  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129,C57BL/6J,FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5062944"  
/tissue\_type="tumor, gross tissue"  
/dev\_stage="10 months"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Mam3"  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH  
Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999)."

ORIGIN

Alignment Scores:  
Pred. No.: 3.36e-102 Length: 708  
Score: 911.00 Matches: 185  
Percent Similarity: 99.47% Conservative: 2  
Best Local Similarity: 98.40% Mismatches: 1  
Query Match: 97.85% Indels: 0  
DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x B1157842 (1-708)

Qy 2 ValValAspLeuLeuTyrrArgAspIleValysThrGlyValValPheGlyAlaSer 21  
Db 59 GTTGTGACCTCTCTGCTGAGACATTAAGAGACTGGAGTGTGTTGGTGCCAGC 118  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrrileAla 41

```

Db      119 TTATTCCTGCTGCTCTGACAGTGTTCAGCAATGTTCAGTGTAAAGCGCTACATTGCC 178
Qy      42  LeuAlaLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAlaIle 61
Db      179 TTGGCCCTGCTCTCTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAAGCTATC 238
Qy      62  GlnIleSerAspGluGlyHisProPheArgAlaTyrIleGluSerGluValAlaIleSer 81
Db      239 CAGAAATCAGATGAAGCCACCCATTCAGGGCATAATTTGGAATCTCAAGTTGCCATATCA 298
Qy      82  GluGluLeuValGlnIleYstYrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db      299 GAGGAATTGGTTCAGAAATATAGTAATTTCTGCTTTGGTCATGTTGAACGACCAATAAAA 358
Qy      102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db      359 GAATTCAGGCGCTCTCTTCTAGTTGATGATTTAGTTGATTCCTCGAAGTTTGCAGTGTG 418
Qy      122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuAla 141
Db      419 ATGTGGGTATTTACTTACCGTTGGTGCCTTTGTTCAATGGTTTGACACTACTGATTTTAGCT 478
Qy      142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db      479 CTGATCTCCTCTTCAGTATCTCTGTTATATATGAACGGCATCAGCGCGGAGATGATCAT 538
Qy      162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      539 TATCTAGGACTTGCAACAAAGAGCGTTAAGGATGCCATGGCCAAAATCCAAAGCAAAATC 598
Qy      182 ProGlyLeuLysArgLysAlaGlu 189
Db      599 CCTGGATTGAAGCGCAAGCAGAA 622

```

## RESULT 32

```

CO0401465
LOCUS      779 bp mRNA linear EST 01-JUL-2004
DEFINITION AGENCOURT_26749547 NIH_MGC_255 Rattus norvegicus cDNA clone
IMAGE:7317070 5', mRNA sequence.
ACCESSION CO0401465
VERSION    1 GI:49583381
KEYWORDS   EST.
SOURCE     Rattus norvegicus (Norway rat)

```

## ORGANISM

```

Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

```

## REFERENCE

```

1 (bases 1 to 779)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892

```

## AUTHORS

```

Email: Gcgsb-r@mail.nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
College of Wisconsin

```

## JOURNAL

```

cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

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## COMMENT

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Plate: L1AM15373 row: 0 column: 20
High quality sequence start: 23
High quality sequence stop: 690.

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## FEATURES

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source     Location/Qualifiers
1..779
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7317070"

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```

/sex="both"
/tissue_type="Brain - Pooled from several tissues from one
or more individuals"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_255"
/notes="organ: brain/CNS; Vector: pExpress-1; Site 1:
ScORV; Site 2: NotI; RNA obtained from brain tissue of 8
wk old animal. Tissues were snap-frozen and kept at -80C
before RNA extraction and purification (TRI-reagent
method). cDNA was primed using oligo-dT primer:
5'-pCAGTGTCTAGATCGGCGGCCG(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb
resulted in an average insert size of 1.7 kb. This primary
library is a normalized (primary library is NIH_MGC_254)
and was constructed by Express Genomics (Frederick, MD).
Note: this is a NIH_MGC library"

```

## ORIGIN

```

Alignment Scores:
Pred. No.:      9,08e-102      Length:      779
Score:          908.00        Matches:    184
Percent Similarity: 98.94%    Conservative: 3
Best Local Similarity: 97.33%  Mismatches:  2
Query Match:     97.53%      Indels:     0
DB:              7          Gaps:         0

```

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US-09-830-972-29_COPY_990_1178 (1-189) x CO0401465 (1-779)
```

```

Qy      1  SerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAla 20
Db      114 TCAGTTGTGACCTCTCTACTGGAGACATTAAGAGACTGGAGTGGTGTGGTGGC 173
Qy      21  SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
Db      174 AGCTTATTCCTGCTGCTCTGACAGTGTTCAGCATTTGTCAGTGTAAAGCGCTACATT 233
Qy      41  AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60
Db      234 GCCTTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGGTGATCCAGGCT 293
Qy      61  IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
Db      294 ATCCAGAAATCAGATGAAGCCACCCATTCAGGGCATATTTAGATCTCGAAGTTGCTATA 353
Qy      81  SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
Db      354 TCAGAGGAATTGGTTTCAGAAATACAGTAATTTCTGCTCTTTGGTTCATGTGAACGACCAATA 413
Qy      101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
Db      414 AAAGAACTGAGCGCGCTTTCTTAGTTGATGATTTAGTTGATTTCTCCCTGAAGTTGCGAGTG 473
Qy      121  LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeu 140
Db      474 TTGATGTGGGTGTTTACTATGTTGGTGCCTTTGTTCAATGGTCTGACACTACTGATTTTA 533
Qy      141  AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
Db      534 GCTCTGATCTCACTCTTCAGTATTTCTGTTATTTATGAACGGCATCAGGTGCGAGATAGAT 593
Qy      161  HisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
Db      594 CATTATCTAGGACTTGCAAAACCAAGAGTGTTAAGAGTGCATGCCCAAAATCCAGCAAAA 653
Qy      181  IleProGlyLeuLysArgLysAlaGlu 189
Db      654 ATCCCTGGATTGAAGCGCAAGCAGAT 680

```

## RESULT 33

```

CO048918
LOCUS      1013 bp mRNA linear EST 14-JUN-2004
DEFINITION ILLUMIGEN_MCQ_38898 Katze WMBR Macaca mulatta cDNA clone
IBIUW:16203 5' similar to_Bases 112 to 991 highly similar to human

```

```

RTN4 (Hs.436349), mRNA sequence.
ACCESSION   CO048918
VERSION     CO048918.1  GI:48688540
KEYWORDS    EST.
SOURCE      Macaca mulatta (rhesus monkey)
ORGANISM    Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
            Cercopitheciinae; Macaca.
REFERENCE   1 (bases 1 to 1013)
AUTHORS     Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
TITLE       Large-scale Rhesus Macaque cDNA Sequencing
JOURNAL     Unpublished (2003)
COMMENT     Contact: C. Magness
            Illumigen Biosciences Inc.
            2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
            Tel: 2063780400
            Fax: 2063780408
            Email: cmagness@illumigen.com
            Sequenced on 2004.05.13. 609 Q20 bases. Library Preparation: Prof.
            Michael Katze Lab at University of Washington DNA Sequencing:
            Illumigen Biosciences Inc. For further information, see
            http://www.macaque.org
            PCR Primers
            FORWARD: CCCTCACTAAAGGGAACAAA
            BACKWARD: CACTATAGGCGAATTGGGTA
            Insert Length: 1013 Std Error: 0.00
            Plate: CL000160 row: G column: 08
            Seq primer: CCCTCACTAAAGGGAACAAA
            POLYA=Yes.

FEATURES             Location/Qualifiers
     1..1013
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     /mol_type="mRNA"
     /strain="Indian"
     /db_xref="taxon:9544"
     /clone="IBIUM:16203"
     /sex="female"
     /dev_stage="adult"
     /lab_host="E. coli SOLR"
     /clone_lib="Katze MMRB"
     /note="Organ: brain; Vector: Uni-ZAP XR; Site 1: Ecor I;
     Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis
     Kit (catalog #200400) and ZAP-CDNA Gigapack III Gold
     Cloning Kit (Catalog #200450)"

ORIGIN
Alignment Scores:
Pred. No.:      1.32e-101      Length:      1013
Score:          908.00      Matches:      186
Percent Similarity: 99.47%      Conservative: 2
Best Local Similarity: 98.41%      Mismatches: 0
Query Match:     97.53%      Indels:      1
DB:              7          Gaps:          0

US-09-830-972-29_COPY_990_1178 (1-189) x CO048918 (1-1013)

Qy      2 ValValAspLeuLeuTyTrpArgAspLeuLysThrGlyValValPheGlyAlaSer 21
      |||
Db      112 GTTGTGACCTCCTCTACTGGAGACATGAGAGACTGGAGTGGTGTGGTGCACG 171
      |||

Qy      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrlleAla 41
      |||
Db      172 CTATTCTCGCTGCTTTCATTGACAGTATTGACATTTGAGTGTGACAGCTTACATTGCC 231
      |||

Qy      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrlsGlyValIleGlnAlaIle 61
      |||
Db      232 TTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAGCTATC 291
      |||

Qy      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrlsLeuGluSerGluValAlaIleSer 81
      |||
Db      292 CAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGGAAGTTGCGATATCT 351
      |||

```

```

Qy      82 GluGluLeuValGlnLysTyTrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
      |||
Db      352 GAGGAGTTGGTTTCAGAGTACAGTAATTTCTGCTCTTGTGTCATGTGAACCTGCACGATAAG 411
      |||

Qy      102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
      |||
Db      412 GAACCTCAGGCCCTCTTCTTAGTTGATGATTAGTTGATTCTCTGAAGTTTGCAGTGTG 471
      |||

Qy      122 MetTrpValPheThrTyTrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
      |||
Db      472 ATGTGGGTATTACTATGTTGGTCCCTGTTTAAATGGTCTGACCTACTGATTTGGCT 531
      |||

Qy      142 LeuIleSerLeuPheSerValProValIleTyTrGluArgHisGlnAlaGlnIleAspHis 161
      |||
Db      532 CTCAATTCACCTCTTCAGTGTTCCTGTTATTATGAACGGCATCAGGCACAGATAGATCAT 591
      |||

Qy      162 TyrlleGlyLeuAlaAsnLysAsn-ValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
      |||
Db      592 TATCTAGGACTTGCAAAATAAGATGGTTAAAGATGCTATGGCTAAATCCAAAGCGAAAT 651
      |||

Qy      181 eProGlyLeuLysArgLysAlaGlu 189
      |||
Db      652 CCCTGGATTGAAGCGCAAAAGCTGAA 676
      |||

RESULT 34
LOCUS     CN801888
DEFINITION ILLUMIGEN MCQ 37222 Katze_MMRB Macaca mulatta cDNA clone
            RTN4 (Hs.436349), mRNA sequence.
ACCESSION CN801888
VERSION    CN801888.1  GI:47697864
KEYWORDS   EST.
SOURCE     Macaca mulatta (rhesus monkey)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
            Cercopitheciinae; Macaca.
REFERENCE   1 (bases 1 to 1018)
AUTHORS     Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
TITLE       Large-scale Rhesus Macaque cDNA Sequencing
JOURNAL     Unpublished (2003)
COMMENT     Contact: C. Magness
            Illumigen Biosciences Inc.
            2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
            Tel: 2063780400
            Fax: 2063780408
            Email: cmagness@illumigen.com
            Sequenced on 2004.05.14. 594 Q20 bases.
            PCR Primers
            FORWARD: CCCTCACTAAAGGGAACAAA
            BACKWARD: CACTATAGGCGGATTTGGGTA
            Insert Length: 1018 Std Error: 0.00
            Plate: CL000272 row: E column: 10
            Seq primer: CCCTCACTAAAGGGAACAAA
            POLYA=No.

FEATURES             Location/Qualifiers
     1..1018
     /organism="Macaca mulatta"
     /mol_type="mRNA"
     /strain="Indian"
     /db_xref="taxon:9544"
     /clone="IBIUM:16016"
     /sex="female"
     /dev_stage="adult"
     /lab_host="E. coli SOLR"
     /clone_lib="Katze MMRB"
     /note="Organ: brain; Vector: Uni-ZAP XR; Site 1: Ecor I;
     Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis
     Kit (catalog #200400) and ZAP-CDNA Gigapack III Gold
     Cloning Kit (Catalog #200450)"

ORIGIN

```





[illegible]

was primed using oligo-dT primer:  
 5'-pGACTAGTCTAGATCGGAGCGGCCCCC(T)25-3' and cloned into  
 the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb  
 resulted in an average insert size of 1.6 kb. This primary  
 library is normalized (non-normalized primary library is  
 NIH MGC 250) and was constructed by Open Biosystems. Note:  
 this is a NIH\_MGC library"

## ORIGIN

Alignment Scores:  
 Pred. No.: 2,426-101 Length: 695  
 Score: 904.00 Matches: 183  
 Percent Similarity: 98.94% Conservative: 3  
 Best Local Similarity: 97.34% Mismatches: 2  
 Query Match: 97.10% Indels: 0  
 DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CV077130 (1-695)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 DB 126 GTTGTGGACCTCTCTACCTGGAGAGACATTAAGAACACTGGAGTGGTGTGGTGGCCAGC 185  
 QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 DB 186 TTATCTCTGCTGCTGCTGACAGTGTTCAGCATGTTCAGTGTACGCGCTACATTGGCC 245  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 DB 246 TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATTAAGGCGGTGATCCAGGCTATC 305  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 306 CAGAAATCAGATGAAGCCACCCATTCAGCGGCATATTTAGAAATCTCAAGTGTCTATATCA 365  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 DB 366 GAGGAATGGTTCAGAAATACAGTAATCTGCTCTTGGTCATGTGAACAGCAATATAA 425  
 QY 102 GluLeuArgGluLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 DB 426 GAACCTGAGCGGGCTTTCTTAGTTGATGATTTAGTTGATTCCTCGAAGTTTGCAGTGTG 485  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuAla 141  
 DB 486 ATGTGGGTGTACTTATGTGTGCTGCTTGTCAATGGTCTGACACTCTGATTTTGTGCT 545  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 DB 546 CTGATCTCACTCTTCAGTATCTCTGTATTATTAAGACGGCATCAGGTGCAGATAGATCAT 605  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 DB 606 TATCTAGGACTTGCACAAACAGAGTGTAAAGATGCCATGGCCAAAATCCAAAGCAAAATC 665  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 DB 666 CTGGATTGAAGCGCAAGGAGAT 689

## RESULT 38

LOCUS BG740561 758 bp mRNA linear EST 15-MAY-2001  
 DEFINITION 602633075F1 NCI\_CGAP\_Skn3 Homo sapiens cDNA clone IMAGE:4778131 5',  
 mRNA sequence.  
 ACCESSION BG740561  
 VERSION BG740561.1 GI:14051214  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 758)  
 AUTHORS NIH-MGC <http://mge.nci.nih.gov/>.

TITLE  
JOURNAL  
COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs@mail.nih.gov  
 Tissue Procurement: James Cleaver, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA  
 Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM10633 row: f column: 20  
 High quality sequence stop: 743.  
 Location/Qualifiers

## FEATURES

source

1..758

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4778131"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_lib="NCI\_CGAP\_Skn3"

/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.5kb. Library constructed by Life  
 Technologies. Note: this is a NCI\_CGAP Library."

## ORIGIN

## Alignment Scores:

Pred. No.: 2,746-101 Length: 758  
 Score: 904.00 Matches: 186  
 Percent Similarity: 98.41% Conservative: 0  
 Best Local Similarity: 98.41% Mismatches: 2  
 Query Match: 97.10% Indels: 1  
 DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BG740561 (1-758)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 DB 130 GTTGTGGACCTCTCTACCTGGAGAGACATTAAGAACACTGGAGTGGTGTGGTGGCCAGC 189  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 DB 190 CTATTCTCTGCTCTTTCATTGACAGTATTCAGCATGTGAGCGTAAACAGCTACATTGCC 249  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 DB 250 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGCTGTGATCCAAGCTATC 309  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 310 CAGAAATCAGATGAAGCGCCACCCATTCAGGCGCATATCTGGAATCTGAAGTGTCTATATCT 369  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 DB 370 GAGGAGTGGTTCAGAGTACAGTAATCTGCTCTTGGTTCATGTGAACGACGATTAAG 429  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 DB 430 GAACTCAGCGCGCTCTCTTAGTTGATTTAGTTGATTTCTCTGAAAGTTTGCAGTGTG 489  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleLeuAla 141  
 DB 490 ATGTGGGTATTTTACCTATGTTGGTGGCTTTGTTTAAATGGTCTGACACTACTGATTTTGGCT 549  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 DB 550 CTCATTTCACTCTTCAGTGTCTCTGTTATTATTAAGCGCATCAGGACAGATAGATCAT 609  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLys-AspAlaMetAlaLysIleGlnAlaLysIle 181  
 DB 610 TATCTAGGACTTGCACAAATGAAGATGTAAACAGATGCTATGGCTGCTAAATCCAAAGCAAAAT 669

Qy	181	eProGlyLeuLysArgLysAlaGlu 189       670 CCTGGATTGAAGCGCAAGCTCAA 694
Db		
RESULT 39		
CF977898		
LOCUS		
DEFINITION	F26A06_048.abl.R Rat retinal ganglion cell Rattus norvegicus cDNA, mRNA sequence.	linear EST 24-JUN-2004
ACCESSION	CF977898	
VERSION	CF977898.1	GI:49173356
KEYWORDS	Rattus norvegicus (Norway rat)	
SOURCE	Rattus norvegicus	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
REFERENCE	1 (bases 1 to 791) Farkas,R.H., Qian,J., Goldberg,J.L., Quigley,H.A. and Zack,D.J. Gene Expression Profiling of Highly Purified Rat Retinal Ganglion Cells Unpublished (2003)	
AUTHORS	Contact: Farkas RH	
TITLE	Department of Ophthalmology Johns Hopkins University School of Medicine 600 North Wolfe Street, Baltimore, MD 21287, USA Tel: 410 502 5230 Fax: 410 502 5382 Email: rfarkas@jhmi.edu.	
JOURNAL		
COMMENT		
FEATURES		
source	Location/Qualifiers	
	1..791	
	/organism="Rattus norvegicus"	
	/mol_type="mRNA"	
	/strain="Sprague-Dawley"	
	/db_xref="taxon:10116"	
	/tissue_type="Retinal Ganglion Cells"	
	/lab_host="DH10B"	
	/clone_lib="Rat retinal ganglion cell"	
	/notes="Organ: Eye; Vector: pDNR-LIB; Site 1: Sfil; Site 2: Sfil; The library was constructed from purified rat retinal ganglion cells. The Creator SMART cDNA Library method (Clontech) was used. EST analysis was performed on the unamplified, non-normalized, non-subtracted library."	
ORIGIN		
Alignment Scores:		
Pred. No.:	2,91e-101	Length: 791
Score:	904.00	Matches: 183
Percent Similarity:	98.94%	Conservative: 3
Best Local Similarity:	97.34%	Mismatches: 2
Query Match:	97.10%	Indels: 0
DB:	7	Gaps: 0
US-09-830-972-29_COPV_990_1178 (1-189) x CF977898 (1-791)		
Qy	2	ValValAspLeuLeuThrTrpArgAspIleLysThrsGlyValValPheGlyAlaSer 21 
Db	167	GTGTGTTGACTCTCTCTGAGAGACATTAAGAGACTGGAGTGGTGTGGTGCCAGC 226 
Qy	22	LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThraTyrlleAla 41 
Db	227	TTATTCTCTGTCGTCTCTGCAGTGTTCAGCATTTGTCAGTGTAAACGCCCTACATTGCC 286 
Qy	42	LeuAlaIleuLeuSerValThrIleSerPheArgIleTyrlLysGlyValIleGlnAlaIle 61 
Db	287	TTGGCCCTGCTCTCGGTGACTATCAGCTTTTAGGATATATAAAGCGGCTGATCCAGGCTATC 346 
Qy	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrlLeuGluSerGluValAlaIleSer 81 
Db	347	CAGAAATCAGATGAAGGCCACCCTTCAGGGCATATTTAGAATCTGAAGTGTCTATACA 406 
Qy	82	GluGluLeuValGlnLysTyrlSerAsnSerAlaLeuGlyHisValAsnCystrHrileLys 101 

```

Score:          904.00          Matches:          185
Percent Similarity: 98.94%      Conservative:      2
Best Local Similarity: 97.88%    Mismatches:        1
Query Match:       97.10%       Indels:            1
DB:               7            Gaps:              0

US-09-830-972-29_COPY_990_1178 (1-189) x CM641703 (1-1081)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 156 GTTGTGGACCTCTCTACTTGGAGAGACATGAAGACACTGGAGTGGTGTGGTGGCCAGC 215
QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 216 CTATTCTCTGCTCTCTCATTCAGCATTTTACGATTTGAGTGTAAACAGCCTACATTCGC 275
QY 42 LeuAlaLeuLeuSerValThrIle-SerPheArgIleTyrLysGlyValIleGlnAlaI 61
Db 276 TTGGCCCTGCTCTCTGTGACCATCANGCTTTAGGATATACAGGGTGTGATCCAGCTAT 335
QY 61 eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 81
Db 336 CCAGAAATCAGATGAAGGCCACCCATTACAGGCATATCTGGAATCTGGAATTCGCGATATC 395
QY 81 rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLy 101
Db 396 TGAGGAGTTGGTTTCAAGATACAGTAATTTCTGCTCTTGGTCTATGTGAACCTGCACGATAA 455
QY 101 sGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLe 121
Db 456 GGAACCTCAGCGCCCTCTCTTAGTGTATTTAGTGTATTTAGTGTATTTAGTGTATTTAGTGT 515
QY 121 uMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAlaI 141
Db 516 GATGTGGTATTTACCTATGTGGTGGTCTTTGTTTAAATGCTGTACGCTACTGATTTTGGC 575
QY 141 aleuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHi 161
Db 576 TCTCAFTTCACTCTTCAGTGTCTCTGTTATTTATGAAACGGCATCAGGCACAGATAGATCA 635
QY 161 sTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIl 181
Db 636 TTATCTAGACTTGCATAATAGATGTTAAAGATGCTATGGCTAAATCCAGCGAAAT 695
QY 181 eProGlyLeuLysArgLysAlaGlu 189
Db 696 CCTGTGATTGAAGCGCAAGCTGAA 720

RESULT 41
BG623462
LOCUS 602648520F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4770077 5',
DEFINITION mRNA sequence.
ACCESSION BG623462
VERSION BG623462.1 GI:13674833
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 747)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

```

```

Plate: LLCM1636 row: g column: 06
High quality sequence stop: 742.
FEATURES
Location/Qualifiers
1..747
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4770077"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_79"
/note="Organ: placenta; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggccgctcgccc); Site 2: SfiI
(ggcccattatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGCGCGCGCCGACATG-DT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.3
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

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## ORIGIN

```

Alignment Scores:
Pred. No.: 4,74e-101 Length: 747
Score: 902.00 Matches: 183
Percent Similarity: 98.39% Conservative: 0
Best Local Similarity: 98.39% Mismatches: 3
Query Match: 96.89% Indels: 0
DB: 4 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x BG623462 (1-747)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db 133 GTTGTGGACCTCTCTACTTGGAGAGACATTAAGAGACTGGAGTGGTGTGGTGGCCAGC 192
QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 193 CTATTCTCTGCTCTCTCATTCAGCATTTTACGATTTGAGTGTAAACAGCCTACATTCGC 252
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 253 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 312
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 313 CAGAAATCAGATGAAGGCCACCCATTACAGGCATATCTGGAATCTGGAATTCGATATCT 372
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db 373 GAGGAGTTGGTTTCAAGATACAGTAATTTCTGCTCTTGGTCTGTAACCTGCACGATAAAG 432
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 433 GAACCTCAGCGCCCTCTCTTAGTGTATTTAGTGTATTTAGTGTATTTAGTGTATTTAGTGT 492
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141
Db 493 ATGTGGGTATTTACCTATGTTGGTGGCTTTGTTTAAATGTTCTGACACTACTGATTTTGGCT 552
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHi 161
Db 553 CTCATTTCATCTCTCAGTGTCTCTGTATTTATGAACGGCATCAGGCACAGATAGATCAT 612
QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 613 TATCTAGGACTTGCATAATAGATGTTTACAGATGCTCTATGTTAAATCCAGCAAAAATC 672
QY 182 ProGlyLeuLysArgLys 187
Db 673 CCTGGATTGAAGCGCAAA 690

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```
RESULT 42
CO259245
LOCUS 4130644 BARC 8BOV Bos taurus cDNA clone 8BOV_51K20 5', mRNA
DEFINITION sequence.
ACCESSION CO259245
VERSION CO259245.1 GI:49144047
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 585)
Baumann, R.G., Baldwin, R.L., Sonstegard, T.S., Van Tassell, C.P. and
Matukumalli, L.K.
Construction and Analysis of a cDNA Library Generated From
Intestinal Muscle and Epithelial Tissues of Holstein Cattle
Unpublished (2004)
Contact: Richard G. Baumann
Bovine Functional Genomics Lab
ANR1

BLDG 162: BARC-EAST, Beltsville, MD 20705, USA
Tel: 3015048604
Fax: 3015048744
Email: rbaumann@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt '-trim_fasta. Vector identified
by cross_match using options -minmatch 12 -minscore 12
Plate: 51 row: K column: 20
Seq primer: CCTATTAGGTGACACTATAGAAC
High quality sequence stop: 585.
Location/Qualifiers
1. 585
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone="8BOV 51K20"
/sex="Female"
/tissue_type="Epithelial, Muscle"
/dev_stage="Lactating, Neonatal"
/lab_host="DH10B TonA"
/clone_lib="BARC 8BOV"
/organ="Organ: Intestine; Vector: pCMVSPORT6.1; Site 1:
Not1, Site 2: EcoRI; Normalized cow cDNA intestinal mRNA
library in pCMVSPORT6.1, constructed from equimolar mRNA
pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 Lactating, Proximal Duodenum,
Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
Duodenum, Jejunum, Distal Ileum"

ORIGIN
Alignment Scores:
Pred. No.: 5,92e-101 Length: 585
Score: 900.00 Matches: 183
Percent Similarity: 99.46% Conservative: 0
Best Local Similarity: 99.46% Mismatches: 1
Query Match: 96.67% Indels: 0
DB: 7 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x CO259245 (1-585)

Qy 2 ValValAspLeuLeuTyrrTrrArgAspIleYsThrGlyValValPheGlyAlaSer 21
Db 32 GTTGTGTACCTCCTCTACTCGAGACATTAAGAACTGGAGTGGTCTCCGGTCCAGC 91
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrrIleAla 41
Db 92 TTGTTCTTCTGCTCTCCTGACAGTATTCAGCATTTGAGTGTACCGCTACATTGCC 151
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrrYsGlyValIleGlnAlaIle 61
|||||
```

```
Db 152 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAGGGTGTGATCCAGCTATC 211
Qy 62 GlnYsSerAspGluGlyHisProPheArgAlaTyrrLeuGluSerGluValAlaIleSer 81
|||||
Db 212 CAGAAATCTGATGAAGGCCACCCATTTCAGGCAATATTTGGAAATCTGAAGTTGCTATATCT 271
|||||
Qy 82 GluGluLeuValGlnYsTyrrSerAsnSerAlaLeuGlyHisValAsnCythrIleYs 101
|||||
Db 272 GAGGAGTTGGTTTCAGAAAGTACAGCAATTCCTCTCTTGGTCATGTTAACTGCACATAAAA 331
|||||
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuYsPheAlaValLeu 121
Db 332 GAATCTCAGACCCCTCTTCTTAGTTGATTTAGTTAGTTCTCTGAGTGTTCAGTGTG 391
|||||
Qy 122 MetTrpValPheThrTyrrValGlyValAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
|||||
Db 392 ATGTGGGTATTACTATGTTGGTCCCTTGTTCATGCTCTGACACTACTAATTTGGCT 451
|||||
Qy 142 LeuIleSerLeuPheSerValProValIleTyrrGluArgHisGlnAlaGlnIleAspHis 161
|||||
Db 452 CTGATTTCACTCTTTCAGTGTCTCTGTTTATTATGAACGGCATCAGGCGCAATAGATCAT 511
|||||
Qy 162 TyrrLeuGlyLeuAlaAsnYsAsnValYsAspAlaMetAlaYsIleGlnAlaYsIle 181
Db 512 TATCTGGGACTTGCAATAAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAATC 571
|||||
Qy 182 ProGlyLeuYs 185
|||||
Db 572 CCTGGATTGAAG 583
|||||

RESULT 43
BI838242
LOCUS 603083162F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5222534 5',
DEFINITION mRNA sequence.
ACCESSION BI838242
VERSION BI838242.1 GI:15949792
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 742)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1559 row: k column: 15
High quality sequence stop: 734.
Location/Qualifiers
1. 742
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5222534"
/lab_host="DH10B"
/clone_lib="NIH_MGC_120"
/organ="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
```

tracking code 025. Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
Pred. No.: 1,11e-100 Length: 742  
Score: 899.00 Matches: 185  
Percent Similarity: 98.93% Conservative: 0  
Best Local Similarity: 98.93% Mismatches: 1  
Query Match: 96.56% Indels: 1  
DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x B1838242 (1-742)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPhe-GlyAlaSe 21  
Db 135 GTTGTGACCTCTGCTACTGGAGAGACATTAAGACAGCTGGAGTGGTGTGTGGTCCAG 194  
QY 21 rLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAl 41  
Db 195 CCTATTTCCTGCTCTTCATTGACAGTATTTCAGCATTTGAGCGTGAACAGCTTACATTCG 254  
QY 41 AleuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaI 61  
Db 255 CTGGCCCTGCTCTCTGTGACCATCAGCTTAGGATATACAGGCTGTGATCCAGCTAT 314  
QY 61 eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 81  
Db 315 CCAGAAATCAGATGAAGGCCACCCATTCAGGCATATCTGGAATCTGGAATCTGCTATATC 374  
QY 81 rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCyThrIleLy 101  
Db 375 TGAGGAGTGGTTCAGAAGTACAGTAATCTGCTCTTGTGTCATGTAAGTTCGAGTGT 494  
QY 101 sGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValle 121  
Db 435 GGAACCTCAGCGGCTCTCTTAGTTCATGATTTAGTTGATCTCTGAAGTTTGCAGTGT 494  
QY 121 uMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAl 141  
Db 495 GATGTGGGTATTACCTATGTGGTGGTCTGTTTAAATGCTGACACTACTGATTTTGGC 554  
QY 141 AleuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsph 161  
Db 555 TCTCATTTCACTCTTCAGTGTTCCTGTATTATGTAACGCGATCAGGCACAGATGATCA 614  
QY 161 sTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysI 181  
Db 615 TTATCTAGGACTTGCAATAAGAAATCTTAAGATGCTATGGCTAAATCCAGCAAAAT 674  
QY 181 eProGlyLeuLysArgLys 187  
Db 675 CCCTGGATTGAAGCGCAAA 693

## RESULT 44

AK034902  
LOCUS AK034902 3533 bp mRNA linear HTC 03-APR-2004  
DEFINITION Mus musculus 12 days embryo embryonic body between diaphragm region  
and neck cDNA, RIKEN full-length enriched library, clone:9430059L06  
product:RETICULON 4 (NEURITE OUTGROWTH INHIBITOR) (NOGO PROTEIN)  
(FOCCN) (GLUT4 VESICLE 20 KDA PROTEIN) homolog [Rattus  
norvegicus], full insert sequence.

ACCESSION AK034902  
VERSION AK034902.1 GI:26084268  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1  
REFERENCE Carninci, P. and Hayashizaki, Y.  
TITLE High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
JOURNAL 99279253  
MEDLINE

10349636  
2  
REFERENCE  
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
JOURNAL 20499374  
MEDLINE 11042159  
PUBMED  
REFERENCE  
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
TITLE RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
JOURNAL 20530913  
MEDLINE 11076861  
PUBMED  
REFERENCE  
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the  
PANTOM Consortium.  
TITLE Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)  
JOURNAL 20530913  
MEDLINE 11076861  
PUBMED  
REFERENCE  
AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
TITLE Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
JOURNAL 20530913  
MEDLINE 11076861  
PUBMED  
REFERENCE  
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
Hori, F., Imotani, D., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T.,  
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,  
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
Sogabe, Y., Tanaka, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
Muramatsu, M. and Hayashizaki, Y.  
TITLE Direct Submission  
SUBMITTED (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.jp,  
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)  
COMMENT cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/  
LOCATION/Qualifiers  
1. 3533  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="FANTOM DB:9430059L06"  
/db\_xref="taxon:10090"  
/clone="9430059L06"  
/tissue\_type="embryonic body between diaphragm region and  
neck"  
/clone\_lib="RIKEN full-length enriched mouse cDNA library"

/dev\_stage="12 days embryo"

misc\_feature

1. 3533  
/note="RETTICULON 4 (NEURITE OUTGROWTH INHIBITOR) (NOCO PROTEIN) (FOOCEN) (GLUT4 VESICLE 20 KDA PROTEIN) homolog (Rattus norvegicus) (SWISSPROT) [Q9UKL1, evidence: FASTA, 95.8%ID, 100%length, match=1068]"

## ORIGIN

## Alignment Scores:

Pred. No.: 2,42e-99 Length: 3533  
Score: 896.00 Matches: 184  
Percent Similarity: 98.94% Conservative: 2  
Best Local Similarity: 97.87% Mismatches: 2  
Query Match: 96.24% Indels: 0  
DB: 3 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AK034902 (1-3533)

Qy 2 ValValAspLeuLeuTyrTrpArgAspLeuLysThrGlyValValPheGlyAlaSer 21  
Db 740 GTTGTGACCTCTCTACTGAGAGACATTAAGAGACTGGAGTGTGTTGGTCCAGC 799  
Qy 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThAlaTyrIleAla 41  
Db 800 TTATTCCTGCTGCTCTCTGACAGTGTTCAGCATTTGTCAAGTGAACGGCTTACATTGCC 859  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 860 TTGGCCCTGCTCTCTGACTATCATCTTAGATATATAGGGTGTGATCCAGCTATC 919  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 920 CAGAAATCAGATGAAGCCACCCATTCAGGCGATATTTGGAATCTGAAGTTGCCATATCA 979  
Qy 82 GluGluLeuValGlnLysTyrSerAnsSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 980 GAGGAATTTGGTTTCAAAAATATAGTAATCTCTGCTTTGGTTCATGTGAACAGCACATAAA 1039  
Qy 102 GluLeuArgGluLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 1040 GAATTTGAGCGGTCTCTCTTAGTGTATGATTTAGTTGATTCCTGAAGTTTGCAGTGTG 1099  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
Db 1100 ATGTGAGTATTACTTACGTGGTGGTCTTGTTCATGTTTGACACTACTGATTTAGCT 1159  
Qy 142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 1160 CTGATCTCACTCTTCAGTATTCTCTTATATATGAACGGCATCAGGCGCAGATAGATCAT 1219  
Qy 162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 1220 TATCTAGGACTTGAACAACAGAGCGTTAAGATGCCATGGCCAAATCCAGCAAAATC 1279  
Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
Db 1280 CTGGAATTGAGCGCAAGACGAA 1303

## RESULT 45

BI079496

LOCUS

DEFINITION 602876306F1 NCI\_CGAP\_Mam2 Mus musculus cDNA clone IMAGE:5008248 5', mRNA sequence.

ACCESSION BI079496

VERSION BI079496.1

KEYWORDS GI:14497826

SOURCE Mus musculus

ORGANISM Mus musculus (house mouse)

REFERENCE 1 (bases 1 to 781)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

## JOURNAL

## COMMENT

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgapsb@mail.nih.gov](mailto:cgapsb@mail.nih.gov)

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLML1052 row: k column: 01

High quality sequence stop: 773.

## FEATURES

source

1. 781

Location/Qualifiers

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="FVB/N-3"

/db\_xref="taxon:10090"

/clones="IMAGE:5008248"

/tissue type="tumor, biopsy sample"

/dev stage="5 months"

/lab\_host="DH10B"

/clone\_lib="NCI\_CGAP Mam2"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Library constructed by Life Technologies. Investigator

providing samples: Gilbert Smith, NIH"

## ORIGIN

## Alignment Scores:

Pred. No.: 4,96e-100 Length: 781  
Score: 894.00 Matches: 182  
Percent Similarity: 98.40% Conservative: 3  
Best Local Similarity: 96.81% Mismatches: 3  
Query Match: 96.03% Indels: 0  
DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BI079496 (1-781)

Qy 2 ValValAspLeuLeuTyrTrpArgAspLeuLysThrGlyValValPheGlyAlaSer 21  
Db 213 GTTGTGACCTCTCTGACTATCATCTTAGGATATATAGGGTGTGATCCAGCTATC 272  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThAlaTyrIleAla 41  
Db 273 TTATTCCTGCTGCTCTCTGACAGTGTTCAGCAATTGTCAAGTGAACGGCTTACATTGCC 332  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 333 TTGGCCCTGCTCTCTGACTATCATCTTAGGATATATAGGGTGTGATCCAGCTATC 392  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 393 CAGAAATCAGATGAAGCCACCCATTCAGGCGATATTTGGAATCTGAAGTTGCCATATCA 452  
Qy 82 GluGluLeuValGlnLysTyrSerAnsSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 453 GAGGAATTTGGTTTCAAAAATATAGTAATCTCTGCTTTGGTTCATGTGAACAGCACATAAA 512  
Qy 102 GluLeuArgGluLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 513 GAATTTGAGCGGTCTCTCTTAGTGTATGATTTAGTTGATTCCTGAAGTTTGCAGTGTG 572  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141  
Db 573 ATGTGGGTATTACTTACGTGGTGGTCTTGTTCATGCTTGTGTCATGTGAACAGCACATAAA 632  
Qy 142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 633 CTGATCTCACTCTTCAGTATTCTCTTATATATGAACGGGATCAGGCGCAGATCATCAT 692  
Qy 162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

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Db      693  TATCTAGGACTTCACAAAGAGCGTTAAGGATGCCATCGGCAGCAAAATCCAGCAAAAATC 752
QY      182  ProGlyLeuLysArgLysAlaGlu 189
Db      753  CCTGGATTGAAGCGCAAGCAGAT 776

RESULT 46
BG699274
LOCUS   602678946F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4811674 5',
DEFINITION mRNA sequence.
ACCESSION BG699274
VERSION   BG699274.1 GI:13967408
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL   1 (bases 1 to 774)
COMMENT   NIH-MGC http://mgc.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
          Contact: Robert Strausberg, Ph.D.
          Email: cgaabs-r@mail.nih.gov
          Tissue Procurement: Niklos Palkovits, M.D., Ph.D.
          cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
          Toshiyuki and Piero Carninci (RIKEN)
          CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM10702 row: 1 column: 11
          High quality sequence stop: 774.

FEATURES
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/organism="Homo sapiens"
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/clone="IMAGE:4811674"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_95"
/notes="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtccgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTT-3', size-selected for average
insert size 2.5 kb and normalized to 10^5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this
is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 6,52e-100 Length: 774
Score: 893.00 Matches: 186
Percent Similarity: 98.42% Conservative: 1
Best Local Similarity: 97.89% Mismatches: 1
Query Match: 95.92% Indels: 2
DB: 4 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x BG699274 (1-774)

QY      2  ValValAspLeuLeuThrValPheSerIleValSerValThrAla 21
Db      169  GTTGTGACTCTCTGACTGGAGAGACATTAGAGACTGGAGTGTGTGGTGCACG 228
QY      22  LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAla 41
Db      229  CTATTCCTGCTGCTTTTCATTGACAGTATTGAGCATTTGAGCGGTACAGCTACATTGCC 288

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QY      42  LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db      289  TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAAGGTGTGATCCAAAGCTATC 348
QY      62  GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db      349  CAGAAATCAGATCAAGGCCACCCATTAGGATATCTGGATCTTGAAGTTGCTATATCT 408
QY      82  GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db      409  GAGGAGNTGGTTTCAGAGGTACAGTAATCTCTGCTCTTGGTTCATGTGAACTGCACGATAAAG 468
QY      102  GluLeuArgArgLeuPheLeu-ValAspAspLeuValAspSerLeuLysPheAlaValle 121
Db      469  GAACTCAGCGCCCTCTTCTAGCTTGTAGTATTAGTCTCTGAAGTTTGCAGTGT 528
QY      121  uMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
Db      529  GATGGGGTATTACTATGTTGGTCCCTGTTTAAAGTCTGACACTACTGATTTTGGC 588
QY      141  aLeuIleSerLeuPheSer-ValProValIleTyrGluArgHisGlnAlaGlnIleAspH 161
Db      589  TCTCATTTCACTCTTTCAGTTGTTCTGTTATTATGACCGCATCAGGCACAGATAGATC 648
QY      161  istYrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysI 181
Db      649  ATTATCTAGGACTTCCAATAGAAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAA 708
QY      181  leProGlyLeuLysArgLysAlaGlu 189
Db      709  TCCCTGGATTGAAGCGCAAGCTGAA 734

RESULT 47
BG691132
LOCUS   603314519F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5354477 5',
DEFINITION mRNA sequence.
ACCESSION BG691132
VERSION   BG691132.1 GI:15653761
KEYWORDS EST.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE     NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished (1999)
          Contact: Robert Strausberg, Ph.D.
          Email: cgaabs-r@mail.nih.gov
          Tissue Procurement: Jeffrey Green M.D.
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM11901 row: e column: 06
          High quality sequence stop: 758.

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/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam6"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

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Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH

## ORIGIN

Alignment Scores:  
 Pred. No.: 9,276-100 Length: 990  
 Score: 893.00 Matches: 184  
 Percent Similarity: 98.41% Conservative: 2  
 Best Local Similarity: 97.35% Mismatches: 2  
 Query Match: 95.92% Indels: 1  
 DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x B1691132 (1-990)

QY 2 ValValAspLeuLeuTyrTTPArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 DB 63 GTTGTGACCTCTCTGCTGACGACATTAAGAAGCTGGAGTGGTGTGGTCCAGC 122  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 DB 123 TTATTCCTGCTGCTCTGACAGCTTTCAGCATTTGTCAGTGAACGGCTTACATTGCC 182  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLys-GlyValIleGlnAla 61  
 DB 183 TTGGCCCTGCTCTGCTGACTATCATGCTTTAGGATATATAACGGGTGTGATCCAGCTAT 242  
 QY 61 eGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 81  
 DB 243 CCAGAAATCAGATGAAGCCACCCATTCAGGCATATTTGGATCTGAAGTTGCCATATC 302  
 QY 81 rGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 DB 303 AGAGAAATTTGGTTTCAGAAATATAGTAATTCCTCTGCTCATGTGAACAGCACAATAA 362  
 QY 101 sGluLeuArgArgLeuPheLeuValAspLeuValAspLeuSerLeuLysPheAlaValLe 121  
 DB 363 AGAATTTGAGCGCTCTCTCTTGTAGTTGATGATTTAGTTGATTCCTCCCTGAAGTTTGCAGTGT 422  
 QY 121 uMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 DB 423 GATGTGGGTATTTACTTACGTTGGTGGCTTGTTCATGTTTGACACTGATGATTTTACG 482  
 QY 141 aleuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHi 161  
 DB 483 TCTGATCTCACTCTTCAGTATTCCTGTTATATATCAACGGCATCAGCGCGAGATGATCA 542  
 QY 161 sTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 DB 543 TTATCTAGGACTTGCAAAACAAGAGCGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAAT 602  
 QY 181 eProGlyLeuLysArgLysAlaGlu 189  
 DB 603 CCTCGATTTGAAGCGCAAAAGCAGAA 627

RESULT 48  
 BG699748  
 LOCUS 784 bp mRNA linear EST 07-MAY-2001  
 DEFINITION 602681431F1 NIH\_MGC\_95 Homo sapiens cDNA clone IMAGE:4814382 5', mRNA sequence.

ACCESSION BG699748  
 VERSION BG699748.1 GI:13968365  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 784)  
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 cDNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: L1AM10709 row: m column: 07  
 High quality sequence stop: 747.  
 Location/Qualifiers

## FEATURES

source

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 /clone="IMAGE:4814382"  
 /tissue\_type="hippocampus"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH\_MGC\_95"  
 /note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3', size-selected for average insert size 2.5 kb and normalized to 10<sup>7</sup> 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 8,83e-100 Length: 784  
 Score: 892.00 Matches: 186  
 Percent Similarity: 98.94% Conservative: 1  
 Best Local Similarity: 98.41% Mismatches: 0  
 Query Match: 95.81% Indels: 2  
 DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BG699748 (1-784)

QY 2 ValValAspLeuLeuTyrTTPArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 DB 169 GTTGTGACCTCTCTGCTGACGACATTAAGAAGCTGGAGTGGTGTGGTCCAGC 228  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 DB 229 CTATTCCTGCTGCTTTCATTCAGCATTTACAGATTGAGCGTGAACGCTTACATTGCC 288  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 DB 289 TTGGCCCTGCTCTCTGTCACCATCAGCTTTAGGATATACAAAGGTGTGATCCAAGCTATC 348  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 349 CAGAAATCAGATGAAGCGCACCCATTCAGGCATATCTGGAATCTGGAATTTGCTATATCT 408  
 QY 82 GluLeuLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 DB 409 GAGGAGTTGGTTTCAGAGTACAGTAATTCCTCTTGGTCAATGTAACCTGACGATAAG 468  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 DB 469 GAACCTCAGCGCCCTCTCTTAGTTGATGATTTAGTTAGTTCTCTGAAGTTTGCAGTGTG 528  
 QY 122 MetTrpValPheThrTyrValGlyAla-LeuPheAsnGlyLeuThrLeuLeuIleAla 141  
 DB 529 ATGTGGGTATTTACGTATGTTGGTCCCTTTGTTAAATGGTCTGACACTTACTGATTTGGC 588  
 QY 141 aLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHi 161  
 DB 589 TCTCATTTCACTCTCTGCTGCTTCTGTTATTTATGACGGCATCAGGCACAGATAGATCA 648  
 QY 161 sTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181

DB: 649 TTATCTAGACCTGCAAAATGAAGATGTTCAAGATGCTATGGCTAAATCCAAAGCAAAAT 708  
 QY 181 eProGly-LeuLysArgLysAla 188  
 DB 709 CCTGGATTGAAGCGCAAGCT 731

RESULT 49  
 AA986233 718 bp mRNA linear EST 28-MAY-1998  
 uc73q12.y1 Sugano mouse liver mlia Mus musculus cDNA clone  
 IMAGE:1431334.5, similar to TR:Q15801 Q15801  
 NEUROENDOCRINE-SPECIFIC PROTEIN C.; mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, P., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.  
 The WashU-HHMI Mouse EST Project  
 Unpublished (1996)  
 Contact: Marra M/Mouse EST Project  
 WashU-HHMI Mouse EST Project  
 Washington University School of MedicineP  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu

TITLE  
 JOURNAL  
 COMMENT

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:915402  
 Possible reversed clone: similarity on wrong strand  
 Seq primer: primer name ambiguous  
 High quality sequence stop: 489..

FEATURES

source  
 1..718  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:1431334"  
 /sex="female"  
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 /lab\_host="DH10B"  
 /clone\_lib="Sugano mouse liver mlia"  
 /notes="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII (CACTGTGG); Site 2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGGCTCTTTTCTTTTCTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTGGCTTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTTAAAGTGTGG and 3' end primer CGACCTGCAGCTCGAGCACA."

ORIGIN

Alignment Scores:  
 Pred. No.: 1.04e-99 Length: 718  
 Score: 891.00 Matches: 180  
 Percent Similarity: 97.87% Conservative: 4  
 Best Local Similarity: 95.74% Mismatches: 4  
 Query Match: 95.70% Indels: 0

DB: 1 Gaps: 0  
 US-09-830-972-29\_copy\_990\_1178 (1-189) x AA986233 (1-718)  
 QY 2 ValValAspLeuLeuTyrTTPArgAspIleLysVslThrGlyValValPheGlyAlaser 21  
 DB 155 GTTGTGACCTCTCTGTACTGGAGACATTAAGAAGACTGGAGTGGTGTGGTGGCCAGC 214  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThralaTyrIleAla 41  
 DB 215 TTATTCCTGCTGCTCTCTGACAGTGTTCAGCAITGTTCAGTGTAAAGCGCTTACATTC 274  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 DB 275 TTGGCCCTGCTCTCTGTGACTATCATCTAGTATATTAAGGGTGTGATCCAAGCTATC 334  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 335 CAGAATTCAGATGAAGGCCACCCANTTCAGGGATATTTGGAAATCTGAAGTTGCCATATCA 394  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 DB 395 GAGGAATTGGTTTCAGAAATATAGTAATCTCTCTTGGTCAATGTGAACAGCACAATAA 454  
 QY 102 GluLeuArgArgLeuPheLeuValAspIleValAspSerLeuLysPheAlaValLeu 121  
 DB 455 GAATTGAGCGCTCTCTTCTAGTATTTAGTTGATTCCTCGAAGTTTCAGCTGTG 514  
 QY 122 MetTTPValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 DB 515 ATGTGGGTATTTACTTACGTGGTGGCTTGTTCANTGGTTTGACACTACTGATTTAGCT 574  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 DB 575 CTGATCTCACTCTTCAGTATTCTCTTATATATGAACGCATCAGCGCGCAGATAGATCAT 634  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 DB 635 TATCTAGGACTTGCACCAAGACGCTTAAGGATGCCATGGCGCAAAATCCAAAGCAAAATC 694  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 DB 695 CCTGGATTGAGCGCAGGCAGAA 718

RESULT 50

BU950008

LOCUS

DEFINITION

BU950008

in63d05.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6126776 5'

similar to TR:Q9Y2Y7 Q9Y2Y7 FOCEN-M. [2] TR:O94962 ;, mRNA

sequence.

ACCESSION

BU950008

VERSION

BU950008.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 569)

AUTHORS

Mellon, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,

Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,

Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,

Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,

Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarishvili, R.,

Williams, T., Jackson, Y., and Bowers, Y.

Endocrine Pancreas Consortium

Unpublished (2000)

TITLE

JOURNAL

COMMENT

Other\_ESTs: in63d05.xl  
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium  
 Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
 MA 02138

Tel: 617-495-1812

Fax: 617-495-8557  
 Email: dmelton@biohp.harvard.edu  
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:  
 Washington University Genome Sequencing Center For information on  
 obtaining a clone please contact: Dr. Hiroshi Inoue  
 (hinoue@im.wustl.edu)  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 488.  
 Location/Qualifiers  
 1. 569  
 /organism="Homo sapiens"  
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 /clone\_lib="HR85 islet"  
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 NotI; Site\_2: XhoI; cDNA made by oligo-dT priming.  
 Size-selected on agarose gel. Average insert size ~1kb. 5'  
 XhoI site was destroyed after directional cloning.  
 Amplified once. Contact information: Hiroshi Inoue, MD,  
 Metabolism Div. (Alan Permutt Lab), Washington University  
 School of Medicine, Box 8127, 660 South Euclid Ave., St.  
 Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:  
 314-362-1916, Fax: 314-747-2692."

# FEATURES source

QY 188 AlaGlu 189  
 |||||  
 Db 552 GCTGAA 557  
 RESULT 51  
 BG296048  
 LOCUS  
 DEFINITION  
 602393712F1 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:4505499 5',  
 mRNA sequence.  
 ACCESSION  
 BG296048  
 VERSION  
 BG296048.1 GI:13058293  
 KEYWORDS  
 EST.  
 SOURCE  
 Mus musculus (house mouse)  
 ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE  
 1 (bases 1 to 749)  
 AUTHORS  
 NIH-MGC http://mgc.nci.nih.gov/  
 TITLE  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL  
 Unpublished (1999)  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: c9apbs-remail.nih.gov  
 Tissue Procurement: The Cepko Laboratory  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM10379 row: g column: 04  
 High quality sequence stop: 745.  
 Location/Qualifiers  
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 /clone\_lib="NIH\_MGC\_94"  
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 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 3.3 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

## FEATURES source

## ORIGIN

Alignment Scores:  
 Pred. No.: 4.59e-99 Length: 749  
 Score: 886.00 Matches: 181  
 Percent Similarity: 98.90% Conservative: 2  
 Best Local Similarity: 97.31% Mismatches: 3  
 Query Match: 95.17% Indels: 0  
 DB: 4 Gaps: 0  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x BG296048 (1-749)  
 QY 2 ValValAspLeuLeuTyrTrrArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 125 GTTGTGACCTCTCTGTGACATTAAGAGACTGGAGTGGTGTGGTGGCCAGC 184  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 185 TTATTCTTCGCTGCTCTCTGACAGTGTTCAGCATTTGACGCTTAACGGCTTACATTGCC 244  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 245 TTGGCCCTGCTCTCTGTGACATTAAGAGACTGGAGTGGTGTGGTGGCCAGC 304  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 305 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCCATATCA 364

QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 365 GAGGAATGGTTTCAGAAATATAGTAATCTGCTCTTGGTCATGTGAACACCAATAAAA 424  
 QY 102 GluLeuArgGlnLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 425 GAATTGAGCGGCTCTCTTAGTTGATGATTTAGTTGATTCCTGGAAGTTTGAGGTG 484  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 485 ATGTGGGATTTACTTACGTTGGTCTGTTGTTCAATGGTTTGACACTACTGATTTAGCT 544  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 545 CTGATCTCACTCTTCATGATTTCTGTTATATATATGAACGCGCATCAGCGGAGATGATCAT 604  
 QY 162 TyrLeuGlyLeuAlaAsnIleValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 605 TATCTAGGACTTGCAAAACAGAGCGTTAAGGATGCGCATGGCCAAATCCAGCAAAATCC 664  
 QY 182 ProGlyLeuLysArgLys 187  
 Db 665 CTGTGGATTGAAGCGCAAG 682

RESULT 52  
 AF125103 1798 bp mRNA linear HTC 22-MAY-2001  
 LOCUS Homo sapiens neuroendocrine specific protein c homolog mRNA,  
 DEFINITION complete cds.  
 ACCESSION AF125103  
 VERSION AF125103.1 GI:5107001  
 KEYWORDS HTC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 1798)  
 Zhang, Q.H., Ye, M., Wu, X.Y., Ren, S.X., Zhao, M., Zhao, C.J., Fu, G.,  
 Shen, Y., Fan, H.Y., Lu, G., Zhong, M., Xu, X.R., Han, Z.G., Zhang, J.W.,  
 Tao, J., Huang, Q.H., Zhou, J., Hu, G.X., Gu, J., Chen, S.J. and Chen, Z.  
 Cloning and functional analysis of cDNAs with open reading frames  
 for 300 previously undefined genes expressed in CD34+ hematopoietic  
 stem/progenitor cells  
 Genome Res. 10 (10), 1546-1560 (2000)  
 20499367  
 11042152  
 REFERENCE 2 (bases 1 to 1798)  
 Ye, M., Zhang, Q., Zhou, J., Shen, Y., Guan, Z., Wu, X., Fan, H., Mao, H.,  
 Dai, M., Huang, Q., Chen, S. and Chen, Z.  
 Human neuroendocrine specific protein c homolog mRNA, complete cds  
 Unpublished  
 TITLE 3 (bases 1 to 1798)  
 Ye, M., Zhang, Q., Zhou, J., Shen, Y., Guan, Z., Wu, X., Fan, H., Mao, H.,  
 Dai, M., Huang, Q., Chen, S. and Chen, Z.  
 Direct Submission  
 JOURNAL Submitted (02-FEB-1999) Shanghai Institute of Hematology, Shanghai  
 Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road II,  
 Shanghai 200025, P. R. China  
 REFERENCE Location/Qualifiers  
 1. 1798  
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 /mol\_type="mRNA"  
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## FEATURES

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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
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## ORIGIN

## Alignment Scores:

Pred. No.: 1.6e-98 Length: 1798  
 Score: 886.00 Matches: 187  
 Percent Similarity: 98.94% Conservative: 0  
 Best Local Similarity: 98.94% Mismatches: 1  
 Query Match: 95.17% Indels: 2  
 DB: 3 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x AF125103 (1-1798)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 248 GTTGTGTGACCTCTCTACTGAGAGACATTAAAGAGCTGGAGTGGTGTGTGGTGCAGC 307  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 308 CTATTCTGCTGCTCTTCAATGACAGTATTCAGATTGTGAGCGTAACACCTACATTGCC 367  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 368 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 427  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 428 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 487  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 488 GAGGAGTTGGTTCAAGATACAGTAATCTCTGCTCTTGGTCATGTGACTGCACGATAAG 547  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 548 GAATCAGCGCGCTCTCTCTAGTATGATTTAGTTGATCTCTCAAGTTTGCAGTGTG 607  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 608 ATGTGGGTATTTACCTATGTTGGTGCCTTGTGTTAATGGTCTGACACTACTGATTTGGGT 667  
 QY 142 LeuIleSerLeu-PheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 668 CTCATTTCACTCTCTCAGTGTCTCTGTTATTTA-GAAGCGCATCAGCACAGATAGATCA 726  
 QY 161 sTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 727 TTATCTAGGACTTGCAAAATAGAAATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAAAT 786  
 QY 181 eProGlyLeuLysArgLysAlaGlu 189  
 Db 787 CCTGTGATTGAAGCGCAAAAGCTGAA 811

## RESULT 53

## CR548792

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

CR548792 683 bp mRNA linear EST 12-JUL-2004  
 DKFZp469H1132\_r1 469 (synonym: pkid1) Pongo pygmaeus CDNA clone  
 DKFZp469H1132 5', mRNA sequence.

CR548792

CR548792.1 GI:50242416

EST.

Pongo pygmaeus (orangutan)

Pongo pygmaeus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.

1 (bases 1 to 683)

Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,

Pobo, G., Han, M. and Wiemann, S.

Pongo pygmaeus mRNA (Bahr, A., Lauber, J., Mewes, H.W., et al.)

Unpublished (2004)

Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp469H1132) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at <http://mips.gsf.de/projects/cdna/>.

## FEATURES

source  
1..683  
/organism="Pongo pygmaeus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9600"  
/clone="DKFZp469H1132"  
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## ORIGIN

Alignment Scores:  
Pred. No.: 5,35e-99 Length: 683  
Score: 885.00 Matches: 179  
Percent Similarity: 98.90% Conservative: 0  
Best Local Similarity: 98.90% Mismatches: 2  
Query Match: 95.06% Indels: 0  
DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CR548792 (1-683)

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 140 GTTGTGACCTCTCTACTGGAGACACATTAGAAGACTGGAGTGGTGTGGTCCAGC 199  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 200 CTATTCTCTGCTCTTTCATTGACAGTATTGACAGTATTGAGTGTAAAGCTTACATTCGCC 259  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 260 TTGGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAAAGGTTGATCCAGCTATC 319  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
Db 320 CAGAAATCAGATGAAGGCCACCCATTACGGGCATATCTGGAATCTGGAATCTGCTATATCT 379  
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 380 GAGGAGTGGTTTCAGAAATACAGTAAATCTGCTCTGTGTCATGTAAGTGCACGATAAG 439  
Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 440 GNACTCAGCGCCCTCTTCTAGTGTATGATTAGTTGATTCTCTGAAGTTGCACTGTG 499  
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
Db 500 ATGTGGGTATTTACCTATGTTGGTGCCTGTTTAAATGCTGTCAGCTACTGATTTGGCT 559  
Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
Db 560 CTCATTCTCACTCTCAGTGCTCCTGTATTTATGAACGGCATCAGGCACAGATAGATCAT 619  
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
Db 620 TATCTAGGACTTGCATAAATGAAGATGTTAAAGATGCTATGGCTAAATTCNAGCGAAATC 679  
Qy 182 Pro 182  
Db 680 CCT 682

## RESULT 54

BI544917  
LOCUS  
DEFINITION 603242368P1 NIH\_MGC\_95 Homo sapiens cDNA clone IMAGE:5284672 5',  
mRNA sequence.  
ACCESSION BI544917  
VERSION BI544917.1 GI:15432229  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 731)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L1A011719 row: h column: 17  
High quality sequence stop: 724.  
FEATURES  
source  
1..731  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5284672"  
/tissue\_type="hippocampus"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_95"  
/note="Organ: brain; Vector: pBluescriptR (modified  
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI  
(gtcgag); Oligo-dT primed using primer  
5'-TTTTTTTTTTTTTTVN-3', size-selected for average  
insert size 2.5 kb and normalized to 10^5. This is a  
primary library enriched for full-length clones and  
constructed using the Cap-trapper method (Carninci, in  
preparation). Library constructed by M. Brownstein  
(NIH/NHGRI, National Institutes of Health). Note: this  
is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
Pred. No.: 1.39e-98 Length: 731  
Score: 882.00 Matches: 179  
Percent Similarity: 99.44% Conservative: 0  
Best Local Similarity: 99.44% Mismatches: 1  
Query Match: 94.74% Indels: 0  
DB: 4 Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x BI544917 (1-731)  
Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
Db 191 GTTGTGACCTCTCTACTGGAGACACATTAGAAGACTGGAGTGGTGTGGTCCAGC 250  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
Db 251 CTATTCTCTGCTCTTTCATTGACAGTATTGACGCTTGTGAGCGTAACAGCTTACATTCGC 310  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
Db 311 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATTAAGGGTGTGATCCAGCTATC 370  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81

Db 371 CAGAAATCAGATGAGAGCCACCATTCAGGCATATCTCGAATCTGCAAGTTCGTATATCT 430

QY 82 GluGluLeuValGlnIlystYrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 |||||  
 Db 431 GAGGAGTTGGTTTTCAGAAAGTACAGTAAATCTCTGCTCTTGGTCAATGCACTGCACGATAAAG 490

QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspLeuValAspLeuValLeu 121  
 |||||  
 Db 491 GAACTCAGGCGCTCTCTCTAGTTGATGATTTAGTTGATCTCTGAAAGTTTCAGGTG 550

QY 122 MetTrpValPheThrYrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 |||||  
 Db 551 AATGGGTAATTTACCTATGTTGGTGGCTTGTGTTAATGGTCTGCACACTACTGATTTGGCT 610

QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 |||||  
 Db 611 CTCATTTCACTCTCTCAGTGTCTCTGTTATTTATGAAACGGCATCAGGCACAGATAGATCAT 670

QY 162 TyrLeuGlyLeuAlaAsnLysValIlyAspAlaMetAlaIlystIleGlnAlaIlystIle 181  
 |||||  
 Db 671 TATCTAGGACTTGCATAAATAAGATGTTAAAGATGCTATGGTAAATAATCCAGCAAAATC 730

RESULT 55  
 BU503291  
 LOCUS AGENCOURT\_8933519 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:6490526  
 DEFINITION 5', mRNA sequence.  
 ACCESSION BU503291  
 VERSION BU503291.1 GI:22809480  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 921)  
 NIH-MGC <http://imgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 EMAIL: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
 Tissue procurement: The Cepko Laboratory  
 cDNA library preparation: Life Technologies, Inc.  
 cDNA library arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM14040 row: h column: 15  
 High quality sequence stop: 627.  
 Location/Qualifiers  
 1..921  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:6490526"  
 /tissue\_type="retina"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 94"  
 /note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 3.3 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

FEATURES  
source

## ORIGIN

## Alignment Scores:

Pred. No.: 1 93e-98 Length: 921  
 Score: 882.00 Matches: 181  
 Percent Similarity: 98.94% Conservative: 5  
 Best Local Similarity: 96.28% Mismatches: 1  
 Query Match: 94.74% Indels: 1  
 DB: 5 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BU503291 (1-921)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 |||||  
 Db 156 GTTGTGTACCTCCTCTACTTGGAGAGACATTAAGAAAGACTGGAGTGGTGTGTGGTGCAGC 215

QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 |||||  
 Db 216 TTATTCCTGCTGCTCTCTGACAGTTCACATTTGTCAGTGTAAACGGCCCTACATTGCC 275

QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 |||||  
 Db 276 TTGGCCCTGCTCTCTGTGACATATCAGCTTTAGATATATAAGGTGTGATCCAGCTATC 335

QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 |||||  
 Db 336 CAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATTTGGAATCTCAAGTTGCCATATCA 395

QY 82 GluGluLeuValGlnIlystYrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 |||||  
 Db 396 GAGGAATTTGGTTTCAGAAATATAGTAATTTCTGCTCTTGGTCAATGCAACAGCAATAAAA 455

QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 |||||  
 Db 456 GAATTTAGGCGTCTCTCTTAGTTGATGATTTAGTTGATTCCTCTGAAGTTTCAGTGTG 515

QY 122 MetTrpValPheThrYrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 |||||  
 Db 516 ATGTGGTATTTACTTACGTTGGTGCCTTGTTCATATGGTTTGACACTACTGATTTAGCT 575

QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 |||||  
 Db 576 CTGATCTCACTCTTCAGTATTCCTGTTATATATGAACGCATCAGCGCGCAGATAGATCAT 635

QY 162 TyrLeuGlyLeuAlaAsnLysValIlyAspAlaMetAlaIlystIleGlnAlaIlystIle 181  
 |||||  
 Db 636 TATCTAGGACTTGCATAAACAAGAGCGTTAAGGATGCGTCCCAATCCAGCAAAATC 695

QY 182 Pro-GlyLeuLysArgLysAla 188  
 |||||  
 Db 696 CCTTGGATTAAGCGCCAAAGC 717

## RESULT 56

## CO504431

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

CO504431 647 bp mRNA linear EST 13-JUL-2004  
 GGEZCB1023A09.g chicken breast muscle - CB1 Gallus gallus cDNA  
 clone GGEZCB1023A09, mRNA sequence.

CO504431  
 CO504431.1 GI:50274617

EST.  
 Gallus gallus (chicken)

Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.

1 (bases 1 to 647)

Alves,H.J., Jorge,E.C., Marchesin,M.L., Monteiro-Vitorello,C.B.,  
 Patricio,M., Leduc,M.C. and Coutinho,L.L.

Discovery of new genes expressed in the chicken breast muscle

Unpublished (2004)

Contact: Helena J. Alves

Laboratory of Animal Biotechnology, Dep. of Animal Production

ESALQ - University of Sao Paulo

Av. Padua Dias, 11, Piracicaba, SP, 13418-900, Brazil

Tel: 55 19 3429 4434

Fax: 55 19 3429 4285

Email: [hjalves@esalq.usp.br](mailto:hjalves@esalq.usp.br) and [llcoutin@esalq.usp.br](mailto:llcoutin@esalq.usp.br)

PCR Primers

BACKWARD: T7.

Location/Qualifiers

1..647

/organism="Gallus gallus"

/mol\_type="mRNA"

## FEATURES

## source

```

/db xref="taxon:9031"
/clone="GB2CB1023A09"
/tissue_type="breast muscle"
/dev_stage="1 and 21 days old"
/lab_host="DH5 alpha"
/clone_lib="chicken breast muscle - CB1"
/notes="Vector: pSPORI1; Site 1: NotI; Site 2: SalI; This
cDNA library was constructed with the SuperScript Plasmid
System with Gateway Technology kit (Invitrogen), following
manufacturer's protocols. Plasmid DNA was purified using a
modified alkaline lysis method. Sequencing reactions were
conducted using the DYEnamic Cycle Sequencing Kit for
MegABACE (Amersham biosciences) according to the
manufacturer's recommendations. Clones were sequenced by
the 5' end with T7 primer. Sequencing reactions were
analyzed on MegaBACE1000 DNA Sequencer (Amersham
biosciences). The quality and clustering of the ESTs were
analyzed using the softwares Phred/Gap3. Only EST
sequences with Phred quality greater than 20 and at least
150 bp were considered for clustering."

```

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.55e-98 Length: 647  
 Score: 881.00 Matches: 176  
 Percent Similarity: 97.34% Conservative: 7  
 Best Local Similarity: 93.62% Mismatches: 5  
 Query Match: 94.63% Indels: 0  
 DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CO504431 (1-647)

```

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 54 GTTGTGGACCTCTTACTGGCGAGACATTAGAAGACAGGAGTGGTGTGGTCCAGC 113

Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 114 TTGTTCTCTGCTCTCTAATAACAGTGTTCAGCATCGTGGAGGTGACAGCTTACATTGCC 173

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 174 TTGGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAAGGGAGTGTATCCAGGCAATC 233

Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 234 CAAAGTCCGATGAAGGCCCATCTTTAGGGCTTACTTGGAGTCTGATGTAGTGTGTGTCT 293

Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCyseThrIleLys 101
Db 294 GAAGAGCTGATTCAGAAATACAGCAGTCTTGTGCTTGTCTCATCAACGGCACAGTCAAG 353

Qy 102 GluLeuArgArgLeuPheLeuValAspSerLeuValAspSerLeuLysPheAlaValLeu 121
Db 354 GAGCTGAGACGCTCTCTCTGCTGATGACCTTGTGTGATCTCTCAAGTTTGCAGTGTG 413

Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
Db 414 ATGTGGGTGTTCACTTACGTGGTGCTCTGTTTAAATGTCGACATTAATGATCTGCT 473

Qy 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 474 TTGATTTCTGCTTTCAGTGTCTCTTATTTATGAGACATCAGGCCAGATCGACCAT 533

Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 534 TATTTGGGACAGTCAACAAGAACCTCAAGATGCGATGGCAAGATCCAAGCAAGATC 593

Qy 182 ProGlyLeuLysArgLysAlaGlu 189
Db 594 CTTGGGCTGAAGCGNCAACTGAG 617

```

RESULT 57

CK357937

LOCUS CK357937 751 bp mRNA linear EST 23-DEC-2003  
 DEFINITION AGENCOURT 17155981 NIH\_MGC\_233 Rattus norvegicus cDNA clone  
 IMAGE:7105386 5', mRNA sequence.

ACCESSION CK357937

VERSION CK357937.1 GI:40323869

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus (Norway rat)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE 1 (bases 1 to 751)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement: Howard Jacobs

cDNA Library Preparation: Express Genomics

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LHAM14964 row: g column: 16

High quality sequence stop: 685.

FEATURES

source

1. 751

/organism="Rattus norvegicus"

/mol\_type="mRNA"

/db\_xref="taxon:10116"

/clone="IMAGE:7105386"

/tissue\_type="heart, pooled"

/lab\_host="DH10B Tona"

/clone\_lib="NIH\_MGC\_233"

/note="Organ: heart; Vector: pExpress-1; Site 1: EcorV;  
 Site 2: NotI; RNA obtained from pooled heart tissue from a  
 mix of male and female animals at 8 wk old. Tissues were  
 snap-frozen and kept at -80C for two days before RNA  
 extraction and purification (Tri-reagent method). cDNA was  
 primed using oligo-dT primer:  
 5'-pCAGTAGTTCTAGATCGGACGCGCCGCTT)25-3' and cloned into  
 the EcorV/NotI sites of pExpress-1. Size-selection >1.4kb  
 resulted in an average insert size of 2 kb. This primary  
 library is not normalized (normalized primary library is  
 NIH\_MGC\_234) and was constructed by Express Genomics  
 (Frederick, MD). Note: this is a NIH\_MGC library."

## ORIGIN

Alignment Scores:

Pred. No.: 1.92e-98 Length: 751  
 Score: 881.00 Matches: 179  
 Percent Similarity: 97.31% Conservative: 2  
 Best Local Similarity: 96.24% Mismatches: 5  
 Query Match: 94.63% Indels: 0  
 DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CK357937 (1-751)

```

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 159 GTTGTGACCTCTCTACTGGAGACATTAGAAGACTGGAGTGGTGTGGTCCAGC 218

Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 219 TTATTCCTGCTGCTCTCTGACAGTGTTCAGCATTTGTCAGTGAACGCTTACATTGCC 278

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

```

Db 279 TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAGGGCGGTGATCCAGGCTATC 338  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaLysSer 81  
 Db 339 CAGAAATCAGATCAGAGCCACCCATTCAGGCGCATATTTAGAAATCTGAAGTTGCTATATCA 398  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 399 GAGGAATTCGGTTTCAGAAATACAGTAATCTGCTCTTTGGTTCATGTGAACAGCAATAAAAA 458  
 QY 102 GluLeuArgGluLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 459 GAACGAGCGCGCTTCTTAGTTGATTTAGTTGATTCCTCGAAGTTTCAGGTGTTG 518  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 519 ATGTGGGTGTTACTTATGTTGGTCTGTTCAATGGTCTGACACTACTGATTTTAGCT 578  
 QY 142 LeuLysSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 579 CTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCAT 638  
 QY 162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 639 TATCTAGGACTTGCAACAGAGTGTTAAGGATGCCATGGCCANNATCCAGCAAAAATC 698  
 QY 182 ProGlyLeuLysArgLys 187  
 Db 699 CCTGGATTGAAGCGCAAG 716

RESULT 58  
 CN219472 821 bp mRNA linear EST 08-APR-2004  
 LOCUS WLA006H01.ab1 WLBRAIN Gallus gallus cDNA 5', mRNA sequence.  
 DEFINITION CN219472  
 VERSION CN219472.1 GI:46298814  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 821)

REFERENCE Savolainen, P., Fitzsimmons, C.J., Arvestad, L., Andersson, L. and  
 Lundberg, J.  
 EST analysis of brain and testis cDNA libraries from White Leghorn  
 and Red Jungle Fowl  
 Unpublished (2004)  
 JOURNAL Contact: Peter Savolainen  
 COMMENT Department of Biotechnology  
 Royal Institute of Technology, KTH  
 SE-106 91 Stockholm, SWEDEN  
 Tel: +46 (0) 8 5537 8481  
 Fax: +46 (0) 8 5537 8335  
 Email: Peter.Savolainen@biotech.kth.se

Seq primer: M13 reverse primer.  
 Location/Qualifiers  
 1..821

FEATURES  
 source  
 1..821  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="White Leghorn"  
 /db\_xref="taxon:9031"  
 /sex="female"  
 /lab\_host="ElectronMAX DH10B (Invitrogen)"  
 /clone\_lib="WLBRAIN"  
 /notes="Organ: brain; Vector: pSPORT-1; Site 1: Hind III;  
 Site 2: EcoRI; The cDNA libraries were created with the  
 Superscript Plasmid System (Invitrogen)."

## ORIGIN

Alignment Scores: 2.9e-98 Length: 821  
 Pred. No.: 880.00 Matches: 176  
 Score:

Percent Similarity: 97.85% Conservative: 6  
 Best Local Similarity: 94.62% Mismatches: 4  
 Query Match: 7 Indels: 0  
 DB: Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CN219472 (1-821)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 177 GTTGTGTGACCTCCTTTACTGGCGAGACATTAAAGACAGAGGAGTGGTGTGGTGCAGC 236  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 237 TTGTCTCTGCTCTCTCATTAAACAGTTCAGCATCGTGAGCGTGACACCTTACATGTC 296  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 297 TTGGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAGGAGGAGTTATCCAGGCAATC 356  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaLysSer 81  
 Db 357 CAAAAGTCCGATGAAGGCCATCCATTTAGGGCTTACTTTGAGTCTGATGTGTGTCT 416  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 417 GAAGAGCTGATTGAGAAATACAGCAGTGTGTGCTGTGTGCATCAACGGCAGTCAAG 476  
 QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 477 GAGCTGAGAGCGCTCTCTTCCTCGTTCATGACTTGGTTGATTCTCTGAAGTTTCAGTGTG 536  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 537 ATGTGGGTGTTTACCTTACCTGCTGCTTTTAAATGGTCTGACATTTACTGATCTGGCT 596  
 QY 142 LeuLysSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 597 TTGATTTCTGCTGTTTCTGAGTGTCTCTGTTATTATGAGACATCAGGCCAGATCGACCAT 656  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 657 TATTTGGGACTAGTGAACAAAGACGTCAAAGATGCGATGGCAAGATCCCAAGCAAGATC 716  
 QY 182 ProGlyLeuLysArgLys 187  
 Db 717 CCTGGCTGAAGCGCAAA 734

## RESULT 59

CK305449

LOCUS

DEFINITION

SB02029A2B02.f1 normalized Keck-Tegu Library SB02 Taeniopygia

guttata cDNA clone SB02029A2B02.f1 5, mRNA sequence.

CK305449

ACCESSION

CK305449.1 GI:44815023

VERSION

EST

KEYWORDS

Taeniopygia guttata

ORGANISM

Taeniopygia guttata

REFERENCE

AUTHORS

1 (bases 1 to 736)

Clayton, D.F., Arnold, A.P., Ball, G.F., Branowitz, E., George, J.M.,

Mello, C.V., Wade, J., Replogle, K., Lewin, H., Band, M., Hernandez, A.

and Liu, L.

The Songbird Neurogenomics Initiative: An Evolving Public Resource

for Study of Genes, Brain, and Behavior

Unpublished (2004)

JOURNAL

COMMENT

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University of Illinois

Bi07 CUSL, 601 S. Goodwin, Urbana, IL 61801, USA

Tel: 217 244 3668

Fax: 217 244 1648

Email: dclayton@uiuc.edu



Base Calling/Quality Scores: PHRED from Washington University Genome Center.  
 Vector Trimming: Cross match from Washington University Genome Center PHRAP suite. Low quality bases (Phred score < 20) were trimmed from both ends of the sequence by an in-house script.  
 This sequence is vector free and at least 200 bp in length. Funded by PHS grant # RO1 NS045264, 'Songbird Neurogenomics Initiative.'

PCR Primers

FORWARD: TAATACGACTCACTATAGG (T7)

BACKWARD: ATTAACCTCACTAAAG (T3)

Insert Length: 736 Std Error: 0.00

Plate: SB02029A2 row: B column: 02

Seq primer: TAATACGACTCACTATAGG (T7)

High quality sequence stop: 736.

#### FEATURES

source

Location/Qualifiers

1..736

/organism="Taeniopygia guttata"

/mol\_type="mRNA"

/db\_xref="taxon:59729"

/clone="SB02029A2B02.f1"

/tissue\_type="brain"

/dev\_stage="late embryo, post-hatch days 1, 10, 20, 45,

and adult (pooled)"

/lab\_host="DH10B"

/clone\_lib="normalized Keck-Tagu Library SB02"

/note="Organ: brain; Vector: pBS II SK(+); Site 1:

EcoRI(5' side of insert); Site 2: NotI (3' side of

insert); The library was constructed and normalized as

described by Bonaldo, M.F., Lennon, G. and Soares, M.B.

(1996), Genome Research 6(9): 791-806. An identifying tag

was added at the 3' during cDNA synthesis:

insertAAAAAAAAAAAAAAAAAATGCGA."

#### ORIGIN

##### Alignment Scores:

Pred. No.: 7,78e-98 Length: 736  
 Score: 876.00 Matches: 175  
 Percent Similarity: 96.81% Conservative: 7  
 Best Local Similarity: 93.09% Mismatches: 6  
 Query Match: 94.03% Indels: 0  
 DB: 7 Gaps: 0

US-09-830-972-29\_copy\_990\_1178 (1-189) x CK305449 (1-736)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 DB 125 GTTGTTGACCTCTTTCTGGCGACATATAGAGACCGGGTGTGTTGGAGCCAGC 184  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 DB 185 TTGTTCTGCTGCTCTCAATTAACAGTGTTCAGCATCGTGAGTGTCCAGCCCTACATTGCC 244  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 DB 245 CTGGCCCTGCTCTCTGTCAACATCAGCTTTAGGATATACAGGAGTATCCAGGCAATC 304  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 305 CAGAGTCTGATGAGGGGCCACCCCTTCAGGGCTTACCTGGACTCGGATGTGGCGGTGTCG 364  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 DB 365 GAGGAGCTCATCCAGAGTACAGCAACGTCGTGCTGGCCACGTCGTAACGGCACCGTCGGG 424  
 QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 DB 425 GAGCTGCGCGCGCTCTCTCTGTCGATGACCTGTGGTATCCCTCAAGTTCGCGAGTATG 484  
 QY 122 MetTrpValPheThrTyrValGlyValAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
 DB 485 ATGTGGTTTTTCACTTACGTGGTGGCTGTGTTCAATGGTCTGACATCTACTGCTGCT 544  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161

DB 545 TTGATTTCCGCTCTTTCAGTGTCTCTTATTATGAGACATCAGGCCCAATCGACCAT 604  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 DB 605 TACCTGGGACTTGTGAACAGAACGTCAAAGATGCCATGGCAAGATCCAGCAAGATC 664  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 DB 665 CTGGGTTGAAGCGCAAAACTGAA 688  
 RESULT 60  
 CK303615  
 LOCUS  
 DEFINITION  
 SB02018AIG04.f1 normalized Keck-Tagu Library SB02 Taeniopygia  
 guttata cDNA clone SB02018AIG04.f1 5, mRNA sequence.  
 ACCESSION  
 CK303615  
 VERSION  
 CK303615.1 GI:44813189  
 KEYWORDS  
 EST.  
 SOURCE  
 Taeniopygia guttata  
 ORGANISM  
 Taeniopygia guttata  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Passeriformes; Estrilidae;  
 Estrilidae; Taeniopygia.  
 REFERENCE  
 1 (bases 1 to 765)  
 AUTHORS  
 Clayton,D.F., Arnold,A.P., Ball,G.F., Brenowitz,E., George,J.M.,  
 Mello,C.V., Wade,J., Reppogle,K., Lewin,H., Band,M., Hernandez,A.  
 and Lib,L.  
 The Songbird Neurogenomics Initiative: An Evolving Public Resource  
 for Study of Genes, Brain, and Behavior  
 Unpublished (2004)  
 JOURNAL  
 COMMENT  
 Contact: David F. Clayton  
 University of Illinois  
 B107 CLSL, 601 S. Goodwin, Urbana, IL 61801, USA  
 Tel: 217 244 3668  
 Fax: 217 244 1648  
 Email: dclayton@uiuc.edu  
 Base Calling/Quality Scores: PHRED from Washington University  
 Genome Center.  
 Vector Trimming: Cross match from Washington University Genome  
 Center PHRAP suite. Low quality bases (Phred score < 20) were  
 trimmed from both ends of the sequence by an in-house script.  
 This sequence is vector free and at least 200 bp in length. Funded  
 by PHS grant # RO1 NS045264, 'Songbird Neurogenomics Initiative.'  
 PCR Primers  
 FORWARD: TAATACGACTCACTATAGG (T7)  
 BACKWARD: ATTAACCTCACTAAAG (T3)  
 Insert Length: 765 Std Error: 0.00  
 Plate: SB02018A1 row: G column: 04  
 Seq primer: TAATACGACTCACTATAGG (T7)  
 High quality sequence stop: 765.  
 Location/Qualifiers  
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 /organism="Taeniopygia guttata"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:59729"  
 /clone="SB02018AIG04.f1"  
 /tissue\_type="brain"  
 /dev\_stage="late embryo, post-hatch days 1, 10, 20, 45,  
 and adult (pooled)"  
 /lab\_host="DH10B"  
 /clone\_lib="normalized Keck-Tagu Library SB02"  
 /note="Organ: brain; Vector: pBS II SK(+); Site 1:  
 EcoRI(5' side of insert); Site 2: NotI (3' side of  
 insert); The library was constructed and normalized as  
 described by Bonaldo, M.F., Lennon, G. and Soares, M.B.  
 (1996), Genome Research 6(9): 791-806. An identifying tag  
 was added at the 3' during cDNA synthesis:  
 insertAAAAAAAAAAAAAAAAAATGCGA."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 8.22e-98 Length: 765

Score: 876.00 Matches: 175  
 Percent Similarity: 96.81% Conservative: 7  
 Best Local Similarity: 93.09% Mismatches: 6  
 Query Match: 94.09% Indels: 0  
 DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CK303615 (1-765)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 119 GTTGTGACCTCTTCTTCTGGGAGACATTAAGAAGACCGGGTGGTGTGGAGCCAGC 178  
 QY 22 LeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 179 TTGTTCTCTGCTCTCTATTAACAGTGTTCAGCATCTGAGTGTCTACAGCCTACATGTC 238  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 239 CTGGCCCTGCTCTCTGTACCATCAGCTTTAGGATATACAGGAGTATTCAGGCCAATC 298  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 299 CAGAAGTCTGTATGAGGGCCACCCCTTCAGGGCTTACCTGGACTCGGATCGGCCGTGTCG 358  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 359 GAGGAGCTCATCAGAGTACAGCAACGCTGCTGGGCCACGCTGAACCGCACCGTCCCG 418  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 419 GAGCTCGGGCGCTCTCTCTGTCGAGACCTGCTGGATTCCTCAAGTTCGAGATTG 478  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 Db 479 ATGTGGTTTTTCACTTACGTGGTGGCTGCTTCAATGGTCTGACATTTACTGATCTGGCT 538  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 539 TTGATTTCGCTCTTCAGTGTCTCTGTATTTATGAGAGACATCAGGCCCAATTCGACCAT 598  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 599 TACCTGGGACTGTGTAACAGAACGTCGAAGATGCCATGGCAAGATCCAGCAAGATC 658  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 Db 659 CCTGGGTTGAAGCGCAAACTGAA 682

## RESULT 61

CK306874 793 bp mRNA linear EST 01-MAR-2004  
 LOCUS SB02042A1A11.f1 normalized Keck-Tagu Library SB02 Taeniopygia  
 DEFINITION guttata cDNA clone SB02042A1A11.f1 5, mRNA sequence.

ACCESSION CK306874  
 VERSION CK306874.1 GI:44816448  
 KEYWORDS EST.

## SOURCE

ORGANISM Taeniopygia guttata  
 Taeniopygia guttata  
 Eukaryota; Metazoa  
 Archosauria; Aves; Neognathae; Passeriformes; Estrilidae;  
 Estrilidae; Taeniopygia.

## REFERENCE

AUTHORS Clayton,D.F., Arnold,A.P., Ball,G.F., Brenowitz,E., George,J.M.,  
 Mello,C.V., Wade,J., Replogle,K., Lewin,H., Band,M., Hernandez,A.  
 and Liu,L.

TITLE The Songbird Neurogenomics Initiative: An Evolving Public Resource  
 for Study of Genes, Brain, and Behavior

## JOURNAL

COMMENT Unpublished (2004)

Contact: David F. Clayton

University of Illinois

8107 CLSU, 601 S. Goodwin,

Tel: 217 244 3668

Fax: 217 244 1648

Email: dclayton@uiuc.edu  
 Base Calling/Quality Scores: PHRED from Washington University  
 Genome Center.  
 Vector Trimming: Cross match from Washington University Genome  
 Center PHRAP suite. Low quality bases (Phred score < 20) were  
 trimmed from both ends of the sequence by an in-house script.  
 This sequence is vector free and at least 200 bp in length. Funded  
 by PHS grant # RO1 NS045264, 'Songbird Neurogenomics Initiative.'

## PCR Primers

FORWARD: TAATACGACTCACTATAGG(T7)

BACKWARD: ATTAACCTCACTAAAG(T3)

Insert Length: 793 Std Error: 0.00

Place: SB02042A1 row: A column: 11

Seq primer: TAATACGACTCACTATAGG (T7)

High quality sequence stop: 793.

## FEATURES

source

1..793

/organism="Taeniopygia guttata"

/mol\_type="mRNA"

/db\_xref="taxon:59729"

/clone="SB02042A1A11.f1"

/tissue\_type="brain"

/dev\_stage="late embryo, post-hatch days 1, 10, 20, 45,

and adult (pooled)"

/lab\_host="DH10B"

/clone\_lib="normalized Keck-Tagu Library SB02"

/note="Organ: brain; Vector: pBS II SK(+); Site\_1:

ECORI(5' side of insert); Site\_2: NotI (3' side of

insert); The library was constructed and normalized

described by Bonaldo, M.F., Lennon, G. and Soares, M.B.

(1996), Genome Research 6(9): 791-806. An identifying tag

was added at the 3' during cDNA synthesis:

insertAAAAAAAAAAAAAAAAAATCGCA."

## ORIGIN

## Alignment Scores:

Pred. No.: 8,668-98 Length: 793  
 Score: 876.00 Matches: 175  
 Percent Similarity: 96.81% Conservative: 7  
 Best Local Similarity: 93.09% Mismatches: 6  
 Query Match: 94.09% Indels: 0  
 DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CK306874 (1-793)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 89 GTTGTGACCTCTTCTTCTGGGAGACATTAAGAAGACCGGGTGGTGTGGAGCCAGC 148  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 149 TTGTTCTCTGCTCTCTATTAACAGTGTTCAGCATCTGAGTGTTCACAGCCTACATGTC 208  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 209 CTGGCCCTGCTCTCTGTACCATCAGCTTTAGGATATACAGGAGTATTCAGGCCAATC 268  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 269 CAGAAGTCTGTATGAGGGCCACCCCTTCAGGGCTTACCTGGACTCGGATCGGCCGTGTCG 328  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 329 GAGGAGCTCATCAGAAGTACAGCAACGCTGCTGGGCCACGCTGAACCGCACCGTCCCG 398  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 389 GAGCTCGGGCGCTCTTCTCTGATGACCTTGGTGGATTCCTCAAGTTCGAGATTG 448  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 Db 449 ATGTGGTTTTTCACTTACGTGGTGGCTTGGTCTCAATGGTCTGACATTACTGATCTGGCT 508

Qy 142 LeuileSerLeuPheSerValProValIleTyGluArgHisGlnAlaGlnIleAspHis 161  
 |||||  
 Db 509 TTGATTTTCGCTCTCAGTCTTCTGTTATTTATGAGACATCAGGCCCAATCGACCAT 568  
 |||||  
 Qy 162 TyrLeuGlyLeuAlaAsnLysValIleAspAlaMetAlaLysIleGlnAlaLysIle 181  
 |||||  
 Db 569 TACCTGGGACTTGTGAACAGAACGTCAAAGATGCGCAAGATCCAGCAAAAGATC 628  
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Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
 |||||

Db 629 CTGGGTTGAAGCGCAAAACTGAA 652  
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## RESULT 62

CK304164

LOCUS

DEFINITION

SB02022B2C10.f1 normalized Keck-Tagu Library SB02 Taeniopygia

guttata cDNA clone SB02022B2C10.f1 5, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Taeniopygia guttata

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Passeriformes; Estrilidae;

Estrildinae; Taeniopygia.

REFERENCE

1 (bases 1 to 852)

AUTHORS

Clayton, D.F., Arnold, A.P., Ball, G.F., Brenowitz, E., George, J.M.,

Mello, C.V., Wade, J., Replogle, K., Lewin, H., Band, M., Hernandez, A.

and Liu, L.

The Songbird Neurogenomics Initiative: An Evolving Public Resource

for Study of Genes, Brain, and Behavior

Unpublished (2004)

Contact: David F. Clayton

University of Illinois

B107 CUSL, 601 S. Goodwin, Urbana, IL 61801, USA

Tel: 217 244 3668

Fax: 217 244 1648

Email: dclayton@uiuc.edu

Base Calling/Quality Scores: PHRED from Washington University

Genome Center.

Vector Trimming: Cross\_match from Washington University Genome

Center PHRAP suite. Low quality bases (Phred score &lt; 20) were

trimmed from both ends of the sequence by an in-house script.

This sequence is vector free and at least 200 bp in length. Funded

by PHS grant # RO1 NS045264, 'Songbird Neurogenomics Initiative.'

PCR Primers

FORWARD: TAATACGACTCACTATAGG (T7)

BACKWARD: ATTAACCTCACTAAG (T3)

Insert Length: 852 Std Error: 0.00

Plate: SB02022B2 row: C column: 10

Seq primer: TAATACGACTCACTATAGG (T7)

High quality sequence stop: 852.

FEATURES

source

1..852

/organism="Taeniopygia guttata"

/mol\_type="mRNA"

/db\_xref="taxon:59729"

/clone="SB02022B2C10.f1"

/tissue\_type="brain"

/dev\_stage="late embryo, post-hatch days 1, 10, 20, 45,

and adult (pooled)"

/lab\_host="DH10B"

/clone\_lib="normalized Keck-Tagu Library SB02"

/note="Organ: brain; Vector: pBS II SK(+); Site: 1:

Score(5', side of insert); Site: 2: NotI (3' side of

insert); The library was constructed and normalized as

described by Bonaldo, M.F., Lennon, G. and Soares, M.B.

(1996). Genome Research 6(9): 791-806. An identifying tag

was added at the 3' during cDNA synthesis:

insertAAAAAAAAAAAAAAAAAATGCGA."

## ORIGIN

## Alignment Scores:

Pred. No.: 9,59e-98 Length: 852  
 Score: 876.00 Matches: 175  
 Percent Similarity: 96.81% Conservative: 7  
 Best Local Similarity: 93.09% Mismatches: 6  
 Query Match: 94.09% Indels: 0  
 DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CK304164 (1-852)

Qy 2 ValValAspLeuLeuTyTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21  
 |||||  
 Db 109 GTTGTGACCTCTCTTCTGCGAGACATTAAAGAACCGGGGTGTGTTGAGCGCAGC 168  
 |||||

Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyIleAla 41  
 |||||  
 Db 169 TTGTTCTGCTGCTCTCATTAACAGTGTTCAGCATCGTGAGTGTACAGCCTACATGCC 228  
 |||||

Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyLysGlyValIleGlnAla 61  
 |||||  
 Db 229 CTGGCCCTGCTCTCTGTCCATCAGCTTTAGGATATACAAAGGAGTTATCCAGGCAATC 288  
 |||||

Qy 62 GlnLysSerAspGluGlyHisPropheArgAlaTyLeuGluSerCluValAlaIleSer 81  
 |||||  
 Db 289 CAGAGTCTGATGAGGGCCACCCCTTACGGGCTTACCTGGACTCGGATGTGGCCGTGTGC 348  
 |||||

Qy 82 GluGluLeuValGlnLysTyTrpSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 |||||  
 Db 349 GAGGAGCTATCCAGAGTACAGCAGCTGTGCTGGGCCACGTAAGCGGACCGCTCCGG 408  
 |||||

Qy 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 |||||  
 Db 409 GAGCTGGCGGCTCTTCTCTCGTCGATGACCTGGTGGATTCCTCAAGTTCGACGATTATG 468  
 |||||

Qy 122 MetTrpValPheThrTyTrpValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 |||||  
 Db 469 ATGTGGTGTTCCTTACCTTACGTTGGTGGCTGTTCATATGCTGTGACATTACTGATCTGGCT 528  
 |||||

Qy 142 LeuIleSerLeuPheSerValProValIleTyGluArgHisGlnAlaGlnIleAspHis 161  
 |||||  
 Db 529 TTGATTCGCTCTTCAGTGTCTCTGTTATTTATGAGACATCAGGCCCAATCCACCAT 588  
 |||||

Qy 162 TyrLeuGlyLeuAlaAsnLysValIleAspAlaMetAlaLysIleGlnAlaLysIle 181  
 |||||  
 Db 589 TACCTGGGACTTGTGAACAGAACGTCAAAGATGCGTCAAGATGCGCAAGATCCAGCAAAAGATC 648  
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Qy 182 ProGlyLeuLysArgLysAlaGlu 189  
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Db 649 CTGGGTTGAAGCGCAAAACTGAA 672  
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## RESULT 63

BG109465

LOCUS

DEFINITION

602280543F1 NIH\_MGC\_86 Homo sapiens cDNA clone IMAGE:4368011 5',

mRNA sequence.

ACCESSION

VERSION

BG109465.1 GI:12602971

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

REFERENCE

1 (bases 1 to 819)

AUTHORS

NIH-MGC http://mgc.ncl.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov  
Plate: LLAMI0021 row: f column: 12  
High quality sequence stop: 647.  
Location/Qualifiers  
1. .819

## FEATURES

source  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4368011"  
/tissue\_type="osteosarcoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 86"  
/note="Organ: bone; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
Average insert size 1.533 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
Pred. No.: 1.05e-97 Length: 819  
Score: 875.50 Matches: 185  
Percent Similarity: 97.88% Conservativeness: 0  
Best Local Similarity: 97.88% Mismatches: 3  
Query Match: 94.04% Indels: 2  
DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BG109465 (1-819)

QY	2	ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer	21
Db	19	GTGTGTGACCTCTCTGCTGAGACATTAAGACAGCTGGAGTGGTGTGGTGGCCAGC	78
QY	22	LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaIleAla	41
Db	79	CTATTCTGCTGCTTCTTACGATGATTGAGCATTTGAGCGTAACAGCTACATGTC	138
QY	42	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla	61
Db	139	TTGGCCCTGCTCTCTGACCATTCAGCTTTAGGATATACAGGGTGTGATCCAAAGTATC	198
QY	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer	81
Db	199	CAGAAATCAGATGAGCGCCACCCATTCAGGCATATCTGGAATCTGAGTGGCTATATCT	258
QY	82	GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys	101
Db	259	GAGGAGTTGGTTCAGAAATACAGTAATTTCTGCTCTTGGTCAATGAACTGCACGATAAAG	318
QY	102	GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu	121
Db	319	GAACTCAGCGGCTCTTCTTAGTTGATGATTTAGTTGATTTCTGGAAGTTGCAGG--TTG	376
QY	122	MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla	141
Db	377	ATGTGGGTATTTACCTATGTTGGTGCTTGTATTAATGGTCTGACATCTGATTTGGCT	436
QY	142	LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis	161
Db	437	CTCATTTTCACTCTTCAGTGTCTCTGTTATTAATGACGCGCATCAGGCACAGATAGATCAT	496
QY	162	TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAla-LysIle	181
Db	497	TATCTAGGACTTGCATAATAAGATGTTAAAGATGCTATGCTTAAATCCAAAGCAAAAT	556
QY	181	eProGlyLeuLysArgGlyAlaGlu	189
Db	557	CCCTGATTGACGCGCAAAAGCTGAA	581

RESULT 64  
COS03803 685 bp mRNA linear EST 13-JUL-2004  
LOCUS GGEZCB1022G02.g chicken breast muscle - CB1 Gallus gallus cDNA  
DEFINITION

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

clone GGEZCB1022G02, mRNA sequence.

COS03803

COS03803.1 GI:50273989

EST.

Gallus gallus (chicken)

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.

1 (bases 1 to 685)

Alves, H.J., Jorge, E.C., Marchesin, M.L., Monteiro-Vitorello, C.B.,  
Patricio, M., Leduc, M.C. and Coutinho, L.L.

Discovery of new genes expressed in the chicken breast muscle

Unpublished (2004)

Contact: Helena J. Alves

Laboratory of Animal Biotechnology, Dep. of Animal Production

ESALQ - University of Sao Paulo

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Email: hjalves@esalq.usp.br and llicoutin@esalq.usp.br

PCR Primers

BACKWARD: T7.

## FEATURES

Source

Location/Qualifiers

1. 685

/organism="Gallus gallus"

/mol\_type="mRNA"

/db\_xref="taxon:9031"

/clone="GGEZCB1022G02"

/tissue\_type="breast muscle"

/dev\_stage="1 and 21 days old"

/lab\_host="DH5 alpha"

/clone\_lib="chicken breast muscle - CB1"

/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; This  
cDNA library was constructed with the SuperScript Plasmid  
System with Gateway Technology kit (Invitrogen), following a  
manufacturer's protocols. Plasmid DNA was purified using a  
modified alkaline lysis method. Sequencing reactions were  
conducted using the Dynamic Cycle Sequencing Kit for  
MegabACE (Amersham Biosciences) according to the  
manufacturer's recommendations. Clones were sequenced by  
the 5' end with T7 primer. Sequencing reactions were  
analyzed on MegaBACE1000 DNA Sequencer (Amersham  
Biosciences). The quality and clustering of the ESTs were  
analyzed using the softwares Phred/Cap3. Only EST  
sequences with Phred quality greater than 20 and at least  
150 bp were considered for clustering."

## ORIGIN

Alignment Scores:

Pred. No.: 9.34e-98 Length: 685  
Score: 875.00 Matches: 175  
Percent Similarity: 96.81% Conservativeness: 7  
Best Local Similarity: 93.09% Mismatches: 6  
Query Match: 93.98% Indels: 0  
DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x COS03803 (1-685)

QY	2	ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer	21
Db	72	GTGTGTGACCTCTCTTACTGGCGAGCATTAAGACAGAGTGGTGTGGTGGCCAGC	131
QY	22	LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaIleAla	41
Db	132	TTGTTCTCTGCTCTCTCATTAACAGTGTTCAGCATCGTCGAGCGTGACAGCTTACATG	191
QY	42	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla	61
Db	192	TTGGCCCTGCTCTTCTGTGACCATCAGCTTTAGGATATACAGGGAGTTATCCAGGCAATC	251
QY	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer	81

Db 252 CAAAGTCCGATGAAGGCCATCCATTAGGGCTTACTTGGAGTCTGATGTAGCTGTCT 311  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 312 GAAGAGCTGATTCAGAAATACAGAGTGTGTGCTTGCTCATCAACGGCACAGTCAAG 371  
 QY 102 GluLeuA:GArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 372 GAGCTGAGACGGCTCTCTCGTGGATGACCTGGTGTGATTTCTCTGAAGTTGACGTGTG 431  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAla 141  
 Db 432 ATGTGGGTGTTACACTTACGTGGTGGCTGTGTTAATGTGCTGACATTACTGATCTGCT 491  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 492 TTGATTTGCTGTTTCAGTGTTCCTGTTATTATATGAGACATCAGGCCACGATCGACCAT 551  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 552 TATTTGGGACTAGTGAACAAGAAGCTCCAAGATGGATGGCCCAAGATCCAGCCCAAGATC 611  
 QY 182 ProGlyLeuLysArgLysAlaGlu 189  
 Db 612 CTGGGCTGAAGCGCAAACTGAG 635

RESULT 65  
 COS81452  
 LOCUS  
 DEFINITION  
 ILLUMIGEN MCQ\_47216 Katze\_MMLV Macaca mulatta cDNA clone  
 IBTUM:17799 5' similar to Bases 83 to 959 highly similar to human  
 RTN4 (Hs.436349), mRNA sequence.

ACCESSION  
 COS81452

VERSION  
 COS81452.1 GI:50412806

KEYWORDS  
 EST.

SOURCE  
 Macaca mulatta (rhesus monkey)

ORGANISM  
 Macaca mulatta

REFERENCE  
 Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.

AUTHORS  
 Large-scale Rhesus Macaque cDNA Sequencing

TITLE  
 Unpublished (2003)

JOURNAL  
 Contact: C. Magness

COMMENT  
 Illumigen Biosciences Inc.

2203 Airport Way S, Suite 450, Seattle, WA 98134, USA

Tel: 2063780400

Fax: 2063780408

Email: cmagness@illumigen.com

Sequenced on 2004.06.24. 532 020 bases. Library Preparation: Prof.

Michael Katze Lab at University of Washington DNA Sequencing:

Illumigen Biosciences Inc. For further information, see

http://www.macaque.org

PCR Primers

FORWARD: CCCTCACTAAAGGGAACAAA

BACKWARD: CACTATAGCGGATTCGGTA

Insert Length: 960. Std Error: 0.00

Plate: CL000396 row: H column: 08

Seq primer: CCCTCACTAAAGGGAACAAA

POLYA=Yes.

FEATURES

Location/Qualifiers

1..960

/organism="Macaca mulatta"

/mol\_type="mRNA"

/strain="Indian"

/db\_xref="taxon:9544"

/clone="IBTUM:17799"

/sex="female"

/dev\_stages="adult"

/lab\_host="Electromax DH10B"

/clone\_lib="Katze MMLV"

/note="Organ: liver; Vector: pDONR 222; Site\_1: BsrG I;

Site 2: BsrG I; Created from CloneMiner cDNA Library  
 Construction kit (catalog #18249-029)"

# ORIGIN

Alignment Scores:  
 Pred. No.: 1.51e-97 Length: 960  
 Score: 875.00 Matches: 180  
 Percent Similarity: 97.34% Conservative: 3  
 Best Local Similarity: 95.74% Mismatches: 4  
 Query Match: 93.98% Indels: 1  
 DB: 7 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x COS81452 (1-960)

QY 3 ValAspLeuLeuTyrTrpArgAspIleLysIleValValPheGlyAlaSerLeu 22  
 Db 84 GTTGACCTCTCTAGTGGAGAGACTTGAAGAAATATGGAGTGGTGTGGCCAGCCTA 143  
 QY 23 PheLeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeu 42  
 Db 144 TTCCTGCTGCTTCTCTTGACAGTATTACAGATTGTGAGTGTAAACAGCCTACATTGCCCTTG 203  
 QY 43 AlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleGln 62  
 Db 204 GCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCCAAAGCTATCCAG 263  
 QY 63 LysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGlu 82  
 Db 264 AAATCAGATGAGGCCACCCATTGAGGCATATCTGGAAATCTGAAGTTGGCATATCTGAG 323  
 QY 83 GluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGlu 102  
 Db 324 GAGTTGGTTCAGAAAGTACAGTAATCTCTCTTGTCTCATGTGAACTGCACGATAAAGGAA 383  
 QY 103 LeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMet 122  
 Db 384 CTCAGGGCCCTCTCTTTAGTTGATGATTAGTTAGTTCTCTGAAAGTTTGCAGTGTGTGATG 443  
 QY 123 TrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLeuAlaLeu 142  
 Db 444 TGGGTATTATCTATGTTGGTGGCTTGTGTTTAAATGTTGACGCTACTGATTTGGCTCTC 503  
 QY 143 IleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyr 162  
 Db 504 ATTTCACTCTTCAGTGTTCCTGTTATTATTAACGGCATCAGGCACAGATAGATCATTTAT 563  
 QY 163 LeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePr 182  
 Db 564 CTAGGACTTGCAAAATAAGAATGTTAAAGATGCTATGGCTAAATATCCAGCGGAAAAATCCC 623  
 QY 182 oGlyLeuLysArgLysAlaGlu 189  
 Db 624 TGGATTGAAGCGCAAGCTGAA 645

RESULT 66

CDS11521

LOCUS

DEFINITION

IMAGE:30405928 5', mRNA sequence.

ACCESSION

CD511521

VERSION

CD511521.1 GI:31443239

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 758)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

CDS11521 758 bp mRNA linear EST 06-JUN-2003

AGENCOURT\_14353136 NIH\_MGC\_187 Homo sapiens cDNA clone

IMAGE:30405928 5', mRNA sequence.

CD511521

CD511521.1

EST.

GI:31443239

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 758)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits  
cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDCM193 row: n column: 17

High quality sequence stop: 614.

#### FEATURES

source

1..758

Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:30405928"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_lib="NIH\_MGC\_187"

/note="Organ: Blood vessels - aorta, basilar and artery;

Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2:

SfiI (ggcgctcgccg); 5' and 3' adaptors were used in

cloning as follows: 5' adaptor sequence:

5'-CACGGCCATTATGCC-3' and 3' adaptor sequence:

5'-ATTCTAGAGCGCGGCGCGGACATG-dT(30)BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.4 kb

(range 0.5-4.0 kb). 14/15 colonies contained inserts by

PCR. This library was enriched for full-length clones and

was constructed by Clontech Laboratories (Palo Alto, CA).

Note: this is a NIH\_MGC Library."

#### ORIGIN

Alignment Scores:

Pred. No.:	1,25e-97	Length:	758
Score:	874.50	Matches:	182
Percent Similarity:	98.39%	Conservative:	1
Best Local Similarity:	97.85%	Mismatches:	1
Query Match:	93.93%	Indels:	2
DB:	6	Gaps:	1

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CD511521 (1-758)

QY	2	ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer	21
Db	148	GTGTGTGACCTCTGTACTGGAGAGACATTAAAGAACCTGGAGTGTGTGGTGGCCAGC	207
QY	22	LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla	41
Db	208	CTATTCTCTGCTTTCATTGACAGTATTCAGCATTTGTGAGCTACACGCTACATTGCC	267
QY	42	LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAlaIle	61
Db	268	TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGTGTGATCCAAAGCTATC	327
QY	62	GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer	81
Db	328	CAGAAATCAGATGAAGCCACCCATTGAGGCGCATATCTGGAATCTGAAGTTGCTATATCT	387
QY	82	GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys	101
Db	388	GAGGAGTTGGTTCAGAAAGTACAGTAAATCTGCTCTTGGTCACTGTAAGTGCAGGTAAG	447
QY	102	GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu	121
Db	448	GAACTCAGGCGCCTCTCTCTAGTTGATGATTTAGTTGATTTCTGAAGTTTCAGGTGTG	507
QY	122	MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeuAla	141
Db	508	ATGTGGGTATTTACCTATGTGTGTGCTGCTTTTAATGGTCTGACACTACTGATTTTGGCT	567
QY	142	LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis	161
Db	568	CTCATTTCACTTTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT	627

QY	162	TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMet-AlaLysIleGlnAlaLysIle	181
Db	628	TATCTAGGACTTGCATAATGAAGATGTTAAAGATGCTATGGCTAAATCCAAAGCAAAA	687
QY	181	ePro--GlyLeuLys	185
Db	688	TCCCCTGGGATTGAAA	703

#### RESULT 67

BG427864

LOCUS

DEFINITION

mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens (human)

EST.

GI:13334370

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QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 266 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 325  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 326 CAGAAATCAGATGAAGGCCACCAATTCAGGCATATCTGGAATCTGAAGTTGCTATATCT 385  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 386 GAGGAGTTGGTTTCAGAGTACAGTAACTCTCTCTGTGGTCATGTGAACCTGCACGATAAG 445  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 446 GAACCTCAGCGGCTCTCTCTAGTTAGTATTTAGTTGATCTCTGAGGTTGTCATGTTG 505  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
 Db 506 ATGTGGGTATTTACCTATGTTGGTGC-CTGTTTAATAGTCTGCACACTACTGATTTGGCT 564  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 565 CTCATTTTCACTCTTCAGTGTCTCTGTCATTTATGAACGGCATCAGGCAAGATAGATCAT 624  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 625 TATCTAGGACTTGCAANTAGAAATGTTACAGATGCTAATGGTAAATCCAGCAAAATC 684  
 QY 182 ProGlyLeuLysArgLys 187  
 Db 685 CCTGGATTGAAGCGCAAG 702

RESULT 68  
 BG400408  
 LOCUS  
 DEFINITION 602464428F1 NIH\_MGC\_75.Homo sapiens cDNA clone IMAGE:4592670 5',  
 mRNA sequence.  
 ACCESSION BG400408  
 VERSION BG400408.1 GI:13293856  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 905)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: CLONTECH Laboratories, Inc.  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ILNL at:  
<http://image.llnl.gov>  
 Plate: LLCW1331 row: g column: 07  
 High quality sequence stop: 708.  
 Location/Qualifiers  
 1..905  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4592670"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NIH\_MGC\_75"  
 /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:  
 SfiI (ggccctcgccg); Site 2: SfiI (ggccattatggcc); 5' and  
 3' adaptors were used in cloning as follows: 5' adaptor  
 sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:  
 5'-ATTCTAGAGCGCGGCGCGGCACATG-dt(30)BN-3' (where B = A,

## FEATURES

C, or G and N = A, C, G, or T). Average insert size 1.65  
 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA). Note: this is a NIH\_MGC Library."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 2,46e-97 Length: 905  
 Score: 873.00 Matches: 182  
 Percent Similarity: 96.84% Conservative: 2  
 Best Local Similarity: 95.79% Mismatches: 4  
 Query Match: 93.77% Indels: 2  
 DB: 4 Gaps: 0  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x BG400408 (1-905)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysIleValValPheGlyAlaSer 21  
 Db 153 GTTGTGACCTCTCTGTACTGGAGACATTAAGAAGACTGGAGTGGTGTGGTCCAGC 212  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 213 CTATTCTTCCTGCTTTCATTGACAGTATTGAGCATTGTGAGCGTAACAGCCTACATGCC 272  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 273 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 332  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 333 CAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCTGAAGTTGCTATATCT 392  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 393 GAGGAGTTGGTTTCAGAGTACAGTAACTCTCTCTGTGTCATGTGAACCTGCACGATAAG 452  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 453 GAACCTCAGCGGCTCTCTCTAGTTAGTATTTAGTTGATTTCTCTGAAAGTTGCACTGTTG 512  
 QY 122 Met-TrpValPheThrTyrValGlyAlaLeuPheAsn-GlyLeuThrLeuLeuIleAla 141  
 Db 513 ATCGTGGGTATTTACCTATGTTGGTGCCTCTGTTACTGGGTCGACACTACTGATTTGGG 572  
 QY 141 laLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspH 161  
 Db 573 CTCTCATTTCACTCTCTCAGTGTCTCTGTTATTTATGAACGGCATCAGGCAAGATAGATC 632  
 QY 161 isTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysI 181  
 Db 633 ATTATCTAGGACTTGCAANTAGAAATGTTAAGATGCTATGGTAAATCCAGCAAA 692  
 QY 181 leProGlyLeuLysArgLysAlaGlu 189  
 Db 693 TCCCTGGATTGAAGCGCAAGTTGAA 718

RESULT 69  
 BU364240  
 LOCUS  
 DEFINITION 603585074F1 CSEQCHN72 Gallus gallus cDNA clone ChEST539d19 5', mRNA  
 sequence.  
 ACCESSION BU364240  
 VERSION BU364240.1 GI:25872241  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 820)  
 Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.

## TITLE A Comprehensive Collection of Chicken cDNAs

JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
 MEDLINE 22335534  
 PUBMED 12445392  
 COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.

## FEATURES

source  
 1. .820  
 Location/Qualifiers  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="Compton Line 151"  
 /db\_xref="taxon:9031"  
 /clone="CHES7539d19"  
 /sex="female"  
 /tissue\_type="cerebrum"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="CSECHN72"  
 /note="Organ: brain; Vector: pBluescript II KS(+); Site\_1: EcoRI; Site\_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Alignment Scores:  
 Pred. No.: 2,85e-97 Length: 820  
 Score: 872.00 Matches: 177  
 Percent Similarity: 96.83% Conservative: 6  
 Best Local Similarity: 93.65% Mismatches: 5  
 Query Match: 93.66% Indels: 1  
 DB: 5 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BU364240 (1-820)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 156 GTTGTGAGCTCTTACTGGCGAGACATTAAAGACAGGAGTGGTGTGGTGGCAGC 215  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 216 TTGTTCTCTGCTCTCATTAACAGTGTTCAGCATCTGAGCGTGACGCTTACATTC 275  
 QY 42 LeuAlaLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 276 TTGGCCCTGCTTCTGTGACCATCAGCTTTAGATATACAGGAGTTATCCAGGCAATC 335  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 336 CAAAGTCCGATGAAGGCCATCCATTAGGCTTACTTGGAGTCTGATGCTAGTGTCT 395  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 396 GAAGAGCTGATCAGAAATACAGCAGTGTGTGCTTGGTCACATCAACGGCAGTCAAG 455  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 456 GAGCTGAGAGCGCTCTTCTCGTTGATGACTTGGTTGATCTCTGAAGTTTCAGTGTG 515

QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleuLeuAla 141  
 Db 516 ATGTGGGTGTTTCACTTACGTTGGTCTGTTTAAATGGTCTGACATTACTGATGGCT 575  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 576 TTGATTTTCGCTGTTTCACTGTTTCTCTGTTTATTAAGAGACATCAGGCCAGATCCACCAT 635  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181  
 Db 636 TATTTGGGACAGTAGTGACACAGAACCTCAAGATGCGATGGCAAGATCCACCAAGATC 695  
 QY 182 Pro-GlyLeuLysArgLysAlaGlu 189  
 Db 696 CTTGGGCTGTGAAGCGCAAACTGAG 720

## RESULT 70

CA322433 817 bp mRNA linear EST 09-JUL-2003  
 UI-W-FX0-ckk-n-21-0-UI.r1 NIH\_BMAP\_FX0 Mus musculus cDNA clone  
 IMAGE:6820918 5', mRNA sequence.  
 CA322433  
 CA322433.1 GI:24540531  
 EST.  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 817)  
 NIH-MGC http://mgs.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-r@mail.nih.gov  
 Tissue Procurement: Dr. Jim Lin, University of Iowa  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 This clone was contributed by the Brain Molecular Anatomy Project  
 (BMAP)  
 Seq primer: pYX-5.  
 Location/Qualifiers  
 1. .817  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="CS7BL/6"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:6820918"  
 /tissue\_type="whole brain"  
 /dev\_stage="embryo 13.5,14.5,16.5,17.5dpc"  
 /lab\_host="DH10B (T1 phage resistant)"  
 /clone\_lib="NIH\_BMAP\_FX0"  
 /note="Organ: Brain; Vector: pYX-Asc; Site\_1: EcoR I;  
 Site\_2: Not I; The library was constructed according  
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
 1996. Denatured RNA was size fractionated on a 1% agarose  
 gel. First strand cDNA synthesis was primed with oligo-dT  
 primer containing a Not I site. Double strand cDNA was  
 size selected according to mRNA size fraction, ligated  
 with EcoR I adaptor, digested with NotI and then cloned  
 directionally into pYX-Asc vector. The library tag  
 sequence located between the Not I site and the polyA tail  
 is ACCGAGACAG. This library was created for the University  
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the  
 Developing Mouse Nervous System', supported by National  
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,  
 program coordinator."

## FEATURES

source

## ORIGIN



## Alignment Scores:

Pred. No.: 5,01e-97 Length: 817  
 Score: 870.00 Matches: 185  
 Percent Similarity: 97.40% Conservative: 2  
 Best Local Similarity: 96.35% Mismatches: 2  
 Query Match: 93.45% Indels: 3  
 DB: 6 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CA322433 (1-817)

QY 1 SerValValAspLeuLeu-TyrTrp-ArgAspIleIysIysThrGlyValValPheGlyA 20  
 DB 41 TCAGTTGTGGCTCTCTGCTGCTCTCTGACAGCTGTTGAGTGTGAGTGTGTTGGTG 100  
 QY 20 laSerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrI 40  
 DB 101 CCAGCTTATCTCTGCTGCTCTCTGACAGCTGTTGAGTGTGAGTGTGAGTGTGAC 160  
 QY 40 leAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnA 60  
 DB 161 TTGCCCTTGCCCTGCTCTCTGCTGCTCTCTGACAGCTGTTGAGTGTGAGTGTGAG 220  
 QY 60 laIleGlnIysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaI 80  
 DB 221 TTTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCCA 280  
 QY 80 leSerGluGluLeuValGlnIysTyrSerAspSerAlaLeuGlyHisValIleCysThrI 100  
 DB 281 TATCAGAGGAATGGTTTCAGAAATATAGTAATCTGCTCTGCTGCTGCTGCTGCTGCTG 340  
 QY 100 leLeuGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuIysPheAlaV 120  
 DB 341 TAAAGAAATTTGAGCGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 400  
 QY 120 alLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuLe 140  
 DB 401 TGTTCATGGGTATTTACTTACGTTGGTGGCTCTGTTCAATGGTTGACACTACTGATTT 460  
 QY 140 euAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleA 160  
 DB 461 TAGCTCTGATCTCCTCTTCAGTATCTCTGTTATATATGACGGCATCAGGGCCAGATAG 520  
 QY 160 epHisTyrLeuGlyLeuAlaAlaIleValAsnValIysAspAlaMetAlaIysIleGlnAla 180  
 DB 521 ATCATTTATCTAGGACTTGCACCAAGAGCGTTTAAAGGATGCCATGCCAAAATCCCAAGCAA 580  
 QY 180 ysIlePro-GlyLeuIysArgIysAlaGlu 189  
 DB 581 AAATCCCTGGGATTGAAGCCANAGCAGAA 610

RESULT 71  
 CD623552/c 659 bp mRNA linear EST 12-JAN-2004  
 LOCUS 5608673H1 FLP Homo sapiens cDNA, mRNA sequence.  
 DEFINITION CD623552  
 ACCESSION CD623552  
 VERSION CD623552.1 GI:40271817  
 EST. EST.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 659)  
 AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
 TITLE Circular rapid amplification of cDNA ends for high-throughput  
 extension cloning of partial genes  
 JOURNAL Genomics 84 (1), 205-210 (2004)  
 COMMENT Contact: Fu GK  
 Incyte Genomics, Inc.  
 3160 Porter Dr., Palo Alto, CA 94304, USA  
 Tel: 6508454102  
 Email: gfu@incyte.com.  
 Location/Qualifiers  
 1..659 source

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone\_lib="FLP"  
 /note="Vector: pDrive Cloning Vector"

## ORIGIN

Alignment Scores:  
 Pred. No.: 4.9e-97 Length: 659  
 Score: 869.00 Matches: 177  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 99.44% Mismatches: 0  
 Query Match: 93.34% Indels: 0  
 DB: 6 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CD623552 (1-659)

QY 12 LysIysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrValPhe 31  
 DB 654 AGGAAGACTGGAGTGGTGTGGTGCCAGCCTATTCTCTGCTGCTTTCATTGACAGTATTC 595  
 QY 32 SerIleValSerValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerPhe 51  
 DB 594 AGCATTTGAGCGGTAAACAGCCTACATTGCCCTTGGCCCTCTCTGTGACCATCAGCTTT 535  
 QY 52 ArgIleTyrIysGlyValIleGlnAlaIleGlnIysSerAspGluGlyHisProPheArg 71  
 DB 534 AGGATATACAGGGTGTGATCCAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGG 475  
 QY 72 AlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGlnIysTyrSerIleSer 91  
 DB 474 GCATATCTGGAATCTGAAGTTGCTATATCTCAGGAGTTGGTTTCAGAGTACAGTAATTC 415  
 QY 92 AlaLeuGlyHisValAsnCysThrIleIysGluLeuArgLeuPheLeuValAspAsp 111  
 DB 414 GCTCTTGCTGATGAACTGCACGATAAAGAACTCAGCGGCTCTCTTAGTTGATGAT 355  
 QY 112 LeuValAspSerLeuIysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeu 131  
 DB 354 TTAGTTGATCTCTGAGTTTGCAGTGTGATGGGTATTTACCTATGTTGGTGGCTTGT 295  
 QY 132 PheIleGlyLeuThrLeuLeuIleAlaLeuIleSerLeuPheSerValProValIle 151  
 DB 294 TTTAATGCTGACACTACTGATTTGGCTCTCATTTTCACCTCTTCAGTGTCTCTGTATT 235  
 QY 152 TyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnIysValIys 171  
 DB 234 TATGAACGGCATCAGGCACAGATAGATCATTTATCTAGGACTTGCAAAATAAGAAATGTTAA 175  
 QY 172 AspAlaMetAlaIysIleGlnAlaIysIleProGlyLeuIysArgIysAlaGlu 189  
 DB 174 GATGCTATGGCTAAAATCCAGCAAAATACCTGGATTGAAGGCCAAGCTGAA 121

## RESULT 72

CD623553 660 bp mRNA linear EST 12-JAN-2004  
 LOCUS 5608673J1 FLP Homo sapiens cDNA, mRNA sequence.  
 DEFINITION CD623553  
 ACCESSION CD623553  
 VERSION CD623553.1 GI:40271818  
 EST. EST.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 660)  
 AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
 TITLE Circular rapid amplification of cDNA ends for high-throughput  
 extension cloning of partial genes  
 JOURNAL Genomics 84 (1), 205-210 (2004)  
 COMMENT Contact: Fu GK  
 Incyte Genomics, Inc.  
 3160 Porter Dr., Palo Alto, CA 94304, USA  
 Tel: 6508454102

## FEATURES

Location/Qualifiers

1..659

source

Email: gfu@incyte.com

Location/Qualifiers

## FEATURES

source

1. .660

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone\_lib="FLP"

/notes="vector: pDrive Cloning Vector"

## ORIGIN

Alignment Scores:  
 Pred. No.: 4,91e-97 Length: 660  
 Score: 869.00 Matches: 177  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 99.44% Mismatches: 0  
 Query Match: 93.34% Indels: 0  
 DB: 6 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CD623553 (1-660)

QY 12 LysLeuThrGlyValValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPhe 31  
 :::  
 Db 6 AGGAAGACTCGAGT 65  
 QY 32 SerLeuValSerValThrAlaTyrLeuAlaLeuLeuSerValThrLeuSerPhe 51  
 :::  
 Db 66 AGCATTTGTGAGCGTAAACAGCTTACATTTGCTTGTGGCCCTCTCTCTGTGACCATGCTTT 125  
 QY 52 ArgLeuTyrLysGlyValLeuGlnAlaLeuGlnLysSerAspGluGlyHisProPheArg 71  
 :::  
 Db 126 AGGATATACAGGGTGTGTATCCAGGTATCCAGGATCCAGGATCCAGGATCCAGGATCCAG 185  
 QY 72 AlaTyrLeuGluSerGluValAlaLeuSerGluGluLeuValGlnLysTyrSerLeuSer 91  
 :::  
 Db 186 GCATATCTGGAATCTGAAGTGTCTATATCTGAGGAGTGTGTGTGTGTGTGTGTGTGTGT 245  
 QY 92 AlaLeuGlyHisValAsnCystrLeuLysGluLeuArgArgLeuPheLeuValAspAsp 111  
 :::  
 Db 246 GCTCTTGT 305  
 QY 112 LeuValAspSerLeuLysPheAlaValLeuMetTyrValPheThrTyrValGlyAlaLeu 131  
 :::  
 Db 306 TTATGT 365  
 QY 132 PheAsnGlyLeuThrLeuLeuLeuAlaLeuLeuSerLeuPheSerValProValLeu 151  
 :::  
 Db 366 TTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCTCTCTCTCTCTCTCTCTCTCTCT 425  
 QY 152 TyrGluArgHisGlnAlaGlnLeuAspHisTyrLeuGlyLeuAlaAsnLysAsnValLys 171  
 :::  
 Db 426 TATGAACGGCATCAGGCAGATAGATCATTTCTAGGACTTGTCAAAATGAAGATGTAAA 485  
 QY 172 AspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLysArgLysAlaGlu 189  
 :::  
 Db 486 GATGCTATGGCTAAATCCAGCAAAATCCCTGGATTGAAGCGCAAGCTGAA 539

RESULT 73  
 BI872386  
 LOCUS 603397035F1 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:5400584 5',  
 DEFINITION mRNA sequence.

ACCESSION BI872386

VERSION BI872386.1 GI:16046048

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov

Tissue Procurement: The Cepko Laboratory

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM12021 row: f column: 09

High quality sequence stop: 754.

Location/Qualifiers

1. .857

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="IMAGE:5400584"

/tissue\_type="retina"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_94"

/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally; oligo-dT primed.

Average insert size 3.3 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.26e-96 Length: 857  
 Score: 867.00 Matches: 184  
 Percent Similarity: 97.89% Conservative: 2  
 Best Local Similarity: 96.84% Mismatches: 1  
 Query Match: 93.13% Indels: 3  
 DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BI872386 (1-857)

QY 2 ValValAspLeuLeuTyrTyrArgAspLeuLysLysThrGlyValValPheGlyAlaSer 21  
 :::  
 Db 130 GTGTGTGACCTCTCTGT 189  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrLeuAla 41  
 :::  
 Db 190 TTATTTCTGCTGCTCTCTGACAGTTCAGCATTTGTAGGATATATAGGGGTGTGATCAAGCTATC 249  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaLe 61  
 :::  
 Db 250 TTGGGCCCTGCTCTCTGTGACTATCATCTATGATATATAGGGGTGTGATCAAGCTATC 309  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaLeuSer 81  
 :::  
 Db 310 CAGAAATCAGATCAAGGCCACCATTCAAGGCATATTTGGATCTGAGTTCGATTCATATCA 369  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCystrLeuLys 101  
 :::  
 Db 370 GAGGAATTTGTTTCAGAAATATAGTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 429  
 QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 :::  
 Db 430 GAAATTTGAGCGCTCTCTCTCTTAGTATTTAGTATTTCCCTGAAAGTTTCAGGTGTG 489  
 QY 122 MetTyrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAlaLeu 141  
 :::  
 Db 490 ATGTGGGTATTTACTTACCTTGTGTCCTTGTTCATGTGTTTGACACTACTGATTTAGTGT 549  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 :::  
 Db 550 CTGATCTCACTCTCTCAGTATTTCTGTATATATGAACGCATCAGCGCAGATAGATCAT 609  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAla-LysIleGlnAla-LysI 181  
 :::  
 Db 610 TATCTAGGACTTGCAGAACAGAGCGTTAGGATGCGATGCGCAAAATCCAGCAAAAAA 669  
 QY 181 leProGlyLeu-LysArgLysAla 188

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Db      670 TCCCTGGATTGGAAGCGCAAGCA 693
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RESULT 74
BU949473
LOCUS
DEFINITION
sequence.
ACCESSION
BU949473
VERSION
BU949473.1
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
EST.
BU949473.1 GI:24200824
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 609)
AUTHORS
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scarce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
TITLE
Endocrine Pancreas Consortium
JOURNAL
Unpublished (2000)
COMMENT
Other ESTs: in67h09.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 471.
FEATURES
source
Location/Qualifiers
1..609
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6127360"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site:1:
NotI; site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
ORIGIN
Alignment Scores:
Pred. No.: 1,376-96 Length: 609
Score: 865.00 Matches: 177
Percent Similarity: 98.33% Conservative: 0
Best Local Similarity: 98.33% Mismatches: 3
Query Match: 92.91% Indels: 0
DB: 5 Gaps: 0
US-09-830-972-29_COPY_990_1178 (1-189) x BU949473 (1-609)
Qy      10 AspileLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThr 29
Db      1 GACATTAGAGATTGGAGTGGTGTGGTGGCCAGCCTATTCTCTTCATTGACA 60
|||||
30 ValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIle 49
|||||
61 GTATTACGATTGTGAGCGTAACGCTACATTGCTTGGCCCTGCTCTCTGTGACCATC 120
|||||
50 SerPheArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisPro 69
|||||
121 AGCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGCCACCCA 180
|||||
70 PheArgAlaTyrLeuGluSerGluValAlaIleSerGluLeuValGlnLysTyrSer 89
|||||
181 TTCAGGGCATATCTGGAATCTGAAAGTTCATATCTGAGGAGTGGTTCAGAAAGTACTGT 240
|||||
90 AsnSerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuVal 109
|||||
241 AATTCTGCTCTTGGTCATGTGAACCTGCACGATAAAGGAACCTCAGCGGCTCTTCTTAGTT 300
|||||
110 AspAspLeuValAspSerLeuLysPheAlaValLeuMetTrrValPheThrTyrValGly 129
|||||
301 GATGATTTAGTTGATTCTCTGAAGTTTGCACTGTTGATGGGTATTTACCTATGTTGGT 360
|||||
130 AlaLeuPheArgGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValPro 149
|||||
361 GCCTTGTGTTAATGTTGTCACACTACTGATTTTGGCTCTCATTTCACTCTTCTAGTTTCT 420
|||||
150 ValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsn 169
|||||
421 GTTATTTATGACCGCATCAGCAGATAGATCATTTATCTAGGACTTGCAAATAGAAAT 480
|||||
170 ValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuLysArgLysAlaGlu 189
|||||
481 GTTAAAGATGCTATGGCTAAATCAAAGCAAAATCCCTGGATTGAAGCGCAAGCTGAA 540
|||||
RESULT 75
BE733819 716 bp mRNA linear EST 15-SEP-2000
601569133F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843729 5',
mRNA sequence.
ACCESSION
BE733819
VERSION
BE733819.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 716)
AUTHORS
NIH-MGC http://mgi.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCMS59 row: a column: 10
High quality sequence stop: 716.
FEATURES
Location/Qualifiers
1..716
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3843729"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_21"
/note="Organ: placenta; Vector: pOTB7; Site:1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by

```

Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

Alignment Scores:  
 Pred. No.: 1,738-96 Length: 716  
 Score: 865.00 Matches: 185  
 Percent Similarity: 98.40% Conservative: 0  
 Best Local Similarity: 98.40% Mismatches: 1  
 Query Match: 92.91% Indels: 3  
 DB: 2 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BE733819 (1-716)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThyGlyValValPheGlyAlaSer 21  
 DB 142 GTTGTGACCTCTGTTACTGGAGACATTAAAGAGCTGGAGTGGTGTGGTGCACG 201  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 DB 202 CTATTCTCTGCTTTCATTGACAGTATTACAGCATTTGAGCGTTACAGCCTACATGGC 261  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIyGlyValIleGlnAlaIle 61  
 DB 262 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAGGCTGTGATCCAGCTATC 321  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 322 CAGAAATCAGATGAAGCCACCATTCAGGCGCATATCTGGAATCTGGAATGCTATATCT 381  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 DB 382 GAGGAGTTGGTTTTCAGAGTACAGTAACTCTGCTTCTGGTCACTGGAACGCGATAAAG 441  
 QY 102 GluLeuArgGluLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 DB 442 GAACTCAGGCGCCCTCTCTTAGTGAATGATTTAGTTGATCTCTGGAAGTTTCAGGTGTG 501  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
 DB 502 ATGTGGGTATTTACCTATGTTGGTGGCTTGTATTAATGGTCTGACACTACTGAT-TTGGCT 560  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 DB 561 CTCAATTTCATCTCTCAGTGTCTCTGTATTATGAACGCGCATCAGGCACAGATAGATCAT 620  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGln-AlaLysI 181  
 DB 621 TATCTAGGACTTGGCAATTAAGATGTTAAGATGCTATGGCTTAATCCAAAGCAAAAT 680  
 QY 181 e-ProGlyLeuLysArgLys 187  
 DB 681 CCCCTGGATTGAAGCGCAAA 700

RESULT 76  
 BG427986 743 bp mRNA linear EST 14-MAR-2001  
 LOCUS 602500385F1 NIH\_MGC\_75 Homo sapiens cDNA clone IMAGE:4613876 5',  
 DEFINITION mRNA sequence.

ACCESSION BG427986  
 VERSION BG427986.1 GI:13334492  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 743)  
 NIH-MGC <http://mgi.nci.nih.gov/>.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL  
 CONTACT: Robert Strausberg, Ph.D.  
 COMMENT Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: CLONTECH Laboratories, Inc.  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 cDNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 cDNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>  
 Plate: LLCMI364 row: j column: 21  
 High quality sequence stop: 716.

Location/Qualifiers  
 1. -743

FEATURES  
 source

/organism="Homo sapiens"  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:4613876"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NIH\_MGC\_75"  
 /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site: 1:  
 SfiI (ggccctcgcc); Site 2: SfiI (ggccattatggc); 5' and  
 3' adaptors were used in cloning as follows: 5' adaptor  
 sequence: 5'-CACGCCATTATGGC-3' and 3' adaptor sequence:  
 5'-ATTCTAGAGCGCGAGCGGCACATG-dt(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size 1.65  
 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA). Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 1,828-96 Length: 743  
 Score: 865.00 Matches: 181  
 Percent Similarity: 96.32% Conservative: 2  
 Best Local Similarity: 95.26% Mismatches: 5  
 Query Match: 92.91% Indels: 2  
 DB: 4 Gaps: 0  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x BG427986 (1-743)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThyGlyValValPheGlyAlaSer 21  
 DB 163 GTTGTGACCTCTGTTACTGGAGACATTAAAGAGCTGGAGTGGTGTGGTGCACG 222  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 DB 223 CTATTCTCTGCTTTCATTGACAGTATTACAGCATTTGAGCGTTACAGCCTACATGGC 282  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIyGlyValIleGlnAlaIle 61  
 DB 283 TTGGCCCTCTCTCTGTGACCATCAGCTTTAGGATATACAGGCTGTGATCCAGCTATC 342  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 DB 343 CAGAAATCAGATGAAGCCACCATTCAGGCGCATATCTGGAATCTGGAATGCTATATCT 402  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 DB 403 GAGGAGTTGGTTTTCAGAGTACAGTAACTCTGCTTCTGGTCACTGGAACGCGATAAAG 462  
 QY 102 GluLeuArgGluLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121  
 DB 463 GAACTCAGGCGCCCTCTCTTAGTGAATGATTTAGTTGATCTCTGGAAGTTTCAGGTGTG 522  
 QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141  
 DB 523 ATGTGGGTATTTACCTATGTTGGTGGCTTGTATTAATGGTCTGACACTACTGATTTGGCT 582  
 QY 142 LeuIleSer-LeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 DB 583 CTCAATTTCATCTCTCAGTGTCTCTGTATTATGAACGCGCATCAGGCACAGATAGATCA 642  
 QY 161 sTyrLeuGlyLeuAlaAsnLysAsnVal-LysAspAlaMetAlaLysIleGlnAlaLysI 181  
 DB 161 sTyrLeuGlyLeuAlaAsnLysAsnVal-LysAspAlaMetAlaLysIleGlnAlaLysI 181

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Db      643 TTATCTAGGACTTGCATAAATAAGAAATGTTACAGATGCTTAATGGTAATAAATCCAAAGCAAAA 702
QY      181 leProGlyLeuLysArgLysAlaGlu 189
Db      703 TCCTGGATTGAAGCGCAAGCTGAC 728

RESULT 77
BI394814
LOCUS   646 bp mRNA linear EST 06-AUG-2001
DEFINITION
p9pin.pk009.15 Normalized Chicken Pituitary/Hypothalamus/Pineal
Library Gallus cDNA clone p9pin.pk009.15 5' similar to
gi|5902016.ref|NP_008939.1| reticulon 4; neuroendocrine-specific
protein c like (foocen) [Homo sapiens] gi|13637055.ref|XP_002439.3|
neuroendocrine-specific protein C like (foocen) [Homo sapiens]
gb|AAD27783.1|AF077050_1 (AF077050) neuroendocri, mRNA sequence.
ACCESSION
BI394814
VERSION
BI394814.1 GI:15088096
KEYWORDS
EST.
SOURCE
Gallus gallus (chicken)
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 646)
Porter,T.E. and Cogburn,L.A.
ESTs from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA
Library USDA/IFAFS Animal Genome Project
Unpublished (2001)
Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.

FEATURES
source
1..646
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Commercial broiler chicken"
/db_xref="taxon:9031"
/clone="p9pin.pk009.15"
/sex="Male and Female"
/dev_stage="Embryonic (d12,d14,d19); post-hatch
(w1,w3,w5,w7,w9)"
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/clone_lib="Normalized Chicken
Pituitary/Hypothalamus/Pineal Library"
/note="Vector: pCMVSPORT6; Library made from equivalent
pools of total RNA isolated from each tissue at different
ages. Single pass sequencing from 5'-end"

ORIGIN
Alignment Scores:
Pred. No.: 2,646-96 Length: 646
Score: 863.00 Matches: 174
Percent Similarity: 95.74% Conservative: 6
Best Local Similarity: 92.55% Mismatches: 8
Query Match: 92.70% Indels: 0
DB: 4 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x BI394814 (1-646)

QY      2 ValValAlaLeuLeuTyrTyrArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db      51 GTTGTGACCTCTTCTTACTGCGGACATTAAGACAGAGGAGTGTGTTGGTCCAGC 110
QY      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db      111 TTGTTCTCTGCTCTCTTACATTAACAGTGTTCAGCATCGTACGCGTGACAGCTTACATGCC 170
QY      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61

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Db      171 TTGGCCCTCTTCTGTGACCATCAGCTTTAGGATATACAGGAGGAGTTATCCAGGCAATC 230
QY      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db      231 CAAAAGTCCGATGAAGGCCATCCATTAGGGCTTACTTGGAGTCTGTAGTCTGTGTCT 290
QY      82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db      291 GAAGAGCTGATTTCAGAAATACAGCAGTGTGTGCTTGGTCACATCAACGGCACAGTCAAG 350
QY      102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db      351 GAGCTGAGACGCTCTTCTCTGCTGATGACCTTGTGTTGATTTCTCTCAAGTTTCAGTGTG 410
QY      122 MetTTPValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAla 141
Db      411 ATGTGGGTGTTTCACTTACGTGGTGCTTGTGTAAATGGTCTGACATTACTTGATCTGGCT 470
QY      142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAephHis 161
Db      471 TTGATTCCTGCTTTCAGTGTCTCTGTTTATTTATGAGACATCAGCCGCCAGATCCACCAN 530
QY      162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
Db      531 TATTGGGACTTNTGAACAAGAACGTCAAAGATGGATGGCAAGATCCAAAGCAAAGATC 590
QY      182 ProGlyLeuLysArgLysAlaGlu 189
Db      591 CCNNCTTGAAGCGCNCNNACTGAG 614

RESULT 78
BI39629
LOCUS   1028 bp mRNA linear EST 25-NOV-2002
DEFINITION
603134795F1 CSEQCHL24 Gallus gallus cDNA clone CHEST117m23 5', mRNA
sequence.
ACCESSION
BI39629
VERSION
BI39629.1 GI:25354039
KEYWORDS
EST.
SOURCE
Gallus gallus (chicken)
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 1028)
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Pong,W.T., Fickie,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
22335534
12445392
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1..1028
/organism="Gallus gallus"
/mol_type="mRNA"
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/db_xref="taxon:9031"
/clone="CHEST117m23"
/dev_stage="16 day embryo"
/lab_host="DH10B"
/clone_lib="CSEQCHL24"
/note="Organ: brain; Vector: pBluescript II KS(+); Site 1:
EcoRI; Site 2: NotI; Modification of pBluescript II KS(+)
[Stratagene] vector to accommodate cDNA produced with the
T-trimmed protocol [Construction of uni-directionally
cloned cDNA libraries from messenger RNA for improved 3'

```

end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BsgI and BamHI sites [5'ggcgctgagcccgatccgagaaaaag] [5'aattcttttttgcgagtcggggctgacgc]

## ORIGIN

Alignment Scores:  
Pred. No.: 5,13e-96 Length: 1028  
Score: 863.00 Matches: 178  
Percent Similarity: 96.34% Conservative: 6  
Best Local Similarity: 93.19% Mismatches: 5  
Query Match: 92.70% Indels: 2  
DB: 5 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BUI39629 (1-1028)

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QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
DB 186 TCAGTTGTTGACCTCTTCTGCGGAGACATTAAAGACAGGAGTGTGTGGTGC 245
QY 21 SerLeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 246 AGCTTGTCTCTGCTCTCATTAACAGTTCAGCATCGTGAGCGTGACAGCTTACATT 305
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAla 60
DB 306 GCCTTGGCCCTGTTCTCTGACCATCAGCTTTAGGATATACAAGGGAGTTATCCAGGCA 365
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 366 ATCCAAAGTCCGATGAAGCCATCCATTAGGCGCTTACTTGAGTCTGATGAGTGTG 425
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
DB 426 TCTGAGAGCTGATTACAGAAATACACAGCTGTGTCTTGTTCACATCAACGCCAGTC 485
QY 101 LysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaVal 120
DB 486 AAGGAGCTGAGAGCGCTCTCTCTGTTGATGACTTGTGTTGATTTCTGAAAGTTGCA 545
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
DB 546 TTGATGGGTGTCTACTTACGTGTGTGCTTGTGTTAATGCTGTGATTTACTGATCTG 605
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
DB 606 GCTTTGATTTCTGCTGTTTCAGTGTCTCTGTTATTTATGAGACATCAGGCCAGATCG 665
QY 161 HisTyrLeuGlyLeuAlaLeuLysAsnValLysAspAlaMetAla-LysIleGlnAlaLys 180
DB 666 CATTATTGGGACTAGTGAACAGAACGTCGAAGATGCGATGCGCAAAAGATCCAAAG 725
QY 180 stlePro-GlyLeuLysArgLysAlaGlu 189
DB 726 GATCCCTGGCTTGAAGCGCAAAACTGAG 754

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RESULT 79  
CD000871  
LOCUS CD000871 735 bp mRNA linear EST 01-MAY-2003  
DEFINITION AGENCOURT 13650322 NIH\_MGC\_186 Homo sapiens cDNA clone  
IMAGE:30321390 5', mRNA sequence.

ACCESSION CD000871  
VERSION CD000871.1 GI:30295402  
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 735)

TITLE NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)  
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: NDCM120 row: 1 column: 07  
High quality sequence stop: 530.

## FEATURES

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/clone="IMAGE:30321390"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_186"  
/note="Organ: Pooled-Skin; Vector: pDNR-LIB; Site 1: SfiI (ggccattggcc); Site 2: SfiI (ggcgctcgcc); Library is oligo-dr primed and directionally cloned. cDNA was prepared from a pooled samples of tissues from Skin, meninges, duramatter, pia matter and choroid plexus. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGGCCGACATG-dt(30)BN-3' (where B = A, C, G or T). Average insert size 1.47 kb (range 0.50-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library"

## ORIGIN

Alignment Scores:  
Pred. No.: 5,63e-96 Length: 735  
Score: 861.00 Matches: 180  
Percent Similarity: 98.36% Conservative: 0  
Best Local Similarity: 98.36% Mismatches: 1  
Query Match: 92.48% Indels: 2  
DB: 6 Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x CD000871 (1-735)

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QY 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
DB 189 GTTGTGACCTCCTCTACTGAGAGACATTAAAGACAGCTGAGTGTGTGGTGCAGC 248
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 249 CTTATCTCTGCTCTTTCATTGACGATTTACGATTTGTGAGCGTAACACGCTTACAT 308
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 309 TTGGCCCTGCTCTCTGTGACCATCAGCTTAGGATATACAAGGTGTGATCCAGTATC 368
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 369 CAGAAATCAGATGAAGGCCACCCATTACGGGCATATCTGGAATCTGAAGTTGCTATAT 428
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
DB 429 GAGGAGTTGGTTTCAGAAATACAGTAAATCTCTCTTGGTCATGTGAACATGACGATA 488
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 489 GAATCAGCGCGCTCTTCTTAGTGTAGTATTTAGTTGATTTCTCTGAAGTTTCAGAT 548
QY 122 MetTrpValPheThrTyrVal-GlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
DB 549 ATGTGGGTATTACCTATGTTTGGTGCCTTGTGTTAATGCTCTGACACTACTGATTGTC 608

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QY 141 aleulleSerLeuPheSer-ValProValilleTyrGluArgHisGlnAlaGlnIleAspH 161  
 Db 609 TCTCATTTCACTCTTCAGTGGTTCCTGTATTATGAACGGCATCAGGCACAGATAGATC 668  
 QY 161 isTyrLeuGlyLeuAlaAsnLysAanValLysAspAlaMetAlaLysIleGlnAlaLysI 181  
 Db 669 ATTATCTAGGACTTCCCAATAAAATGTTAAAGATGCTATGGCTAAAAATCCAGCCAAA 728  
 QY 181 lePro 182  
 Db 729 TCCCT 733  
 RESULT 80  
 CN791158  
 LOCUS 4125836 BARC 8BOV Bos taurus cDNA clone 8BOV\_41013 5', mRNA  
 DEFINITION linear EST 26-MAY-2004  
 ACCESSION CN791158.1 GI:47687138  
 VERSION CN791158.1  
 KEYWORDS EST.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 677)  
 Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.P. and  
 Matukumalli,L.K.  
 Construction and Analysis of a cDNA Library Generated From  
 Intestinal Muscle and Epithelial Tissues of Holstein Cattle  
 Unpublished (2004)  
 JOURNAL Contact: Richard G. Baumann  
 COMMENT Bovine Functional Genomics Lab  
 ANRI  
 BLDG 162: BARC-EAST, Beltsville, MD 20705, USA  
 Tel: 3015048604  
 Fax: 3015048744  
 Email: rbaumann@anri.barc.usda.gov  
 Single pass sequencing. Bases called and trimmed with phred  
 0.000925 using options -trim\_alt '- -trim\_fasta. Vector identified  
 by cross\_match using options -minmatch 12 -minscore 18  
 Plate: 41 row: O column: 13  
 Seq primer: CCTATTAGTGACACTATAGAAC  
 High quality sequence stop: 677.  
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 Location/Qualifiers  
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 /clone="8BOV 41013"  
 /sex="Female"  
 /tissue\_type="Epithelial, Muscle"  
 /dev\_stage="Lactating, Neonatal"  
 /lab\_host="DH10B TonA"  
 /note="Organ: Intestine; Vector: pCMVSPORT6.1; Site 1:  
 Not1; Site 2: EcoRI; Normalized cow cDNA intestinal  
 library in pCMVSPORT6.1, constructed from equimolar mRNA  
 pools derived from 5 sources, 4 lactating intestinal, 1  
 neonatal intestinal 4/5 Lactating, Proximal Duodenum,  
 Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal  
 Duodenum, Jejunum, Distal Ileum"

QY 2 ValValAspLeuLeuTyrTrrArgAspIleLysLysThrGlyValValPheGlyAlaSer 21  
 Db 156 GTTGTGGACCTCCCTCTACTGGAGAGACATTAAAGAGACTGGAGTGGTGTGGTCCACG 215  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
 Db 216 TTGTTCTCTGCTGCTCTGCTGACAGATTTACGACATTGTGAGTGTAAACGGCTTACATTGCC 275  
 QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61  
 Db 276 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAGGGGTGTGATCCAGCGTATC 335  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81  
 Db 336 CAGAAATCTGATGAAGCCACCACTTCAGGCGATATTGGGAATCTGAAGTTGCTATATCT 395  
 QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101  
 Db 396 GAGGAGTTGGTTTCAGAGTACAGCAATTTCTCTCTTGGTTCATGTTAACTGCACATAAAA 455  
 QY 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
 Db 456 GAACCTCAGACGCCCTCTTCTTAGTTGATGATTAGTTGATTCTCTGAAGTTTGCAGTGTG 515  
 QY 122 MetTrpValPheThrTyrValGlyValAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 Db 516 ATGTGGGTATTACCTATGTTGGTGGCTTGTTCATGTCGTGACACTACTAATTTGGCT 575  
 QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161  
 Db 576 CTGATTTCACTCTTCAGTGTTCCTGTTATTATTGAACGGCATCAGGCCCAATAGATCAT 635  
 QY 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAla 175  
 Db 636 TATCTGGACTTGCAATAAGATGTTAAAGATGCTATGGCT 677  
 RESULT 81  
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 LOCUS 603133909F1 CSEQCHL24 Gallus gallus cDNA clone ChEST115a3 5', mRNA  
 DEFINITION sequence.  
 ACCESSION BUI38907  
 VERSION BUI38907.1 GI:25353139  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 759)  
 Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
 Ford,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
 A Comprehensive Collection of Chicken cDNAs  
 Curr. Biol. 12 (22), 1965-1969 (2002)  
 JOURNAL 2235534  
 MEDLINE 12445392  
 PUBMED 12445392  
 COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612089930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.  
 Location/Qualifiers  
 1..759  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="White Leghorn, Hisex"  
 /db\_xref="taxon:9031"  
 /clone="ChEST115a3"

FEATURES  
 source  
 Alignment Scores:  
 Pred. No.: 8.86e-96 Length: 677  
 Score: 859.00 Matches: 174  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 92.27% Indels: 0  
 DB: 7 Gaps: 0

ORIGIN

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/dev stage="16 day embryo"
/lab_host="DH10B"
/clone_lib="CSQCHL24"
/Note="Organ: Brain; Vector: pBluescript II KS(+); Site 1:
EcoRI; Site 2: NotI; Modification of pBluescript II KS(+)
[Stratagene] vector to accommodate cDNA produced with the
T-trimmed protocol. (Construction of uni-directionally
cloned cDNA libraries from messenger RNA for improved 3'
end DNA sequencing by Glenn Fu, et al. U.S. Patent #
6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
Ligate in double stranded adaptor containing BsgI and
BamHI sites [5'ggcgctgcagcccgatccgagaaaaag]
[5'aattcttttttcggatccg999ctgcagc]
```

## ORIGIN

## Alignment Scores:

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Pred. No.: 1-85e-95 Length: 759
Score: 857.00 Matches: 176
Percent Similarity: 96.81% Conservative: 6
Best Local Similarity: 93.62% Mismatches: 6
Query Match: 92.05% Indels: 1
DB: 5 Gaps: 0
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US-09-830-972-29\_COPY\_990\_1178 (1-189) x BUI38907 (1-759)

```
QY 2 ValValAspLeuLeuTyrTrpArgAspLysLysThrGlyValValPheGlyAlaSer 21
DB 137 GTTGTGAGCTCTTACTGGCAGACATTAAAGACAGGAGTGGTGTGGTGCAGC 196
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 197 TTGTTCTCTGCTCTCATTAACAGTGTTCAGCATCGTGAGCGTGACCTTACATGGC 256
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 257 TTGGCCCTGCTTCTCTGACCATCAGCTTTAGGATATACAGGAGTATCCAGGCAATC 316
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 317 CAAAGTCGCGATGAGGCCATCCATTTAGGGCTTACTTGGAGTCTGATAGTGTGTCT 376
QY 82 GluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAenCysThrIleLys 101
DB 377 GAAGAGCTGATTCAGAAATACAGCAGTGTGTGCTTGGTCACATCAACGCGCAGTCAAG 436
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 437 GAGCTGAGAGCGCTCTCTCGTTGATGACTTGGTTGATTCCTGAAGTTTCAGGTGG 496
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuLeuAla 141
DB 497 ATGTGGGTGTCACTTACGTGGTGGCTGCTTTAAATGGTCTGACATTTACTGATCTGG 556
QY 142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAphHis 161
DB 557 TTGATTCGCTGTTCAGTGTCTCTGTTATTTATGAGAGACATCAGGCCAGATCGACCAT 616
QY 162 TyrLeuGlyLeuAlaAenLysAenValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
DB 617 TATTTGGGACTAGTGACAGAACGTCACAA-GATGCGATGGCAAGATCCAGCAAGATC 675
QY 182 ProGlyLeuLysArgLysAlaGlu 189
DB 676 CTTGGGCTGAAGCGCAAACTGAG 699
```

## RESULT 82

## CR771568

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LOCUS CR771568 684 bp mRNA linear EST 23-SEP-2004
DEFINITION DKFZp469C2337_r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
ACCESSION DKFZp469C2337 5', mRNA sequence.
VERSION CR771568
KEYWORDS CR771568.1 GI:52614841 EST.
```

SOURCE  
ORGANISM

Pongo pygmaeus (orangutan)

Pongo pygmaeus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pongo.

## REFERENCE

1 (bases 1 to 694)

## AUTHORS

Ottewaelder, B., Obermaier, B., Deutschenbaure, S., Schaipp, A.,

Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and

Wiemann, S.

## TITLE

Pongo pygmaeus mRNA (Ottewaelder, B., Obermaier, B.,

Deutschenbaure, S., et al.)

## JOURNAL

Unpublished (2004)

## COMMENT

Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert. Clone from S. Wiemann,  
Molecular Genome Analysis, German Cancer Research Center (DKFZ);  
Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix  
(Martinsried/Germany) within the cDNA sequencing consortium of the  
German Genome Project. This clone (DKFZp469C2337) is available at  
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in  
Berlin, Germany. Please contact RZPD for ordering:  
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp469C2337

Further information about the clone and the sequencing project is  
available at http://mips.gsf.de/projects/cdna/.

## FEATURES

source

location/Qualifiers

1..684

/organism="Pongo pygmaeus"

/mol\_type="mRNA"

/db\_xref="taxon:9600"

/clone="DKFZp469C2337"

/tissue\_type="kidney"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="469 (synonym: pkid1)"

/note="Vector: pSport1\_Sfi; Site\_1: SfiI; Site\_2: SfiIb"

## ORIGIN

## Alignment Scores:

```
Pred. No.: 3.75e-95 Length: 684
Score: 854.00 Matches: 173
Percent Similarity: 99.43% Conservative: 0
Best Local Similarity: 99.43% Mismatches: 1
Query Match: 91.73% Indels: 0
DB: 7 Gaps: 0
```

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CR771568 (1-684)

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QY 2 ValValAspLeuLeuTyrTrpArgAspLysLysThrGlyValValPheGlyAlaSer 21
DB 162 GTTNTGACCTCTCTTACTGGAGACACATTAAAGACCTGGAGTGGTGTGGTGCAGC 221
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 222 CTATTCTGCTGCTTTCATTGACAGTATTTCAGCATTTGTGAGTGTAAACAGCTTAC 281
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
DB 282 TTGGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAGGGTGTGATCCAGCTATC 341
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 342 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAAATCTGAAGTTGCTATCT 401
QY 82 GluGluLeuValGlnLysTyrSerAenSerAlaLeuGlyHisValAenCysThrIleLys 101
DB 402 GAGGAGTTGGTTTCAGAAGTACAGTAATCTCTCTTGTGTCACTGTGAACGTGCACGATA 461
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 462 GAACCTCAGCGCCTCTCTTCTAGTATTTAGTATCTCTGAAGTTTCAGGTGTG 521
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAenGlyLeuThrLeuLeuAla 141
```



```

Db      522 ATGTGGGATTACCTATGTTGGTGGCTGTTTAAATGGTCTGACGCTACTGATTTGGCT 581
Qy      142 LeuileSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db      582 CTCATTTTCACTCTTTCAGTGTCTCTGTTATTATGAACGGCATCAGGCACAGATAGATCAT 641
Qy      162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAla 175
Db      642 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGGCT 683

RESULT 83
BU848611      813 bp      mRNA      linear      EST 16-OCT-2002
AGENCY      10276498 NIH MGC 144 Mus musculus cDNA clone
IMAGE      6596409 5', mRNA sequence.

ACCESSION      BU848611
VERSION
KEYWORDS
SOURCE
ORGANISM      Mus musculus (house mouse)
REFERENCE      NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS      National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE      Unpublished (1999)
JOURNAL
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: c9apbs-r@mail.nih.gov
              Tissue Procurement: Dr. Michael Brownstein
              cDNA Library Preparation: Michael Brownstein Laboratory
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLCW2825 row: p column: 09
              High quality sequence stop: 160.

FEATURES
source
1. 813
   /organism="Mus musculus"
   /mol_type="mRNA"
   /db_xref="taxon:10090"
   /clone="IMAGE:6596409"
   /lab_host="DH10B (T1-phage-resistant)"
   /clone_lib="NIH MGC 144"
   /note="Organ: Brain; Vector: pDNR-LIB; Site 1: SfiI
         (ggccatagggc); Site 2: SfiI (ggccgcctggcc); cDNA made
         by oligo-dT priming and directionally cloned. 5' and 3'
         adaptors were used in cloning as follows:
         5'-AAGCAGTGTATCAACGAGAGTGCGCATTCAGCGCGG-3' and
         5'-ATTCTAGAGCGCGCGCGGCGACATG-DT(30)NN-3'. Full-length
         enriched library was constructed using the Clontech
         Creator SMART kit and size-selected to contain the 0.2-0.5
         kb size fraction (other fractions present in NIH MGC 143).
         Library created in the laboratory of M. Brownstein (NIH,
         NIH). Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.:      4.8e-95      Length:      813
Score:          854.00      Matches:    179
Percent Similarity: 95.79%      Conservative: 3
Best Local Similarity: 94.21%      Mismatches: 6
Query Match:    91.73%      Indels:    2
Db:             5          Gaps:      0

US-09-830-972-29_COPY_990_1178 (1-189) x BU848611 (1-813)

Qy      2 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db      159 GTTGTGACCTCCTGCTACTGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGGCCAGC 218
Qy      22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41

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Db      219 TTATTCCTGCTGCTGCTCTCTGACAGTGTTCAGCATTTGTCAGTGTAAACGCCCTACATTCGC 278
Qy      42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db      279 TTGGCCCTGCTCTCTGTGACTATCAGCTTTTAGGATATATAAGGGTGTGTATCAAGCTATC 338
Qy      62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db      339 CAGAAATCAGATGAAGGCCACCCATTTCAGGCGCATTTTGGATCTGAAGTTGCCATATCA 398
Qy      82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db      399 GAGGAATTTGGTTTCAAAATATAGTAATTTCTCTTGTGTCATGTGAACAGCACAATAAAA 458
Qy      102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db      459 GAATTGAGCGCTCTCTTCTTAGTTGATGATTTAGTTGATTCCTCGAAGTTTCAGTGTG 518
Qy      122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
Db      519 ATGTGGGTATTACTAGTGTGGTGGCTTGTTCATGTTGACACTACTGATTTAGCT 578
Qy      142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db      579 CTGATCTCACTCTTCAGTATTCTCTTATATATGAACGGCATCAGCGCGCAGATAGATCAT 638
Qy      162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMet-AlaLysIleGlnAlaIle 181
Db      639 TATCTAGGACTTGC AAAACACAGCGGTAAAGATGCCATGCCATGNNCAAAATCCCAAGCAAAAT 698
Qy      181 eProGlyLeu-LysArgLysAlaGlu 189
Db      699 CCTTGGATTGANGCGCAAAACAGNA 724

RESULT 84
BU847877      614 bp      mRNA      linear      EST 05-SEP-2001
LOCUS      603192073P1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5263026 5',
DEFINITION      mRNA sequence.
ACCESSION      BU847877
VERSION      BU847877.1 GI:15435189
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              NIH-MGC http://mgi.nci.nih.gov/.
              National Institutes of Health, Mammalian Gene Collection (MGC)
              Unpublished (1999)
              Contact: Robert Strausberg, Ph.D.
              Email: c9apbs-r@mail.nih.gov
              Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
              cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
              Toshiyuki and Piero Carninci (RIKEN)
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM11663 row: b column: 19
              High quality sequence stop: 614.

FEATURES
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1. 614
   /organism="Homo sapiens"
   /mol_type="mRNA"
   /db_xref="taxon:9606"
   /clone="IMAGE:5263026"
   /tissue_type="hippocampus"
   /lab_host="DH10B"
   /clone_lib="NIH_MGC_95"
   /note="Organ: brain; Vector: pBluescriptR (modified)

```

pbluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores: 7.56e-95 Length: 614  
Pred. No.: 851.00 Matches: 174  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 91.41% Gaps: 0  
DB: 4

US-09-830-972-29\_COPY\_990\_1178 (1-189) x B1547877 (1-614)

QY 16 ValValPheGlyAlaSerLeuPheLeuSerLeuThrValPheSerIleValSer 35  
Db 7 GTGGTGTGGTCCAGCCTATTCTGCTGCTTCATTGACAGTATTCAGCATTTGTGAGC 66

QY 36 ValThrAlaTyrlleAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrls 55  
Db 67 GTAACAGCCTACATTCCTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAG 126

QY 56 GlyValIleGlnAlaIleGlnIlySerAspGluGlyHisProPheArgAlaTyrlleGlu 75  
Db 127 GGTGTGATCCAGCTATCCAGAAATCAGATGAAGGCCATTCAGGGCATATCTGGAA 186

QY 76 SerGluValAlaIleSerGluGluLeuValGlnIlySerSerAsnSerAlaLeuGlyHis 95  
Db 187 TCTGAAGTTGCTATATCTCAGGAGTGGTTTCAGAACTACAGTAATTCCTGTCAT 246

QY 96 ValAsnCysThrIleIlySerGluLeuArgArgLeuPheLeuValAspSerValAspSer 115  
Db 247 GTGAACCTGCAGCAGTAAAGAACTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTC 306

QY 116 LeuIlyPheAlaValLeuMetTrpValPheThrTyrlleValGlyAlaLeuPheAsnGlyLeu 135  
Db 307 CTGAAGTTGCAGTGTGATGGGATTTACCTATGTTGGCCCTGTTTAAATGTCGTCG 366

QY 136 ThrLeuLeuIleAlaLeuIleSerLeuPheSerValProValIleTyrlleGluArgHis 155  
Db 367 ACACACTGATTTGGCTCTCATTTCTCAGTGTTCTCTGTTATTTATGAAGCGCAT 426

QY 156 GlnAlaGlnIleAspHisTyrlleGlyLeuAlaAsnIlyAsnValIlyAspAlaMetAla 175  
Db 427 CAGGCACAGATGATCATTTATCTAGGACTTGCAGAAATGAAGATGTTAAAGATGCTATGCT 486

QY 176 LysIleGlnAlaIlyIleProGlyLeuIlyAsnGlyAlaGlu 189  
Db 487 AATATCCAGCAAAAATCCCTGGATTGAAGCGCAAGAGCTGAA 528

## RESULT 85

CN429726 708 bp mRNA linear EST 16-MAY-2004  
LOCUS 170005934467 GRN\_PRENU Homo sapiens cDNA 5', mRNA sequence.

## DEFINITION

CN429726

## ACCESSION

CN429726.1 GI:47417320

## VERSION

EST.

## KEYWORDS

Source

## SOURCE

Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## REFERENCE

AUTHORS

1 (bases 1 to 708)  
Bradenberger, R., Wei, H., Zhang, S., Lei, S., Mura, J., Fisk, G.J.,  
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,  
Lebkowski, J. and Stanton, L.W.

## TITLE

Transcriptome characterization elucidates signaling networks that

## JOURNAL

## COMMENT

control human ES cell growth and differentiation  
Nat. Biotechnol. 22 (6), 707-716 (2004)  
Contact: Brandenberger R  
Regenerative Medicine  
Geron Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: rbrandenberger@geron.com  
Insert Length: 708 Std Error: 0.00.

## FEATURES

## Source

1..708  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="embryonic stem cell, retinoic acid and  
mitogen-treated hES cell line H7"  
/clone\_lib="GRN PRENU"  
/note="oligo dT-primed, full-length enriched cDNA library  
from hES cell line H7 (p29) maintained in feeder-free  
conditions. Embryoid bodies were generated in the presence  
of all-trans retinoic acid and mitogens."

## ORIGIN

Alignment Scores: 9.27e-95 Length: 708  
Pred. No.: 851.00 Matches: 174  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 91.41% Gaps: 0  
DB: 7

US-09-830-972-29\_COPY\_990\_1178 (1-189) x CN429726 (1-708)

QY 16 ValValPheGlyAlaSerLeuPheLeuSerLeuThrValPheSerIleValSer 35  
Db 1 GTGGTGTGGTCCAGCCTATTCTGCTGCTTCATTGACAGTATTCAGCATTTGTGAGC 60

QY 36 ValThrAlaTyrlleAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrls 55  
Db 61 GTAAACAGCCTACATTCCTGGCCCTGCTCTGTGACCATCAGCTTTAGGATATACAAG 120

QY 56 GlyValIleGlnAlaIleGlnIlySerAspGluGlyHisProPheArgAlaTyrlleGlu 75  
Db 121 GGTGTGATCCAGCTATCCAGAAATCAGATGAAGGCCATTCAGGGCATATCTGGAA 180

QY 76 SerGluValAlaIleSerGluGluLeuValGlnIlySerSerAsnSerAlaLeuGlyHis 95  
Db 181 TCTGAAGTTGCTATATCTCAGGAGTGGTTTCAGAACTACAGTAATTCCTGCTGTCAT 240

QY 96 ValAsnCysThrIleIlySerGluLeuArgArgLeuPheLeuValAspSerValAspSer 115  
Db 241 GTGAACCTGCAGCAGTAAAGAACTCAGCGCCCTCTCTTAGTTGATGATTTAGTTGATTC 300

QY 116 LeuIlyPheAlaValLeuMetTrpValPheThrTyrlleValGlyAlaLeuPheAsnGlyLeu 135  
Db 301 CTGAAGTTGCAGTGTGATGGGATTTACCTATGTTGGCCCTGTTTAAATGTCGTCG 360

QY 136 ThrLeuLeuIleAlaLeuIleSerLeuPheSerValProValIleTyrlleGluArgHis 155  
Db 361 ACACACTGATTTGGCTCTCATTTCTCAGTGTTCTCTGTTATTTATGAAGCGCAT 420

QY 156 GlnAlaGlnIleAspHisTyrlleGlyLeuAlaAsnIlyAsnValIlyAspAlaMetAla 175  
Db 421 CAGGCACAGATGATCATTTATCTAGGACTTGCAGAAATGAAGATGTTAAAGATGCTATGCT 480

QY 176 LysIleGlnAlaIlyIleProGlyLeuIlyAsnGlyAlaGlu 189  
Db 481 AATATCCAGCAAAAATCCCTGGATTGAAGCGCAAGAGCTGAA 522

## RESULT 86

## BG568630

## LOCUS

BG568630 755 bp mRNA linear EST 10-APR-2001

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DEFINITION 602587637F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4716393 5',
mRNA sequence.
ACCESSION BG568630
VERSION BG568630.1 GI:13576283
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 755)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM1564 row: j column: 10
High quality sequence stop: 719.
Location/Qualifiers
1..755
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4716393"
/lab host="DH10B (T1 phage-resistant)"
/clone lib="NIH MGC 76"
/note="organ: liver; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggcccttcggcc); Site 2: SfiI (ggccattggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.85
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

FEATURES
source
BG428512 906 bp mRNA linear EST 14-MAR-2001
LOCUS 602501030F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4614679 5',
DEFINITION mRNA sequence.
ACCESSION BG428512
VERSION BG428512.1 GI:13335018
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 906)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM1366 row: l column: 08
High quality sequence stop: 730.
Location/Qualifiers
1..906
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4614679"
/lab host="DH10B (T1 phage-resistant)"
/clone lib="NIH MGC 75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccgcttcggcc); Site 2: SfiI (ggccattggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores: 1.32e-94 Length: 906
Pred. No.: 851.00 Matches: 184
Score: 96.86% Conservative: 2
Percent Similarity: 95.81% Mismatches: 3
Best Local Similarity: 91.41% Indels: 4
Query Match: 4 Gaps: 0
DB: 4

US-09-830-972-29_COPY_990_1178 (1-189) x BG568630 (1-755)

Qy 2 ValValAspLeuLeuTyTrpArgAspIleLysLysThrGlyValValPheGlyAlaSer 21
Db GTTGTGTACCTCCTGTACTGGAGACATTAAGAGACTGGAGTGTGTGTGGTGGCCAGC 237
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrlleAla 41
Db CTATTCTCTGCTTTCATTGACAGTATTGACATTGTGAGCGTAACAGCCTACATTGCC 297
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyLysGlyValIleGlnAlaIle 61
Db TTGGCCCTCGCTCTGTGACCATCATCAGCTTTAGGATATACAAAGGGTGTGATCAAGCTATC 357
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyLysLeuGluSerGluValAlaIleSer 81
Db CAGAATATAGATGAAGGCCACCCATTACAGGCATATCTGGATCTGAAGTGTCTATATCT 417
Qy 82 GluGluLeuValGlnLysTyTrpSerAsnSerAlaLeuGlyHisValAsnCyThrIleLys 101
Db GAGGAGTTGGTTTCAGAAAGTACAGTAATTTCTGCTCTGGGTCTATGTGAACTGCACGATAAG 477

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Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121
Db GAATCAGGCGCCCTCTTCTTAGTGTATGATTTAGTTGATTTCTCTGAAGTTTGCATGTTG 537
Qy 122 MetTrpValPheThrTyTrpValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141
Db ATGTGGGTATTATCTATGTTGGTTCCTTTGTTTAAATGCTCTGACACTACTGAT-TTGGCT 596
Qy 142 LeuLeuSerLeuPheSerValProValIleTyGluArgHisGlnAlaGlnIleAspHis 161
Db CTCAATTCACCTCTTCAGTGTTCCTGTTATTATGAACGCGCATCAGGCACAGATGATCAT 656
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAla-MetAlaLysIleGlnAla--Lys 180
Db TATCTAGACCTTGCATTAAGAATGTTACAGATGCTAATGTTAAATCCAAAGCAAAA 716
Qy 181 IleProGlyLeuLysArgLysAlaGlu 189
Db ATCCCTGATTTGAAGCGCAAAAGTGAA 743

RESULT 87
BG428512 906 bp mRNA linear EST 14-MAR-2001
LOCUS 602501030F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4614679 5',
DEFINITION mRNA sequence.
ACCESSION BG428512
VERSION BG428512.1 GI:13335018
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 906)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM1366 row: l column: 08
High quality sequence stop: 730.
Location/Qualifiers
1..906
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4614679"
/lab host="DH10B (T1 phage-resistant)"
/clone lib="NIH MGC 75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccgcttcggcc); Site 2: SfiI (ggccattggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores: 1.32e-94 Length: 906
Pred. No.: 851.00 Matches: 184
Score: 96.86% Conservative: 0
Percent Similarity: 98.40% Mismatches: 2
Best Local Similarity: 98.40%

```

```

Query Match: 91.41% Indels: 3 Gaps: 0
DB: 4

US-09-830-972-29_COPY_990_1178 (1-189) x BG428512 (1-906)

QY 2 ValValAspLeuLeuTyrTrpArgAspIleValLeuThrGlyValValPheGlyAlaSer 21
DB 103 GTTGTGACCTCTGTTCTGGAGACATTAGAGACATGGAGTGGTGTGGTGGCCAGC 162
QY 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
DB 163 CTATTCCTGCTGCTTTCATTCAGCAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 222
QY 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAlaIle 61
DB 223 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 282
QY 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
DB 283 CAGAAATCAGATGAGCGCCACCATTCAGGCATATCTGGAATCTGGAATCTGATATATCT 342
QY 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
DB 343 GAGGAGTGTGTTTCAGAAAGTACAGTAATCTGCTCTTGGTCATGTGAAGTGCAGTAAAG 402
QY 102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
DB 403 GAACTCAGCGCGCTCTCTTAGTGTGATGATTTAGTTGATTTCTCTGAAGTTTGCAGTGTG 462
QY 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAla 141
DB 463 ATGTGGGTATTTACCTATGTTGGTGGCTGTTTAAATGGTCTGACACTACTGATTTTGGT- 521
QY 142 LeuIleSerLeuPheSerValProValIleTyrGlu-ArgHisGlnAlaGlnIleAspHi 161
DB 522 CTCATTTCACTCTTCAGTGTCTCTGTTATTTATGAACCGGCATCAGGCACAGATATCA 581
QY 161 sTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysI 181
DB 582 TTATCTAGGACTTGCAAATGAAGAATGTTAAAGATGCTATGGT-AAAATCCAAAGCAAAAT 640
QY 181 eProGlyLeuLysArgLys 187
DB 641 CCTGTGATTGAGCGCAAA 659

RESULT 88
LOCUS BUI09449
DEFINITION BUI09449 915 bp mRNA linear EST 25-NOV-2002
sequence.
BUI09449
VERSION BUI09449.1 GI:25312699
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 915)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
22335534
12445392
COMMENT Department of Molecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

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FEATURES
source
Location/Qualifiers
1..915
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, HiseX"
/db_xref="taxon:9031"
/clone="ChEST95f15"
/dev_stage="22"
/lab_host="DH10B"
/clone_lib="CSQCHL13"
/note="Organ: limbs; Vector: pBluescript II KS(+); Site 1:
EcoRI; Site 2: NotI; Modification of pBluescript II KS(+)
[Stratagene] vector to accommodate cDNA produced with the
T-trimmed protocol (Construction of uni-directionally
cloned cDNA libraries from messenger RNA for improved 3'
end DNA sequencing by Glenn Fu, et al. U.S. Patent #
6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
Ligate in double stranded adaptor containing BsgI and
BamHI sites [5'ggcgggtgcagcccgatccgaaaaaaag]
[5'aattcttttttcggatccg999gtcgacgc]"

ORIGIN
Alignment Scores:
Pred. No.: 1,78e-94 Length: 915
Score: 850.00 Matches: 175
Percent Similarity: 96.30% Conservative: 7
Best Local Similarity: 92.53% Mismatches: 7
Query Match: 91.30% Indels: 1
DB: 5 Gaps: 0

US-09-830-972-29_COPY_990_1178 (1-189) x BUI09449 (1-915)

QY 1 SerValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAla 20
DB 127 GCGGTTGTGGTGTGCTCTTACTTGGCGAGACATTAAAGACAGAGGTGGTGTGGTGGC 186
QY 21 SerGluPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIle 40
DB 187 AGCTTGTTCCTGCTGCTCTCATTAACAGTGTTCAGCACTCGTGGGTGACAGCTTACAT 246
QY 41 AlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAla 60
DB 247 GCCTTGGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAAGGAGTATTCAGGCA 306
QY 61 IleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIle 80
DB 307 ATCCAAAAGTCCGATGAAGGCCATCCATTTAGGGCTTACTTGGAGTCTGATGTAGCTGTG 366
QY 81 SerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIle 100
DB 367 TCTGAAGAGCTGATTCAGAAATACAGCAGTGTGTGCTTGGTGCATCAACCGCACAGTTC 426
QY 101 LysGluLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaVal 120
DB 427 AAGGAGCTGAGACGCTCTTCTCGTTGATGATCTTGGTGTGTTCTCTGAAGTT-TCAGTGTG 485
QY 121 LeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeu 140
DB 486 TTGATGTGGGTGTTTCACTTACCTTGGTGGCTTGTGTTTAAATGGTCTGACATTTACTGACTGTG 545
QY 141 AlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAsp 160
DB 546 GCTTTGATTTCCGCTGTTCTGAGTGTTCCTGTTATTTATGAGAGACATCAGGCCCATCGAC 605
QY 161 HistyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLys 180
DB 606 CATTAATGGGAGCTAGTGAACAAGAACGTCAAAGATGCGATGCGTGAAGATGCAAGCAAG 665
QY 181 IleProGlyLeuLysArgLysAlaGlu 189
DB 666 ATCCCTGGGCTGAAGCGCAAAATTTGAG 692

RESULT 89

```

BQ807975  
LOCUS NISC kkl12d10.v1 NCI CGAP Brn72 Macaca mulatta cDNA clone EST 31-JUL-2002  
DEFINITION IMAGE:5331139 5', mRNA sequence.  
ACCESSION BQ807975  
VERSION BQ807975.1 GI:22032184  
KEYWORDS EST.  
SOURCE Macaca mulatta (rhesus monkey)  
ORGANISM Macaca mulatta  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.  
REFERENCE 1 (bases 1 to 619)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
cDNA Library Preparation:  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL  
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC)  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
info@image.llnl.gov  
Plate: LLAM11840 row: H column: 20  
Seq primer: M13RP1 reverse primer (ABI).  
FEATURES  
source  
location/Qualifiers  
1..619  
/organism="Macaca mulatta"  
/mol\_type="mRNA"  
/db\_xref="taxon:9544"  
/clone="IMAGE:5331139"  
/tissue\_type="hypothalamus"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NCI CGAP Brn72"  
/Note="Organ: brain; Vector: pCMV-SPORT6.1; Site 1: Not I; Site 2: EcoRV; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.2 kb. Constructed by Invitrogen. Note: this is a NCI\_CGAP Library."

Alignment Scores:  
Pred. No.: 1 35e-94 Length: 619  
Score: 849.00 Matches: 171  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 98.84% Mismatches: 0  
Query Match: 91.19% Indels: 0  
DB: 5 Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x BQ807975 (1-619)

Qy 2 ValValAspLeuLeuTyrrpArgAspIlelyslsThrglyValValPheGlyAlaSer 21  
Db 100 GTTGTGACCTCCTCTACTGGAGACATGAAGAGCTGGAGTGGTGTGGTGGCCAGC 159  
Qy 22 LeuPheLeuLeuLeuSerleuThrValPheSerlleValSerValThrAlaTyrrileAla 41  
Db 160 CTATTTCCTGCTGCTTTTCATTGACATATTGACGATTGTGAGTGTAAACAGCCTACATTGCC 219  
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrrLysGlyValIleGlnAlaIle 61  
Db 220 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAGGGGTGTGATCAAGCTATC 279  
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrrLeuGluSerGluValAlaIleSer 81  
Db 280 CAGAAATCAGATGAAGGCCACCATTCAGGCGATATCTGGAATCTGAAGTGGCATATCT 339  
Qy 82 GluGluLeuValGlnLysTyrrSerAnsSerAlaLeuGlyHisValAsnCysThrIleLys 101  
Db 340 GAGGAGTGGTTTCAGAAGTACAGTAATTCCTGCTCTTGGTCTATGTGAACTGACCGATAAG 399

Qy 102 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAlaValLeu 121  
Db 400 GAACCTCAGCGCCCTCTCTTAGTTAGTATGATTAGTTAGTTCTCTGAAGTTTCAGTGTG 459  
Qy 122 MetTrpValPheThrTyrrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
Db 460 ATGTGGGTATTATACCTATGTTGGTGGCTTGTATTATGCTGACGCTACTGATTTGGCT 519  
Qy 142 LeuLysSerLeuPheSerValProValIleTyrrGluArgHisGlnAlaGlnIleAspHis 161  
Db 520 CTCATTTTCACCTCTTCAGGTGTTCTGTATTATTAACGCGCATCAGGCACAGATATCAT 579  
Qy 162 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMet 174  
Db 580 TATCTAGGACTTGCAATAAGAAATGTTAAAGATGCTATG 618  
RESULT 90  
CR771272 644 bp mRNA linear EST 23-SEP-2004  
LOCUS DKFZP469F2235 r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone  
DEFINITION DKFZP469F2235 5', mRNA sequence.  
ACCESSION CR771272  
VERSION CR771272.1 GI:52614545  
KEYWORDS EST.  
SOURCE Pongo pygmaeus (orangutan)  
ORGANISM Pongo pygmaeus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pongo.  
REFERENCE 1 (bases 1 to 644)  
AUTHORS Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.  
TITLE Pongo pygmaeus mRNA (Poustka, A., Albert, R., Moosmayer, P., et al.)  
JOURNAL Unpublished (2004)  
COMMENT Contact: MIPS  
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert. Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; any. Please contact RZPD for ordering:  
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZP469F2235  
Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.  
FEATURES  
source  
location/Qualifiers  
1..644  
/organism="Pongo pygmaeus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9600"  
/clone="DKFZP469F2235"  
/tissue\_type="kidney"  
/dev\_stages="adult"  
/lab\_host="DH10B"  
/clone\_lib="469 (synonym: pkid1)"  
/Note="Vector: pSport1\_Sfi; Site\_1: SfiI; Site\_2: SfiIb"

Alignment Scores:  
Pred. No.: 1 91e-94 Length: 644  
Score: 848.00 Matches: 172  
Percent Similarity: 97.73% Conservative: 0  
Best Local Similarity: 97.73% Mismatches: 4  
Query Match: 91.08% Indels: 0  
DB: 7 Gaps: 0  
US-09-830-972-29\_COPY\_990\_1178 (1-189) x CR771272 (1-644)

Qy 2 ValValAspLeuLeuTyrrpArgAspIlelyslsThrglyValValPheGlyAlaSer 21  
Db 115 GTTGTGACCTCCTCTACTGGAGACATTAAGAGACTGGAGTGGTGTGGTGGCCAGC 174  
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerlleValSerValThrAlaTyrrileAla 41

```

Db      175 CTATTCTGCTGCTTTCATTGACAGTATTACAGATTGTGAGTGTAAACAGCCTACATTGCC 234
QY      42  LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrIleGlyValIleGlnAlaIle 61
        |||||
Db      235 TTGGCCCTGCTTTCGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 294
QY      62  GlnIleSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
        |||||
Db      295 CAGAAATCAGATGAAGCCACCCATTACAGGCATATCTGGAATCTGGAATGTGATATATCT 354
QY      82  GluGluLeuValGlnIleTyrSerAenSerAlaLeuGlyHisValAsnCysThrIleIle 101
        |||||
Db      355 GAGGAGTTGNNTCAGAGTACAGTAATCTGCTCTTGGTCATGTCAGTGCAGTAAG 414
QY      102 GluLeuArgArgLeuPheLeuValAspLeuValAspSerIleuIysPheAlaValLeu 121
        |||||
Db      415 GAATTCANGCGCNCCTCTCTAGTTGATGATTTAGTTGATTTCTGGAATTTGAGTGTG 474
QY      122 MetTTPValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrIleuIleAla 141
        |||||
Db      475 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACGCTACTGATTTTGGCT 534
QY      142 LeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAepHis 161
        |||||
Db      535 CTCATTTCACTCTTCAGTGTTCCTGGTTATTTAATGAACGGCATCAGGCACAGATAGATCAT 594
QY      162 TyrLeuGlyLeuAlaAlaIleValIleValIleValIleValIleValIle 177
        |||||
Db      595 TATCTAGGACTTGCAAAATGAAGATGTTAAAGATGCTATGCTAAATATC 642

RESULT 91
BG696431      991 bp      mRNA      linear      EST 07-MAY-2001
LOCUS      602659532F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4802911 5',
DEFINITION      mRNA sequence.
ACCESSION      BG696431
VERSION      BG696431.1 GI:13961567
KEYWORDS      EST.
SOURCE      Homo sapiens
ORGANISM      Homo sapiens (human)
REFERENCE      1 (bases 1 to 991)
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL      NIH-MGC http://mgs.nci.nih.gov/.
COMMENT      National Institutes of Health, Mammalian Gene Collection (MGC)
              Unpublished (1999)
              Contact: Robert Strausberg, Ph.D.
              Email: cgabbs-r@mail.nih.gov
              Tissue Procurement: James Cleaver, M.D.
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
              Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: L1AM10697 row: 0 column: 08
              High quality sequence stop: 763.
              Location/Qualifiers
                1..991
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:4802911"
                  /lab_host="PH10B (T1 phage-resistant)"
                  /clone_lib="NCI CGAP Skn3"
                  /notes="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
                  Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                  Average insert size 1.5kb. Library constructed by Life
                  Technologies. Note: this is a NCI_CGAP Library."

FEATURES
source
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="IMAGE:4802911"
  /lab_host="PH10B (T1 phage-resistant)"
  /clone_lib="NCI CGAP Skn3"
  /notes="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
  Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
  Average insert size 1.5kb. Library constructed by Life
  Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Alignment Scores:      6.25e-94      Length:      991
Pred. No.:

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Score:      846.00      Matches:      181
Percent Similarity:      97.33%      Conservative:      1
Best Local Similarity:      96.79%      Mismatches:      3
Query Match:      90.87%      Indels:      3
DB:      4      Gaps:      0

US-09-830-972-29_COPY_990_1178 (1-189) x BG696431 (1-991)

QY      4  AspLeuLeuTyrTTPArgAspIleIysIysThrGlyValValPheGlyAlaSerLeuPhe 23
        |||||
Db      216 GACCTCTCTGACTCGAGAGACATTAAAGAACTGCGAGTGGTGTGGTCCAGCCTATTTC 275
QY      24  LeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAla 43
        |||||
Db      276 CTGCTGCTTTTCATTACAGTATTACAGCATTTGAGCGTAACAGCCTACATGCTTGGCC 335
QY      44  -LeuLeuSerValThrIleSerPheArgIleTyrIysGlyValIleGlnAlaIleGlnly 63
        |||||
Db      336 CTGTCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAGCTATCCAGAA 395
QY      63  sSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluG 83
        |||||
Db      396 ATCAGATGAAGGCCACCCCATTCAGGCGCATATCTGGAATCTGAAGTTGCTATATCTGAGGA 455
QY      83  uLeuValGlnIysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleIysGluLe 103
        |||||
Db      456 GTAGGTTTCAGAAAGTACAGTAATCTGCTCTTGGTCATGTGAACATGCACGATAAGAACT 515
QY      103 uArgArgLeuPheLeuValAspLeuValAspSerLeuIysPheAlaValLeuMetTr 123
        |||||
Db      516 CAGGCGCCTCTTCTAGTTGATGATTTAGTTGATTTCTGGAAGTTTGCAAGTTTGATGTG 575
QY      123 pValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLeuAla 143
        |||||
Db      576 GGTATTTACCTATGTTGGTGCCTTGTAAATGGTCTGACACTACTGAT-TTGGCTCTCAT 634
QY      143 eSerLeuPheSerValProValIleTyrGluArgHisGlnAla-GlnIleAspHisTyrL 163
        |||||
Db      635 TTCACCTTTCAGTGTTCCTGTTATTATGACGGCATCAGGCAACAGATAGATCATATTC 694
QY      163 euGlyLeuAlaAlaIleValIleValIleValIleValIleValIleGlnAlaIleProG 183
        |||||
Db      695 TAGGACTTGCATAATGAAGATGTCAAAGATGCTATGGTAAATCCAGCAAAATCCCTG 754
QY      183 llyLeuIysArgIysAla 188
        |||||
Db      755 GATTGAAGCGCAAAAGC 771

RESULT 92
BI548612      815 bp      mRNA      linear      EST 05-SEP-2001
LOCUS      603189563F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5261007 5',
DEFINITION      mRNA sequence.
ACCESSION      BI548612
VERSION      BI548612.1 GI:15435924
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 815)
AUTHORS      Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE      Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL      NIH-MGC http://mgs.nci.nih.gov/
COMMENT      National Institutes of Health, Mammalian Gene Collection (MGC)
              Unpublished (1999)
              Contact: Robert Strausberg, Ph.D.
              Email: cgabbs-r@mail.nih.gov
              Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
              cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
              Toshinuki and Piero Carninci (RIKEN)
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:

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http://image.llnl.gov  
 Plate: LLAM11657 row: n column: 16  
 High quality sequence stop: 757.

# FEATURES

source  
 1..815  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5261007"  
 /tissue\_type="hippocampus"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH\_MGC\_95"  
 /note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcagc); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 5.45e-94 Length: 815  
 Score: 845.50 Matches: 183  
 Percent Similarity: 96.32% Conservativeness: 0  
 Best Local Similarity: 96.32% Mismatches: 5  
 Query Match: 90.82% Indels: 3  
 DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x B1548612 (1-815)

QY 2 ValValAspLeuLeuThrValPheSerLeuLeuValPheGlyAlaSer 21  
 Db 169 GTTGTGACCTCTCTGACCATCAGCTTAGGATATACAGGGGTGATCCAGCTATC 348  
 QY 22 LeuPheLeuLeuSerLeuThrValPheSerLeuLeuValPheAlaVal 41  
 Db 229 CTATTCCTGCTGCTTTCATGACATATTGACATTTGAGCGTAACAGCTTACATGCC 288  
 QY 42 LeuAlaLeuLeuSerValThrLeuSerPheArgLeuLeuValPheGlyAlaVal 61  
 Db 289 TTGGCCCTGCTCTGTCACCATCAGCTTAGGATATACAGGGGTGATCCAGCTATC 348  
 QY 62 GlnLysSerAspGluGlyHisProPheArgAlaThrLeuGluSerGluValAlaLeuSer 81  
 Db 349 CAGAAATCAGATGAAGGCCACCGATTTCAGGCGCATATCTGGAATCTGGAAGTTGCTATATCT 408  
 QY 82 GluGluLeuValGlnLysThrSerAsnSerAlaLeuGlyHisValAsnCysThrLeuLys 101  
 Db 409 GAGGAGTTGGTTTCAAGATGACAGTAATTTCTGCTTTGCTGATGTAACCTGACGATAAAG 468  
 QY 102 GluLeuArgArgLeuPheLeuValAsp-AspLeuValAspSerLeuLysPheAlaVal 121  
 Db 469 GACCTAGCCGCTCTTCTAGTACCTGATTTAGTATCTCTGAGTTGAGTGT 528  
 QY 121 uMetTrpValPheThrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 Db 529 GATGGGGTATTACCTATGTTGGTCCCTTGTATTAATGCTCTGACACTACTGATTTTGGC 588  
 QY 141 aleuLeuSerLeuPheSer-ValProValIleThrGluArgHisGlnAlaGlnIleAspH 161  
 Db 589 TCTCATTTTCACTTTTCACTGTTCTCTGTTATTTATGAACGGCATCAGGACAGATAGATC 648  
 QY 161 isTrpLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysI 181  
 Db 649 ATTATCTAAGACTGC--ATAAGATGTTAAGGATGCTATGTTAAATCCAGCAAAA 706  
 QY 181 leProGlyLeuLysArgLysAlaGlu 189  
 Db 707 TCCCTGGATTGAAGGCCAAAGTTGAA 732

## RESULT 93

AV702687  
 LOCUS AV702687 719 bp mRNA linear EST 08-OCT-2000  
 DEFINITION AV702687 ADB Homo sapiens cDNA clone ADBBB01 5', mRNA sequence.  
 ACCESSION AV702687  
 VERSION AV702687.1 GI:10719017  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 719)  
 AUTHORS Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G.,  
 Xiao, H., Xu, X., Li, N., Qian, B., Liu, P., Qu, J., Gao, X., Cheng, Z.,  
 Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S.,  
 Zhong, M., Lu, G., Hu, R., Chen, J., Chen, Z. and Han, Z.  
 TITLE Homo sapiens cDNA ADB clones  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Zeguang Han  
 Chinese National Human Genome Center at Shanghai  
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
 201203, P. R. China  
 Tel: 86-21-50801919 (ex.45)  
 Fax: 86-21-50801922  
 Email: hanzg@chgc.sh.cn  
 This clone is available at CHGC in Shanghai.  
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 1..719  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="ADBBB01"  
 /tissue\_type="Adrenal gland"  
 /dev\_stage="Adult"  
 /lab\_host="SOLR"  
 /clone\_lib="ADB"  
 /note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2:  
 XhoI"

## ORIGIN

Alignment Scores:  
 Pred. No.: 6.99e-94 Length: 719  
 Score: 844.00 Matches: 176  
 Percent Similarity: 97.78% Conservativeness: 0  
 Best Local Similarity: 97.78% Mismatches: 3  
 Query Match: 90.66% Indels: 1  
 DB: 1 Gaps: 0  
 US-09-830-972-29\_COPY\_990\_1178 (1-189) x AV702687 (1-719)  
 QY 11 IleLysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuSerLeuThrVal 30  
 Db 1 ATTAAGAAGACTGGAGTGTGTTGGTGCCAGCTATTCTCTGCTGCTTTCATTGACAGTA 60  
 QY 31 PheSerIleValSerValThrAlaThrIleAlaLeuAlaLeuSerValThrIleSer 50  
 Db 61 TTCAGCATTTGAGCGTAACAGCTTACATTCCTTGGCCCTGCTCTGTGACCAATCAGC 120  
 QY 51 PheArgIleThrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPhe 70  
 Db 121 TTTAGGATATACAGGGTGTGATCCAGCTATCCAGAAATCAGATGAAGGCCACCAATTC 180  
 QY 71 ArgAlaThrLeuGluSerGluValAlaIleSerGluLysValGlnLysThrSerAsn 90  
 Db 181 AGGCGATATCTCGAATCTGAGTTGCTATATCTGAGGAGTTGGTTTCAGAGTACAGTAAT 240  
 QY 91 SerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAsp 110  
 Db 241 TCTGCTCTTGCTGATGAACTGCACCAATAAAGAACTCAGCGGCTCTTCTTAGTTGAT 300  
 QY 111 AspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrValGlyAla 130





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/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="ChEST11g8"
/sex="Female"
/tissue_type="cerebrum"
/dev_stages="adult"
/lab_host="DH10B"
/clone_lib="CSPQCHL15"
/note="Organ: brain; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; Modification of pBluescript II KS(+) [Stratagene] vector to accommodate cDNA produced with the 1-trimmed protocol (construction of uni-directionally cloned cDNA libraries from messenger RNA for improved end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BspI and BamHI sites [5'ggcgcgtcagcccgagtcgcaaaaaag] [5'aattcttttttcggatccgggctgcagc]"

```

## ORIGIN

Alignment Scores:  
 Pred. No.: 3 83e-93 Length: 961  
 Score: 839.50 Matches: 175  
 Percent Similarity: 96.28% Conservative: 6  
 Best Local Similarity: 93.02% Mismatches: 7  
 Query Match: 90.17% Indels: 2  
 DB: 5 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BUL16200 (1-961)

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Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 175 GTTGTGACCTCTTTACTGGCGACATTAAGAGACAGGAGTGTGTGGTCCAGC 234
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 235 TTGTTCTCGCTGCTCTCAATTAACAGTGTTCAGCATCGTGAGCGTGACAGCTTACATTC 294
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 295 TTGGCCCTGCTTTCTGTGACCATCAGCTTTAGGATATCAAGGGAGTTATCCAGGCAATC 354
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 355 CAAGAAGTCGATGAAGCCATCAATTTAGGCGCTTACTTGGAGTCTGTGATGCTGTGCT 414
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db 415 GAAGAGCTGATTTCAGAAATACAGCATGCTTGTGCTTGTGTCATCAACGGCAGCTCAAG 474
Qy 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 475 GAGCTGAGACGCTCTTCTGTTGATGACTTGTGTGATCTCTGAAGTTTGCAGTGTG 534
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeuAla 141
Db 535 ATGTGGGTGTTCACTTACGTTGGTCCCTGTTTATGCTGCTGACATTACTGATGCT 594
Qy 142 LeuLeuSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 161
Db 595 TTGATTTCCGCTTTCAGTGTTCCTGTTATTTATGAGAGACATCAGGCCAGATCGACCAT 654
Qy 162 TyrLeuGlyLeuAlaAsnLysValIleAspAlaMetAlaLysIleGlnAlaLysIle 181
Db 655 TATTGGGAGCTAGTGAACAAGAACCTCAAGATGCGATGCGGC-AAAGATCCAAGCAAGAT- 712
Qy 182 ProGlyLeuLysArgLysAlaGlu 189
Db 713 CCTGGGCTGAAGCGCAAACTGAG 736

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RESULT 96  
 BG698881  
 LOCUS

BG698881 665 bp mRNA linear EST 07-MAY-2001

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DEFINITION 602703292F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4800455 5',
mRNA sequence.
ACCESSION BG698881
VERSION BG698881.1 GI:13966613
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 665)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM10691 row: h column: 24
High quality sequence stop: 662.
Location/Qualifiers
1. 665
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4800455"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Skn3"
/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

```

## ORIGIN

Alignment Scores:  
 Pred. No.: 2 61e-93 Length: 665  
 Score: 839.00 Matches: 179  
 Percent Similarity: 98.90% Conservative: 0  
 Best Local Similarity: 98.90% Mismatches: 2  
 Query Match: 90.12% Indels: 2  
 DB: 4 Gaps: 0

US-09-830-972-29\_COPY\_990\_1178 (1-189) x BG698881 (1-665)

```

Qy 2 ValValAspLeuLeuTyrTrpArgAspIleLysThrGlyValValPheGlyAlaSer 21
Db 123 GTTGTGACCTCTTCTGTGACGACATTAAGAGACTGGAGTGTGTGGTCCAGC 182
Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41
Db 183 CTATTCCTGCTGCTTTTCAATTCAGCATGTTTTCAGCATGTTGAGCGCTTACATTCGCC 242
Qy 42 LeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIle 61
Db 243 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATCAAGGGTGTGATCCAAGCTATC 302
Qy 62 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSer 81
Db 303 CAGAAATCAGATGAAGGCCACCCATTTCAGGCGATATCTGGATCTGAAGTTGCTATATCT 362
Qy 82 GluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 101
Db 363 GAGGAGTGGTTTCAGAAAGTACAGTAATCTCTCTTGTTCATGTGAACCTGCACGATAAG 422
Qy 102 GluLeuArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeu 121
Db 423 GAAGTCAGGGCGCTCTTTCTTTAGTTGATGATTTAGTTCTCTCTGAAGTTTGCAGTGTG 482
Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuIleLeuAla 141

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```

Db      483  AATGGGTAATTTACCTATGTTGGTCTGTTTAAATGGTCTGACACTACTGAT-TTGGCT 541
      |||
Qy      142  LeuileSerLeuPheSerValProValIleTyrGluAArgHisGlnAlaGlnIleAspHis 161
      |||
Db      542  CTCATTTCACCTCTTCAGTGTCTCTGTTATTATGAACGCGCATCAGCACAGATAGATCAT 601
      |||
Qy      162  TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysIleGlnAlaLysIle 181
      |||
Db      602  TATCTAGGACTTGCATAAAGATGTTAAAGATGCTATGCT-AAATCCAAGCAAAATC 660
      |||
Qy      182  Pro 182
      |||
Db      661  CCT 663

CO505196      669 bp      mRNA      linear      EST 13-JUL-2004
GGEZEB1026A09.9 embryo breast muscle - EBI Gallus gallus CDNA clone
GGEZEB1026A09, mRNA sequence.
CO505196
CO505196.1 GI:50275382
EST.
Gallus gallus (chicken)
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
Alves H.J., Jorge E.C., Marchesin M.L., Monteiro-Vitorello, C.B.,
Patricio, M., Ledur, M.C. and Coutinho, L.L.
Discovery of new genes expressed in the chicken breast muscle
Unpublished (2004)
Contact: Helena J. Alves
Laboratory of Animal Biotechnology, Dep. of Animal Production
ESALQ - University of Sao Paulo
Av. Pádua Dias, 11, Piracicaba, SP, 13418-900, Brazil
Tel: 55 19 3429 4434
Fax: 55 19 3429 4285
Email: hjalves@esalq.usp.br and llicoutin@esalq.usp.br
PCR Primers
BACKWARD: T7

FEATURES             Location/Qualifiers
     source           1..669
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9031"
                     /clone="GGEZEB1026A09"
                     /tissue_type="breast muscle"
                     /dev_stage="embryos with 9 and 17 days old"
                     /lab_host="DH5 alpha"
                     /clone_lib="embryo breast muscle - EBI"
     notes            cDNA library was constructed with the SuperScript Plasmid
                     System with Gateway Technology kit (Invitrogen), following
                     manufacturer's protocols. Plasmid DNA was purified using a
                     modified alkaline lysis method. Sequencing reactions were
                     conducted using the DYEnamic Cycle Sequencing Kit for
                     MegABACE (Amersham Biosciences) according to the
                     manufacturer's recommendations. Clones were sequenced by
                     the 5' end with T7 primer. Sequencing reactions were
                     analyzed on MegABACE1000 DNA Sequencer (Amersham
                     Biosciences). The quality and clustering of the ESTs were
                     analyzed using the softwares Phred/Cap3. Only EST
                     sequences with phred quality greater than 20 and at least
                     150 bp were considered for clustering."

ORIGIN
Alignment Scores:
Pred. No.:      2.63e-93      Length:      669
Score:          839.00      Matches:    175
Percent Similarity: 96.28%      Conservative: 6
Best Local Similarity: 93.09%      Mismatches: 6

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Query Match:      90.12%      Indels:      2
DB:               7          Gaps:       0

US-09-830-972-29_copy_990_1178 (1-189) x CO505196 (1-669)

Qy      3  ValAspLeuLeuTyrTip-AtgAspIleLysLysThrGlyValValPheGlyAlaSerLe 22
      |||
Db      43  GTTGACCTCCCTTACTGNCGAGACATTAAGAAAGACAGAGTGGTGT-TGGTCCAGCTT 101
      |||
Qy      22  uPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLe 42
      |||
Db      102  GTTCTGCTGCTCTCATTAAACAGTGTTCAGCATCGTGCAGCGTGCAGAGCTTACATTGCCCTT 161
      |||
Qy      42  uAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGlyValIleGlnAlaIleG 62
      |||
Db      162  GGCCCTGCTTCTGTGACCATCAGCTTTAGGATATACAAAGGAGTATATCCAGGCAATCCA 221
      |||
Qy      62  nLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerG 82
      |||
Db      222  AAGTCCCGATGAAGGCCATCCATTTAGGCTTACTTTGGAGTCTGATGATGCTGTCTGA 281
      |||
Qy      82  uGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysG 102
      |||
Db      282  AGAGCTGATTTCAGAAATACAGCAGTGTGCTGCTGCATCAACGCGCACAGTCAAGCA 341
      |||
Qy      102  uLeuArgArgLeuPheLeuValAspLeuValAspSerLeuLysPheAlaValLeuMe 122
      |||
Db      342  GCTGAGACGCTCTTCCTCGTTGATGACTTGGTGTGATTCTCTGAAAGTTTGCAGTGTGAT 401
      |||
Qy      122  tTrrValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleAlaLe 142
      |||
Db      402  GTGGGTGTTCATTAGTTAGTGGTCCCTGTTTAATGGTCTGACATTTACTGATGATGCTGCTTT 461
      |||
Qy      142  uIleSerLeuPheSerValProValIleTyrGluAArgHisGlnAlaGlnIleAspHisT 162
      |||
Db      462  GATTTTCGCTGTTTCAGTGTTCCTGCTGTTATTATGAGAGACATCAGGCCAGATCGACCATTA 521
      |||
Qy      162  rLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIleBr 182
      |||
Db      522  TTTGGGACTAGTGAACAGACGTCAGAGATCGATGCGCAAGATCCCAAGATCCCAAGCAAGATCCC 581
      |||
Qy      182  oGlyLeuLysArgLysAlaGlu 189
      |||
Db      582  TGGGCTGAAGCCCAAAACTGAG 603
      |||

RESULT 98
CN429705
LOCUS      676 bp      mRNA      linear      EST 16-MAY-2004
DEFINITION 1700600430685 GRN_PNEU Homo sapiens cDNA 5', mRNA sequence.
ACCESSION  CN429705
VERSION     CN429705.1 GI:47417299
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 676)
            Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
            Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
            Lebkowski, J. and Stanton, L.W.
            Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
            Nat. Biotechnol. 22 (6), 707-716 (2004)
JOURNAL
COMMENT     Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 676 Std Error: 0.00.
            Location/Qualifiers
            1..676
FEATURES             source

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Db 532 ATGTGGGTTCACCTACGTGGTGGTCTGTTTAAATGTTGCTGACATCTACTGACTGGCT 591  
 Qy 142 LeuileSerLeuPheSerValProValileTyrGluArgHisGlnAlaGlnleAspHis 161  
 Db 592 TTGATTTCGCTGTTCACTGCTCTCTGTTTATTTATGAGACATCAGGCCCGATCGACCAT 651  
 Qy 162 TyrLeuGlyLeuAlaAsnLysValLysAspAlaMetAlaLysileGlnAlaLysile 181  
 Db 652 TATTTGGGACTAGTGAACAGAACGTCAAAGATGCGATGCGCAAGATCCCAAGCAAGATC 711  
 Qy 182 ProGlyLeu-LysArgLysAlaGlu 189  
 Db 712 CTGGGCTGAAGCGCAAACTGAG 736

CB956475 735 bp mRNA linear EST 29-APR-2003  
 AGENCOURT 13665211 NIH MGC 184 Homo sapiens cDNA clone  
 IMAGE:30353314 5', mRNA sequence.  
 CB956475  
 VERSION CB956475.1 GI:30212592  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 735)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Cloned Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: NDCM153 row: n column: 11  
 High quality sequence stop: 619.  
 Location/Qualifiers

## FEATURES

1..735  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:30353314"  
 /lab\_host="PH10B (T1 phage-resistant)"  
 /clone\_lib="NIH MGC 184"  
 /note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site\_1:  
 Sfil (ggcattatggcc); Site\_2: Sfil (ggcgcctggcc);  
 Library is oligo-dr primed and directionally cloned. cDNA  
 was prepared from a glandular pool of tissues from thyroid,  
 parathyroid, adrenal, cortex and pineal gland. 5' and 3'  
 adaptors were used in cloning as follows: 5' adaptor  
 sequence: 5'-CAGGCCATATGACC-3' and 3' adaptor sequence:  
 5'-ATTCTAGCCGCGCCGCGCATG-3' (30)BN-3' (where B = A,  
 C, or G and N = A, C, or T). Average insert size 1.38  
 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA). Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 8 17e-93 Length: 735  
 Score: 835.50 Matches: 177  
 Percent Similarity: 97.25% Conservative: 0  
 Best Local Similarity: 97.25% Mismatches: 2  
 Query Match: 89.74% Indels: 3  
 DB: 6 Gaps: 1

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 Qy 22 LeuPheLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAla 41  
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 Qy 122 MetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuAla 141  
 Db 549 ATGTGGTATTTACCTATGTTGGTGGCTTGTAAATGGTCTGACACTACTGATTTGGCT 608  
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 Db 669 TATCTAGACTTGCATAATAAGAATGGTTAAAGATGCTATGGGCTAAATAATCCCAAGCAA 728  
 Qy 180 Ys 180  
 Db 729 AA 730

Search completed: June 19, 2005, 10:16:59  
 Job time : 2580 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:29:05 ; Search time 24.5171 Seconds  
(without alignments)  
2960.058 Million cell updates/sec

Title: US-09-830-972-29\_COPY\_990\_1178

Perfect score: 931

Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRAE 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1714042

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:\*

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- 3: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep.\*
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- 19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
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- 22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	931	100.0	1192	9	US-09-789-386-2
5	931	100.0	1192	14	US-10-060-036-71
6	931	100.0	1192	15	US-10-060-036-71
7	931	100.0	1192	16	US-10-060-036-71
8	931	100.0	1192	16	US-10-060-036-71
9	931	100.0	1192	16	US-10-060-036-71
10	927	99.6	1192	9	US-09-893-348-25
11	927	99.6	1192	15	US-10-660-946-1

12	927	99.6	199	16	US-10-810-653-25
13	927	99.6	373	9	US-09-789-386-6
14	927	99.6	373	9	US-09-789-386-6
15	927	99.6	373	9	US-09-789-386-6
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18	927	99.6	373	16	US-10-060-036-72
19	927	99.6	373	16	US-10-060-036-72
20	927	99.6	373	17	US-10-060-036-72
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22	920	98.8	199	15	US-10-060-036-72
23	918	98.6	199	11	US-09-789-386-6
24	915	98.3	1162	16	US-10-653-423-10
25	915	98.3	1162	16	US-10-653-423-10
26	908	97.5	1163	9	US-09-893-348-18
27	908	97.5	1163	16	US-10-810-653-18
28	905	97.2	379	14	US-10-205-194-164
29	904.5	97.2	1163	15	US-10-267-502-431
30	904	97.1	199	9	US-09-893-348-21
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32	904	97.1	360	9	US-09-893-348-20
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38	682	73.3	776	15	US-10-267-502-430
39	682	73.3	776	16	US-10-723-860-1481
40	681	73.1	777	14	US-10-205-219-93
41	681	73.1	780	15	US-10-267-502-432
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43	665	71.4	267	15	US-10-660-946-8
44	624.5	67.1	236	9	US-09-729-674-20
45	624.5	67.1	236	9	US-09-765-205-26

ALIGNMENTS

RESULT 1

US-09-789-386-2  
; Sequence 2, Application US/09789386  
; Patent No. US20020010324A1  
; GENERAL INFORMATION:  
; APPLICANT: MICHALOVICH, DAVID  
; APPLICANT: PRINJHA, RABINDER KUMAR  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP-30165-C1  
; CURRENT APPLICATION NUMBER: US/09/789.386  
; CURRENT FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: U.K. 9916898.1  
; PRIOR FILING DATE: 1999-07-19  
; PRIOR APPLICATION NUMBER: U.K. 9816024.5  
; PRIOR FILING DATE: 1998-07-22  
; PRIOR APPLICATION NUMBER: US 09/359,208  
; PRIOR FILING DATE: 1999-07-22  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-789-386-2

Query Match 100.0%; Score 931; DB 9; Length 1192;  
Best Local Similarity 100.0%; Pred. No. 1.1e-83;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SVVDLLYWRDIKKTGVVFGASFLLSLTVTSVSYVTAIYIALLSVTSIPRIYKGVIOA 60  
Db 1004 SVVDLLYWRDIKKTGVVFGASFLLSLTVTSVSYVTAIYIALLSVTSIPRIYKGVIOA 1063  
Qy 61 IQKSDGHPFRAYLSEVAISEELVQKYSNAGLHVNCTIKELRRLFLVDLVDLSKFAV 120

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Db 1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKVNDAMAKIOAK 1183
QY 181 IPGLKRAE 189
Db 1184 IPGLKRAE 1192

RESULT 2
US-09-758-140-6
; Sequence 6, Application US/09758140
; Patent No. US20020012965A1
; GENERAL INFORMATION:
; APPLICANT: Strittmatter, Stephen M.
; TITLE OF INVENTION: NO. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth
; FILE REFERENCE: 44574-5073-US
; CURRENT APPLICATION NUMBER: US/09/758,140
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/175,707
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,378
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-140-6

Query Match 100.0%; Score 931; DB 9; Length 1192;
Best Local Similarity 100.0%; Pred. No. 1.1e-83;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60
Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1063
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Db 1064 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITKELRRLFLVDDLDVSLKFAV 1123
QY 121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKVNDAMAKIOAK 180
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QY 181 IPGLKRAE 189
Db 1184 IPGLKRAE 1192

RESULT 3
US-09-893-348-23
; Sequence 23, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michael
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19

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QY 181 IPGLKRAE 189
Db 1184 IPGLKRAE 1192

RESULT 4
US-09-972-599A-6
; Sequence 6, Application US/09972599A
; Patent No. US20020077295A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; TITLE OF INVENTION: NOCO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
; FILE REFERENCE: C077 CIP US
; CURRENT APPLICATION NUMBER: US/09/972,599A
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/236,378
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-599A-6

Query Match 100.0%; Score 931; DB 9; Length 1192;
Best Local Similarity 100.0%; Pred. No. 1.1e-83;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-348-23

Query Match 100.0%; Score 931; DB 9; Length 1192;
Best Local Similarity 100.0%; Pred. No. 1.1e-83;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60
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Db 1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKVNDAMAKIOAK 1183
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Db 1184 IPGLKRAE 1192

RESULT 4
US-09-972-599A-6
; Sequence 6, Application US/09972599A
; Patent No. US20020077295A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; TITLE OF INVENTION: NOCO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
; FILE REFERENCE: C077 CIP US
; CURRENT APPLICATION NUMBER: US/09/972,599A
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/236,378
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
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; SOFTWARE: PatentIn Ver. 2.1
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; ORGANISM: Homo sapiens
US-09-972-599A-6

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Db 1184 IPGLKRAE 1192

RESULT 5  
US-10-060-036-71  
; Sequence 71, Application US/10060036  
; Publication No. US20030073144A1  
; GENERAL INFORMATION:  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Persing, David H.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Jiang, Yugu  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER  
; FILE REFERENCE: 210121.566  
; CURRENT APPLICATION NUMBER: US/10/060,036  
; CURRENT FILING DATE: 2002-01-30  
; NUMBER OF SEQ ID NOS: 4560  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 71  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-060-036-71

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Best Local Similarity 100.0%; Pred. No. 1.1e-83;  
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Db 1064 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDLSLKFAV 1123  
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QY 181 IPGLKRAE 189  
Db 1184 IPGLKRAE 1192

RESULT 6  
US-10-267-502-429  
; Sequence 429, Application US/10267502  
; Publication No. US20040071700A1  
; GENERAL INFORMATION:  
; APPLICANT: Galant, Ron  
; APPLICANT: Kim, Jaeseob  
; TITLE OF INVENTION: Obesity Linked Genes  
; FILE REFERENCE: LSD-07416  
; CURRENT APPLICATION NUMBER: US/10/267,502  
; CURRENT FILING DATE: 2003-01-27  
; NUMBER OF SEQ ID NOS: 439  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 429  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-267-502-429

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Db 1064 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDLSLKFAV 1123  
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QY 181 IPGLKRAE 189  
Db 1184 IPGLKRAE 1192

RESULT 7  
US-10-327-213-9  
; Sequence 9, Application US/10327213  
; Publication No. US20040121341A1  
; GENERAL INFORMATION:  
; APPLICANT: FILBIN, MARIE T.  
; APPLICANT: DOMENICONI, MARCO  
; APPLICANT: CAO, ZIXUAN  
; TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)  
; TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION  
; FILE REFERENCE: CUNY/003  
; CURRENT APPLICATION NUMBER: US/10/327,213  
; CURRENT FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-327-213-9

Query Match 100.0%; Score 931; DB 16; Length 1192;  
Best Local Similarity 100.0%; Pred. No. 1.1e-83;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1063  
QY 61 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDLSLKFAV 120  
Db 1064 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDLSLKFAV 1123  
QY 121 LMWVFTYVGFALFNGTLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAK 180  
Db 1124 LMWVFTYVGFALFNGTLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAK 1183  
QY 181 IPGLKRAE 189  
Db 1184 IPGLKRAE 1192

RESULT 8  
US-10-466-258-9  
; Sequence 9, Application US/10466258  
; Publication No. US20040132096A1  
; GENERAL INFORMATION:  
; APPLICANT: GLAXO GROUP LIMITED  
; TITLE OF INVENTION: ASSAY  
; FILE REFERENCE: P80966 GCW

```

RESULT 11
US-10-660-946-1
; Sequence 1, Application US/10660946
; Publication No. US20040063131A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Au-Young, Janice
; Goli, Surya K.
; Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9

```



;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
;; STREET: 3174 Porter Drive  
;; CITY: Palo Alto  
;; STATE: CA  
;; COUNTRY: U.S.  
;; ZIP: 94304  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FastSeq Version 1.5  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/660,946  
;; FILING DATE: 12-Sep-2003  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/228,213A  
;; FILING DATE: <Unknown>  
;; APPLICATION NUMBER: 08/700,607  
;; FILING DATE: <Unknown>  
;;  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Billings, Lucy J.  
;; REGISTRATION NUMBER: 36,749  
;; REFERENCE/DOCKET NUMBER: PF-0114 US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-855-0555  
;; TELEFAX: 415-845-4166  
;;  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 199 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; IMMEDIATE SOURCE:  
;; LIBRARY: <Unknown>  
;; CLONE: Consensus  
;;  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-660-946-1  
  
Query Match 99.6%; Score 927; DB 15; Length 199;  
Best Local Similarity 100.0%; Pred. No. 2.9e-84;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61  
Db 12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 71  
  
Qy 62 QKSDEGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLDVSLKFAVL 121  
Db 72 QKSDEGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLDVSLKFAVL 131  
  
Qy 122 MWFTYVGALENGLLTLLILALISLFSVPVYVERHQAQIDHYLGLANKNVKDMAKIQAKI 181  
Db 132 MWFTYVGALENGLLTLLILALISLFSVPVYVERHQAQIDHYLGLANKNVKDMAKIQAKI 191  
  
Qy 182 PGLKRAE 189  
Db 192 PGLKRAE 199  
  
RESULT 12  
US-10-810-653-25  
; Sequence 25, Application US/10810653  
; Publication No. US2004025318A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN, Irun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SCHWARTZ-2A  
  
Query Match 99.6%; Score 927; DB 15; Length 199;  
Best Local Similarity 100.0%; Pred. No. 2.9e-84;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61  
Db 12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 71  
  
Qy 62 QKSDEGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLDVSLKFAVL 121  
Db 72 QKSDEGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLDVSLKFAVL 131  
  
Qy 122 MWFTYVGALENGLLTLLILALISLFSVPVYVERHQAQIDHYLGLANKNVKDMAKIQAKI 181  
Db 132 MWFTYVGALENGLLTLLILALISLFSVPVYVERHQAQIDHYLGLANKNVKDMAKIQAKI 191  
  
Qy 182 PGLKRAE 189  
Db 192 PGLKRAE 199  
  
RESULT 12  
US-10-810-653-25  
; Sequence 25, Application US/10810653  
; Publication No. US2004025318A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN, Irun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SCHWARTZ-2A

;; CURRENT APPLICATION NUMBER: US/10/810,653  
;; CURRENT FILING DATE: 2004-03-29  
;; PRIOR APPLICATION NUMBER: US/09/893,348  
;; PRIOR FILING DATE: 2001-06-28  
;; PRIOR APPLICATION NUMBER: US 09/314,161  
;; PRIOR FILING DATE: 1999-05-19  
;; PRIOR APPLICATION NUMBER: US 09/218,277  
;; PRIOR FILING DATE: 1998-12-22  
;; PRIOR APPLICATION NUMBER: PCT/US98/14715  
;; PRIOR FILING DATE: 1998-07-21  
;; PRIOR APPLICATION NUMBER: IL 124500  
;; PRIOR FILING DATE: 1998-05-19  
;; NUMBER OF SEQ ID NOS: 29  
;; SOFTWARE: Patent in version 3.1  
;; SEQ ID NO 25  
;; LENGTH: 199  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-810-653-25  
  
Query Match 99.6%; Score 927; DB 16; Length 199;  
Best Local Similarity 100.0%; Pred. No. 2.9e-84;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61  
Db 12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 71  
  
Qy 62 QKSDEGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLDVSLKFAVL 121  
Db 72 QKSDEGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLDVSLKFAVL 131  
  
Qy 122 MWFTYVGALENGLLTLLILALISLFSVPVYVERHQAQIDHYLGLANKNVKDMAKIQAKI 181  
Db 132 MWFTYVGALENGLLTLLILALISLFSVPVYVERHQAQIDHYLGLANKNVKDMAKIQAKI 191  
  
Qy 182 PGLKRAE 189  
Db 192 PGLKRAE 199  
  
RESULT 13  
US-09-789-386-6  
; Sequence 6, Application US/09789386  
; Patent No. US2002001032A1  
; GENERAL INFORMATION:  
; APPLICANT: MICHALOVICH, DAVID  
; APPLICANT: PRINJHA, RABINDER KUMAR  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP-30165-C1  
; CURRENT APPLICATION NUMBER: US/09/789,386  
; CURRENT FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: U.K. 9916898.1  
; PRIOR FILING DATE: 1999-07-19  
; PRIOR APPLICATION NUMBER: U.K. 9816024.5  
; PRIOR FILING DATE: 1998-07-22  
; PRIOR APPLICATION NUMBER: US 09/359,208  
; PRIOR FILING DATE: 1999-07-22  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
;; LENGTH: 373  
;; TYPE: PRT  
;; ORGANISM: HOMO SAPIENS  
US-09-789-386-6  
  
Query Match 99.6%; Score 927; DB 9; Length 373;  
Best Local Similarity 100.0%; Pred. No. 6.4e-84;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61  
Db 186 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 245

QY 62 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCCTIKELRRLFLVDDLVDSLKFAYL 121  
DB 246 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCCTIKELRRLFLVDDLVDSLKFAYL 305  
QY 122 MVVFTVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKI 181  
DB 306 MVVFTVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKI 365  
QY 182 PGLKRAE 189  
DB 366 PGLKRAE 373

RESULT 14  
US-09-765-205-6  
; Sequence 6, Application US/09765205  
; Patent No. US20020034800A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Li  
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES  
; FILE REFERENCE: 1458.004/200130.449  
; CURRENT APPLICATION NUMBER: US/09/765,205  
; CURRENT FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: US/09/212,440  
; PRIOR FILING DATE: 1998-12-16  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 373  
; TYPE: PRT  
; ORGANISM: human  
US-09-765-205-6

Query Match 99.6%; Score 927; DB 9; Length 373;  
Best Local Similarity 100.0%; Pred. No. 6.4e-84;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 VDLYWRDIIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61  
DB 186 VDLYWRDIIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 245  
QY 62 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCCTIKELRRLFLVDDLVDSLKFAYL 121  
DB 246 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCCTIKELRRLFLVDDLVDSLKFAYL 305  
QY 122 MVVFTVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKI 181  
DB 306 MVVFTVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKI 365  
QY 182 PGLKRAE 189  
DB 366 PGLKRAE 373

RESULT 15  
US-09-893-348-24  
; Sequence 24, Application US/09893348  
; Patent No. US20020072493A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACH-SCHWARTZ, Michal  
; APPLICANT: COHEN, Irun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE  
; FILE REFERENCE: EIS-SCHWARTZ=2A  
; CURRENT APPLICATION NUMBER: US/09/893,348  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 24  
; LENGTH: 373  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-893-348-24

Query Match 99.6%; Score 927; DB 9; Length 373;  
Best Local Similarity 100.0%; Pred. No. 6.4e-84;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 VDLYWRDIIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61  
DB 186 VDLYWRDIIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 245  
QY 62 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCCTIKELRRLFLVDDLVDSLKFAYL 121  
DB 246 QKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCCTIKELRRLFLVDDLVDSLKFAYL 305  
QY 122 MVVFTVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKI 181  
DB 306 MVVFTVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKI 365  
QY 182 PGLKRAE 189  
DB 366 PGLKRAE 373

Search completed: June 16, 2005, 13:04:04  
Job time : 24.5171 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:31:51 ; Search time 27.2927 Seconds  
(without alignments)  
2678.292 Million call updates/sec

Title: US-09-830-972-29\_COPY\_990\_1178

Perfect score: 931

Sequence: 1 SWVDLLYWRDIKTKGVFGA.....VKDAMAKIQAKIPGLKRAE 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	931	100.0	893	3 AAY95012	Aay95012 Human sec
2	931	100.0	983	6 ABU11573	Abu11573 Human MDD
3	931	100.0	1178	3 AAY71311	Aay71311 Human neu
4	931	100.0	1192	3 AAY56967	Aay56967 Human MAG
5	931	100.0	1192	4 AAB82349	Aab82349 Human NOG
6	931	100.0	1192	4 AAU04591	Aau04591 Human NOG
7	931	100.0	1192	5 ABG30938	Abg30938 Human NOG
8	931	100.0	1192	5 ABP68600	Abp68600 Human pan
9	931	100.0	1192	5 ABB81078	Abb81078 Human neu
10	931	100.0	1192	6 ABR59667	Abr59667 Human NOG
11	931	100.0	1192	8 ADO08103	Ado08103 Human pol
12	931	100.0	1192	8 ADO26400	Ado26400 Human tru
13	931	100.0	1192	8 ADP45551	Adp45551 Human NOG
14	931	100.0	1192	8 ADP67234	Adp67234 Human NOG
15	931	100.0	1192	8 ADR13966	Adr13966 Human NOG
16	928	99.7	200	4 AAB64514	Aab64514 Human sec
17	927	99.6	199	2 AAU53947	Aau53947 Human NSP
18	927	99.6	199	2 AAU78313	Aau78313 Fragment
19	927	99.6	199	3 AAB12805	Aab12805 Human NSP
20	927	99.6	199	4 AAB82348	Aab82348 Human NOG
21	927	99.6	199	5 ABB81080	Abb81080 Human neu
22	927	99.6	199	8 ADP67236	Adp67236 Human NOG
23	927	99.6	373	3 AAY53624	Aay53624 A bone ma
24	927	99.6	373	3 AAY56969	Aay56969 Human MAG
25	927	99.6	373	3 AAB24242	Aab24242 Human NOG

## ALIGNMENTS

### RESULT 1

AAY95012  
ID AAY95012 standard; protein; 893 AA.

XX AC AAY95012;

XX XX  
DT 19-JUN-2000 (first entry)

DE Human secreted protein vb22\_1, SEQ ID NO:64.

XX Human; secreted protein; cancer; tumour; cardiovascular disorder;  
KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;  
KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;  
KW neurodegenerative disease; asthma; contraceptive.

XX Homo sapiens.

XX WO200011015-A1.

XX PD 02-MAR-2000.

XX PF 24-AUG-1999; 99WO-US019351.

XX PR 24-AUG-1998; 98US-0097638P.

PR 24-AUG-1998; 98US-0097659P.

PR 09-SEP-1998; 98US-0099618P.

PR 28-SEP-1998; 98US-0102092P.

PR 25-NOV-1998; 98US-0109978P.

PR 23-DEC-1998; 98US-0113645P.

PR 23-DEC-1998; 98US-0113646P.

PR 23-AUG-1999; 99US-00379246.

XX (ALPH-) ALPHAGEN INC.

XX Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;

XX WPI; 2000-224657/19.

XX New secreted or transmembrane proteins and polynucleotides encoding them,  
XX useful for treating neurodegenerative disorders, autoimmune diseases and  
XX cancer.

XX Claim 73; Page 322-325; 357pp; English.

XX The invention relates to 40 human secreted proteins (AAY94981-Y95020),  
XX and cDNA sequences encoding them (AA23423-A23462). The secreted proteins  
XX of the invention include those that are thought to be only partially  
XX secreted, i.e., transmembrane proteins. The proteins of the invention may

26 927 99.6 373 4 AAB82350  
27 927 99.6 373 5 AAM47954  
28 927 99.6 373 5 ABG30937  
29 927 99.6 373 5 ABP68601  
30 927 99.6 373 5 ABB81079  
31 927 99.6 373 7 ADI63044  
32 927 99.6 373 7 ADK67503  
33 927 99.6 373 8 ADP67235  
34 924 99.2 1192 7 ADK67502  
35 923 99.1 291 4 AAM93484  
36 923 99.1 291 8 ADL31138  
37 920 98.8 199 7 ADK67504  
38 918 98.6 199 2 AAY35903  
39 918 98.6 199 8 ADP19211  
40 915 98.3 1162 8 ADT89537  
41 908 97.5 361 3 AAY71385  
42 908 97.5 1163 3 AAY71310  
43 908 97.5 1163 3 AAY71384  
44 908 97.5 1163 5 ABB81074  
45 908 97.5 1163 8 ADO26399

Aab82350 Human NOG  
Aam47954 Human RTN  
Abg30937 Human NOG  
Abp68601 Human pan  
Abb81079 Human neu  
Adi63044 Human apo  
Adk67503 Human RTN  
Adp67235 Human NOG  
Adk67502 Human RTN  
Aam93484 Human pol  
Adl31138 Human pro  
Adk67504 Human RTN  
Aay35903 Extended  
Adp19211 Human sec  
Adt89537 Mus muscu  
Aay71385 Alternati  
Aay71310 Rat neuro  
Abb81074 Rat neuro  
Ado26399 Rat trunc

CC exhibit one or more activities selected from the following: cytokine  
 CC activity; cell proliferation; differentiation; immune modulation;  
 CC haematopoiesis regulation; tissue growth activity; activin/inhibin  
 CC activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic  
 CC activity; anti-inflammatory activity; and tumour inhibition activity. The  
 CC proteins may be administered to patients as vaccines, and the nucleotides  
 CC may be used as part of a gene therapy regime. Diseases or conditions that  
 CC may be treated using the proteins or nucleotides of the invention include  
 CC autoimmune diseases; genetic disorders; haemophilia; cardiovascular  
 CC diseases; cancer; bacterial, fungal and viral infections, especially HIV;  
 CC multiple sclerosis; rheumatoid arthritis; pulmonary inflammation;  
 CC Guillain-Barre syndrome; insulin dependent diabetes mellitus; and  
 CC allergic reactions such as asthma and anaemia. They may also be used for  
 CC treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal  
 CC diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease  
 CC and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin  
 CC activity may additionally be useful as contraceptives. Nucleic acid  
 CC sequences of the invention may be used in chromosome mapping, and as a  
 CC source of diagnostic primers and probes. The present sequence represents  
 CC one of the 40 proteins of the invention  
 XX  
 SQ Sequence 893 AA;

Query Match 100.0%; Score 931; DB 3; Length 893;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-92;  
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAIALALLSVTISFRIYKGVIOA 60  
 Db 705 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAIALALLSVTISFRIYKGVIOA 764  
 QY 61 IOKSDEGHFPFRAYLSEVAISEELVQKYSNSALGHVNCITIKELRRLFLVDLVDLSLKFAV 120  
 Db 765 IOKSDEGHFPFRAYLSEVAISEELVQKYSNSALGHVNCITIKELRRLFLVDLVDLSLKFAV 824  
 QY 121 LMWVFTYVGCALFNGLLTLLILALISLFSVPVYVERHOAQIDHYGLANKNVKDMAXIOAK 180  
 Db 825 LMWVFTYVGCALFNGLLTLLILALISLFSVPVYVERHOAQIDHYGLANKNVKDMAXIOAK 884  
 QY 181 IPGLKRAE 189  
 Db 885 IPGLKRAE 893

RESULT 2  
 ABU11573  
 ID ABU11573 standard; protein; 983 AA.  
 AC  
 XX ABU11573;

DT 12-FEB-2003 (first entry)

XX Human MDDT polypeptide SEQ ID 520.

KW MDDT; human; disease detection and treatment molecule polypeptide;  
 KW anti-inflammatory; immunosuppressive; osteoparic; cytostatic; anti-HIV;  
 KW haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;  
 KW gene therapy; protein replacement therapy; cell proliferative disorder;  
 KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;  
 KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;  
 KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;  
 KW psoriasis; hepatitis.

XX Homo sapiens.

XX WO20027949-A2.

XX 10-OCT-2002.

XX 27-MAR-2002; 2002WO-US009944.

XX 28-MAR-2001; 2001US-0279619P.

XX 29-MAR-2001; 2001US-0280067P.

PR 29-MAR-2001; 2001US-0280068P.  
 PR 16-MAY-2001; 2001US-0291280P.  
 PR 17-MAY-2001; 2001US-0291829P.  
 PR 17-MAY-2001; 2001US-0291849P.  
 PR 19-JUN-2001; 2001US-0299428P.  
 PR 20-JUN-2001; 2001US-0299776P.  
 PR 20-JUN-2001; 2001US-0300001P.

XX (INCY-) INCYTE GENOMICS INC.

XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;  
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshay SR;  
 PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;  
 PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;  
 PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;  
 XX WPI; 2003-058431/05.  
 DR N-PSDB; ABX34563.

XX New purified disease detection and treatment molecule proteins and  
 PT polynucleotides, useful for diagnosing, treating or preventing cancers  
 PT (e.g. leukemia or sarcoma), anaemia, Crohn's disease, AIDS, osteoporosis  
 PT or hepatitis.

XX Claim 27; SEQ ID NO 520; 339pp + Sequence Listing; English.

XX This invention describes a novel disease detection and treatment molecule  
 CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,  
 CC osteoparic, cytostatic, anti-HIV, haemostatic, nephrotropic,  
 CC antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides  
 CC and the polypeptides of the invention can be used for gene therapy,  
 CC protein replacement therapy and are useful for treating a variety of  
 CC diseases or conditions. These polypeptides or polynucleotides are  
 CC particularly useful for diagnosing, treating or preventing cell  
 CC proliferative disorders (e.g. cancers including adenocarcinoma,  
 CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's  
 CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's  
 CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or  
 CC hepatitis. ABU11450-ABU11845 represent the MDDT polynucleotides encoded  
 CC by ABU11450-ABU11845, described in the disclosure of the invention. NOTE:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 983 AA;

Query Match 100.0%; Score 931; DB 6; Length 983;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-92;

Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAIALALLSVTISFRIYKGVIOA 60  
 Db 795 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAIALALLSVTISFRIYKGVIOA 854

QY 61 IOKSDEGHFPFRAYLSEVAISEELVQKYSNSALGHVNCITIKELRRLFLVDLVDLSLKFAV 120  
 Db 855 IOKSDEGHFPFRAYLSEVAISEELVQKYSNSALGHVNCITIKELRRLFLVDLVDLSLKFAV 914

QY 121 LMWVFTYVGCALFNGLLTLLILALISLFSVPVYVERHOAQIDHYGLANKNVKDMAXIOAK 180  
 Db 915 LMWVFTYVGCALFNGLLTLLILALISLFSVPVYVERHOAQIDHYGLANKNVKDMAXIOAK 974

QY 181 IPGLKRAE 189

Db 975 IPGLKRAE 983

RESULT 3

AAAY71311

ID AAAY71311 standard; protein; 1178 AA.

XX AC

XX AAAY71311;

DT 02-NOV-2000 (first entry)  
XX Human neurite growth inhibitor Nogo.  
XX Human; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;  
KW central nervous system; neoplastic disease; antiproliferative; glioma;  
KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
KW structural plasticity; screening.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH Misc-difference 187 /label= Unknown  
FT Misc-difference 188 /label= Unknown  
FT Misc-difference 189 /label= Unknown  
FT Misc-difference 190 /label= Unknown  
FT Misc-difference 221 /label= Unknown  
FT Misc-difference 328 /label= Unknown  
FT Misc-difference 477 /label= Unknown  
FT Region /note= "Region specifically described in claim 16"  
FT Region 977. .1012  
FT Region 994. .1174  
FT Region /note= "Region specifically described in claim 16"  
FT Region 1079. .1113  
FT Region /note= "Region specifically described in claim 16"  
XX WO200031235-A2.  
XX 02-JUN-2000.  
XX 05-NOV-1999; 99WO-US026160.  
XX 06-NOV-1999; 98US-0107446P.  
XX (SCHW/) SCHWAB M E.  
XX (CHEN/) CHEN M S.  
XX Schwab ME, Chen MS;  
XX WPI; 2000-400052/34.  
XX Nogo proteins and nucleic acids useful for treating neoplastic disorders  
XX of the central nervous system and inducing regeneration of neurons.  
XX Claim 11; Fig 13; 122pp; English.  
XX The present sequence is a human Nogo protein which is a potent neural  
XX cell growth inhibitor and is free of all central nervous system (CNS)  
XX myelin material with which it is natively associated. The human Nogo  
XX sequence was derived by aligning human expressed sequence tags (ESTs)  
XX e.g. AA158636, AA333267, AA081783, AA167765, AA092565, AA081525  
XX and AA081840 with the rat Nogo sequence. Nogo proteins and fragments  
XX displaying neurite growth inhibitory activity are used in the treatment  
XX of neoplastic disease of the CNS e.g. glioma, glioblastoma,  
XX medulloblastoma, craniopharyngioma, ependyoma, pinealoma,  
XX haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma,  
XX neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.  
XX Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo  
XX activity can be used to treat or prevent hyperproliferative or benign  
XX dysproliferative disorders e.g. psoriasis and tissue hypertrophy.  
XX Ribozymes or antisense Nogo nucleic acids can be used to inhibit  
XX production of Nogo protein to induce regeneration of neurons or to  
XX promote structural plasticity of the CNS in disorders where neurite

CC growth, regeneration or maintenance are deficient or desired. The animal  
CC models can be used in diagnostic and screening methods for predisposition  
CC to disorders and to screen for or test molecules which can treat or  
CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are  
CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the  
CC specification. However the specification does not include sequences for  
CC these SEQ ID numbers  
XX SQ Sequence 1178 AA;  
Query Match 100.0%; Score 931; DB 3; Length 1178;  
Best Local Similarity 100.0%; Pred. No. 6.6e-92;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVVLLYWRDIKKTGVVFGASLFLLLSLTVPFSIVSYVAYIALALSVTISFRIYKGVQA 60  
DB 990 SVVLLYWRDIKKTGVVFGASLFLLLSLTVPFSIVSYVAYIALALSVTISFRIYKGVQA 1049  
QY 61 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCITIKELRRLFLVDDLVDLSLKFV 120  
DB 1050 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCITIKELRRLFLVDDLVDLSLKFV 1109  
QY 121 LMWFTTYVGFALFNGLTLLILALISLFSVPVIYERHQAIQIDHYGLANKVNDAMAKIOAK 180  
DB 1110 LMWFTTYVGFALFNGLTLLILALISLFSVPVIYERHQAIQIDHYGLANKVNDAMAKIOAK 1169  
QY 181 IPGLKRAE 189  
DB 1170 IPGLKRAE 1178  
RESULT 4  
AA556967  
ID AA556967 standard; protein; 1192 AA.  
XX AC AA556967;  
XX 25-APR-2000 (first entry)  
XX Human MAGI polypeptide.  
XX MAGI protein; neuroendocrine-specific protein; neuropathy; human;  
XX spinal injury; neuronal degeneration; neuromuscular disorder; cancer;  
XX psychiatric disorder; developmental disorder; inflammatory disorder;  
XX stroke; cytostatic; cerebroprotective; neuroprotective.  
XX Homo sapiens.  
XX WO200005364-A1.  
XX 03-FEB-2000.  
XX 21-JUL-1999; 99WO-GB002360.  
XX 22-JUL-1998; 98GB-00016024.  
XX 19-JUL-1999; 99GB-00016898.  
XX (SMK ) SMITHLINE BEECHAM PLC.  
XX Michalovich D, Prinjha RK;  
XX WPI; 2000-182693/16.  
XX N-PSDB; AAZ56886.  
XX Novel polypeptides related to neuroendocrine-specific proteins and  
XX polynucleotides useful for diagnosis of various diseases and for  
XX treatment of cancer and neurological disorders.  
XX Claim 2; Page 20-21; 35pp; English.  
XX The invention relates to human MAGI protein, which is similar to  
XX neuroendocrine-specific protein. The MAGI protein can be expressed by  
XX standard recombinant methodology. The MAGI polypeptides, polynucleotides

CC and antibodies are useful for treating diseases, including neuropathies,  
 CC spinal injury, neuronal degeneration, neuromuscular disorders,  
 CC psychiatric disorders and developmental disorders, cancer, stroke, and  
 CC inflammatory disorders. The polynucleotide is also useful for chromosome  
 CC localization and for tissue expression studies. The present sequence  
 CC represents the human MAGI protein

XX Sequence 1192 AA;

Query Match 100.0%; Score 931; DB 3; Length 1192;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-92;  
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVVDLLYWRDIKKTGVVFGASLFLLSLTWFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
 DB 1004 SVVDLLYWRDIKKTGVVFGASLFLLSLTWFSIVSVTAYIALALLSVTISFRIYKGVIOA 1063  
 QY 61 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFAV 120  
 DB 1064 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFAV 1123  
 QY 121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYGLANKNVKDMAKIOAK 180  
 DB 1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYGLANKNVKDMAKIOAK 1183

RESULT 5

AAB82349  
 ID AAB82349 standard; protein; 1192 AA.

AC AAB82349;

DT 23-JUL-2001 (first entry)

DE Human NOGO-A protein.

XX NOGO-A; human; chromosome 2p21; neuropathy; spinal injury; brain injury;  
 KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;  
 KW neuromuscular disorder; psychiatric disorder; developmental disorder;  
 KW neuroprotective; nontropic; neuroleptic; antiparkinsonian;  
 KW cerebroprotective; neuroleptic; diagnosis; therapy.

XX Homo sapiens.

XX WO200136631-A1.

XX 25-MAY-2001.

XX 14-NOV-2000; 2000WO-GB0004345.

XX 15-NOV-1999; 99GB-00026995.

XX 24-JAN-2000; 2000GB-00001550.

XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Michalovich D, Prinjha R;

XX WPI; 2001-343822/36.

XX N-PSDB; AAF90324.

XX New polypeptide designated NOGO-C is a splice variant of the human NOGO  
 PT gene and may be useful in the treatment of neural disorders including  
 PT Alzheimer's and Parkinson's diseases.

XX Disclosure; Page 26-27; 25pp; English.

XX The present sequence is that of human NOGO-A. NOGO-A is a previously  
 CC known splice variant of the human NOGO gene on chromosome 2p21. The  
 CC invention relates to a novel splice variant, NOGO-C (see AAB82348). It

CC provides NOGO-C polypeptides and polynucleotides, and methods for  
 CC producing such polypeptides by recombinant techniques. Also disclosed are  
 CC methods for utilizing NOGO-C polypeptides and polynucleotides in the  
 CC treatment of diseases including neuropathies, spinal injury, brain  
 CC injury, stroke, neuronal degeneration, for example Alzheimer's disease  
 CC and Parkinson's disease, neuromuscular disorders, psychiatric disorders  
 CC and developmental disorders. Also provided are methods for identifying  
 CC agonists and agonists for use in treating conditions associated with NOGO  
 CC -C imbalance, and diagnostic assays for detecting diseases associated  
 CC with inappropriate NOGO-C activity or levels

XX Sequence 1192 AA;

Query Match 100.0%; Score 931; DB 4; Length 1192;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-92;  
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVVDLLYWRDIKKTGVVFGASLFLLSLTWFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
 DB 1004 SVVDLLYWRDIKKTGVVFGASLFLLSLTWFSIVSVTAYIALALLSVTISFRIYKGVIOA 1063  
 QY 61 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFAV 120  
 DB 1064 IQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFAV 1123  
 QY 121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYGLANKNVKDMAKIOAK 180  
 DB 1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYGLANKNVKDMAKIOAK 1183  
 QY 181 IPGLKRAE 189  
 DB 1184 IPGLKRAE 1192

RESULT 6

AAU04591  
 ID AAU04591 standard; protein; 1192 AA.

XX AC AAU04591;

DT 26-SEP-2001 (first entry)

XX Human Nogo protein.

XX Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein;  
 KW cranial trauma; cerebral trauma; spinal cord injury; stroke;  
 KW demyelinating disease; multiple sclerosis; monophasia demyelination;  
 KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis;  
 KW Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy;  
 KW Pelizaeus-Merzbacher disease; Spongy degeneration; Alexander's disease;  
 KW Canavan's disease; metachromatic leukodystrophy; viral infection;  
 KW Krabbe's disease.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FT Domain 1054..1119  
 FT /label= Lumenal extracellular domain  
 FT /note= "This sequence is specifically claimed"

FT Peptide 1055..1094  
 FT /label= Pep1  
 FT /note= "Receptor binding inhibitory peptide. This  
 FT sequence is specifically claimed"

FT Peptide 1064..1088  
 FT /label= Pep2  
 FT /note= "Receptor binding inhibitory peptide. This  
 FT sequence is specifically claimed"

FT Peptide 1074..1098  
 FT /label= Pep3  
 FT /note= "Receptor binding inhibitory peptide. This  
 FT sequence is specifically claimed"

FT Peptide 1084..1108  
 FT /label= Pep4



Db 1124 LMWFTYVGALFNGLLTLLILALISLPSVPIYERHOAQIDHYLGLANKNVKDAMAKIOAK 1183

QY 181 IPGLKRAE 189

Db 1184 IPGLKRAE 1192

## RESULT 8

ABP68600

ID ABP68600 standard; protein; 1192 AA.

XX

AC ABP68600;

XX 14-JAN-2003 (first entry)

DT

DE Human pancreatic cancer expressed protein SEQ ID NO 71.

KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;

KW Cytostatic; tumour.

XX

OS Homo sapiens.

XX

PN WO200260317-A2.

XX

PD 08-AUG-2002.

XX

PF 30-JAN-2002; 2002WO-US002781.

XX

PR 30-JAN-2001; 2001US-0265305P.

PR 31-JAN-2001; 2001US-0265682P.

PR 09-FEB-2001; 2001US-0267568P.

PR 21-MAR-2001; 2001US-0278651P.

PR 28-APR-2001; 2001US-0287112P.

PR 16-MAY-2001; 2001US-0291631P.

PR 12-JUL-2001; 2001US-0305484P.

PR 20-AUG-2001; 2001US-0313999P.

PR 27-NOV-2001; 2001US-0333626P.

XX (CORI-) CORIXA CORP.

XX

XX Benson DR, Kalos MD; Lodes MJ, Persing DH, Hepler WT, Jiang Y;

XX WPI; 2002-627435/67.

DR N-PSDB; ABV94680.

XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for  
PT diagnosing, preventing and/or treating cancer, particularly pancreatic  
PT cancer.

XX

PS Claim 2; SEQ ID NO 71; 300pp + Sequence Listing; English.

XX

XX The invention relates to an isolated polynucleotide (I) comprising: (a)  
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)  
CC complements of (a); (c) sequences consisting of at least 20 contiguous  
CC residues of (a); (d) sequences that hybridize to (a), under moderately  
CC stringent conditions; (e) sequences having at least 75% or 90% identity  
CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-  
CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer  
CC in a patient and compositions comprising polypeptides, polynucleotides,  
CC antibodies, fusion proteins, T cell populations and antigen presenting  
CC cells expressing the polypeptide are useful in treating pancreatic cancer  
CC and stimulating an immune response. The polynucleotides can be used as  
CC probes or primers for nucleic acid hybridisation, in the design and  
CC preparation of ribozyme molecules for inhibiting expression of the tumour  
CC polypeptides and proteins in the tumour cells, in vaccines and for gene  
CC therapy. Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at fcp.wipo.int/pub/published\_pct\_sequences

XX Sequence 1192 AA;

SQ

Query Match 100.0%; Score 931; DB 5; Length 1192;  
Best Local Similarity 100.0%; Pred. No. 6.7e-92;

Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVVDLLYWRDIKKTGVFGASLFLLLSLTTFVSIVSVTAIALALLSVTISFRIYKGVIOA 60

Db 1004 SVVDLLYWRDIKKTGVFGASLFLLLSLTTFVSIVSVTAIALALLSVTISFRIYKGVIOA 1063

QY 61 IOKSDEGHPPFRAYLSEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFAV 120

Db 1064 IOKSDEGHPPFRAYLSEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFAV 1123

QY 121 LMWFTYVGALFNGLLTLLILALISLPSVPIYERHOAQIDHYLGLANKNVKDAMAKIOAK 180

Db 1124 LMWFTYVGALFNGLLTLLILALISLPSVPIYERHOAQIDHYLGLANKNVKDAMAKIOAK 1183

QY 181 IPGLKRAE 189

Db 1184 IPGLKRAE 1192

## RESULT 9

ABE81078

ID ABE81078 standard; protein; 1192 AA.

XX

AC ABE81078;

XX

DT 05-NOV-2002 (first entry)

XX

DE Human neurotransmitter receptor protein Nogo-A.

XX

KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;

KW central nervous system; peripheral nervous system; tranquilizer; Nogo;

KW vulnary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;

KW neurologic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;

KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;

KW neurotransmitter receptor; human; receptor.

XX

OS Homo sapiens.

XX

XX US2002072493-A1.

XX

XX 13-JUN-2002.

XX

XX 28-JUN-2001; 2001US-00893348.

XX

XX 19-MAY-1998; 98IL-00124500.

XX

XX 21-JUL-1998; 98WO-US014715.

XX

XX 22-DEC-1998; 98US-00218277.

XX

XX 19-MAY-1999; 99US-00314161.

XX

XX (YEDA ) YEDA RES &amp; DEV CO LTD.

XX

XX Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;

XX Moalem G;

XX

XX WPI; 2002-607255/65.

XX

XX N-PSDB; ABN86601.

XX

XX Promoting nerve regeneration and preventing neuronal degeneration in the

XX central/peripheral nervous system from injury/disease, comprises

XX administering nervous system-specific activated T cells/antigen, or

XX analogs/peptides.

XX

XX Example; Page 53-56; 93pp; English.

XX

XX The invention relates to promoting nerve regeneration or conferring

XX neuroprotection and preventing or inhibiting neuronal degeneration in the

XX central/peripheral nervous system (NS). The method involves administering

XX NS-specific activated T cells, NS-specific antigen, its analogue or its

XX peptide, a nucleotide sequence the NS-specific antigen or its analogue or

XX combinations. The method is useful for promoting nerve regeneration and

XX preventing neuronal degeneration in central/peripheral nervous system

XX from injury/disease, where the injury is spinal cord injury, blunt

XX trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or



CC damages caused by surgery such as tumour excision. The disease is not an  
 CC autoimmune disease or neoplasm. The disease results in a degenerative  
 CC process occurring in either gray or white matter or both. The disease is  
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,  
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and  
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such  
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral  
 CC neuropathies associated with various diseases, including but not limited  
 CC to uremia, porphyria, hypoglycemia, Sjogren Larsson syndrome, acute  
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary  
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption  
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-  
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins  
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia  
 CC telangiectasia, Friedreich's ataxia, amyloid polynuropathies,  
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's  
 CC disease, or lipoproteinemia. The present sequence represents the human  
 CC neurotransmitter receptor protein Nogo-A, an example of NS-specific  
 CC antigen

XX Sequence 1192 AA;

Query Match 100.0%; Score 931; DB 5; Length 1192;

Best Local Similarity 100.0%; Pred. No. 6.7e-92;

Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDDLWYRDIKKTGVFGASFLLLSLTVFSIVSTAYIALALSVTISFRIYKGVIOA 60  
 DB 1004 SVDDLWYRDIKKTGVFGASFLLLSLTVFSIVSTAYIALALSVTISFRIYKGVIOA 1063  
 QY 61 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNTIKELRRLFLVDLVDLSLKFAV 120  
 DB 1064 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNTIKELRRLFLVDLVDLSLKFAV 1123  
 QY 121 LMWVFTYVYGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAK 180  
 DB 1124 LMWVFTYVYGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAK 1183  
 QY 181 IPGLKRAE 189  
 DB 1184 IPGLKRAE 1192

RESULT 10

ABR59667  
 ID ABR59667 standard; protein; 1192 AA.

AC ABR59667;

XX 22-JUL-2003 (first entry)

XX Human NogoA protein.

XX Human; Nogo receptor; NGR; CTS domain; neuroprotective; gene therapy;  
 KW axonal growth; central nervous system; CNS; Nogo; spinal cord injury;  
 KW cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;  
 KW demyelinating disease; multiple sclerosis; monophasic demyelination;  
 KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis.

OS Homo sapiens.

XX WO2003031462-A2.

XX 17-APR-2003.

XX 04-OCT-2002; 2002WO-US032007.

XX 06-OCT-2001; 2001US-00972599.

XX (UYVA ) UNIV YALE.

XX Strittmatter SM;

XX WPI; 2003-393433/37.  
 DR N-PSDB; ACC81048.  
 XX New human Nogo receptor polypeptides and nucleic acids, useful for  
 PT decreasing inhibition of axonal growth by a central nervous system  
 PT neuron, or in treating central nervous system disease, disorder or  
 XX injury, e.g. spinal cord injury.  
 PS Disclosure; Page 131-135; 148pp; English.

XX The invention relates to a novel nucleic acid encoding a polypeptide  
 CC comprising amino acid residues 27-309 of a 473 amino acid sequence (PI,  
 CC human Nogo receptor (NGR) NTRRCT domain), or residues 27-309 of PI with  
 CC 1-20 conservative amino acid substitutions, and less than a complete CTS  
 CC domain, provided that a partial CTS domain, if present, consists of no  
 CC more than the first 39 consecutive residues. The nucleic acid of the  
 CC invention has neuroprotective activity. The polynucleotide may have a use  
 CC in gene therapy. The nucleic acid is useful for decreasing inhibition of  
 CC axonal growth by a central nervous system (CNS) neuron. The Ngr  
 CC polypeptide or an agent inhibits the binding of Nogo to Ngr or Ngr-  
 CC dependent signal transduction in the central nervous system neuron may be  
 CC used in treating central nervous system disease, disorder or injury, e.g.  
 CC spinal cord injury. Expression of an Ngr protein may be associated with  
 CC inhibition of axonal regeneration following cranial, cerebral or spinal  
 CC trauma, stroke or a demyelinating disease, such as multiple sclerosis,  
 CC monophasic demyelination, encephalomyelitis, multifocal  
 CC leukoencephalopathy, panencephalitis, or Krabbe's disease. The present  
 CC sequence is used in the exemplification of the invention

XX Sequence 1192 AA;

Query Match 100.0%; Score 931; DB 6; Length 1192;

Best Local Similarity 100.0%; Pred. No. 6.7e-92;

Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDDLWYRDIKKTGVFGASFLLLSLTVFSIVSTAYIALALSVTISFRIYKGVIOA 60  
 DB 1004 SVDDLWYRDIKKTGVFGASFLLLSLTVFSIVSTAYIALALSVTISFRIYKGVIOA 1063  
 QY 61 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNTIKELRRLFLVDLVDLSLKFAV 120  
 DB 1064 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNTIKELRRLFLVDLVDLSLKFAV 1123  
 QY 121 LMWVFTYVYGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAK 180  
 DB 1124 LMWVFTYVYGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAK 1183  
 QY 181 IPGLKRAE 189  
 DB 1184 IPGLKRAE 1192

RESULT 11

ADO08103

ID ADO08103 standard; protein; 1192 AA.

XX ADO08103;

XX 01-JUL-2004 (first entry)

XX Human polypeptide #65.

XX Human; fat cell number; fat cell size; obesity; diabetes; anorectic;  
 KW antidiabetic.

XX Homo sapiens.

XX US2004071700-A1.

XX 15-APR-2004.

XX 09-OCT-2002; 2002US-00267502.



PF 09-DEC-2003; 2003WO-EP013960.  
 XX  
 PR 10-DEC-2002; 2002GB-00028832.  
 XX  
 PA (NOVS ) NOVARTIS AG.  
 PA (NOVS ) NOVARTIS PHARMA GMBH.  
 XX (UYZU-) UNIV ZUERICH.  
 XX  
 PI Barake C, Mir AK, Oertle T, Schnell L, Schwab ME, Vitaliti A;  
 PI Zurini M;  
 XX  
 XX WPI; 2004-468818/44.  
 DR N-PSDB; ADP45550.  
 XX  
 XX New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-D20 or NogoA623-640, useful in preparing a composition for treating CNS injury or neurodegenerative disorders.  
 PT  
 PT  
 XX  
 PS Claim 1; SEQ ID NO 5; 121pp; English.  
 XX  
 CC The present invention describes a binding molecule which binds to human NogoA polypeptide, human NiG, human NiG-D20 or human NogoA 623-640 with a dissociation constant of less than 100nM. Also described: (1) a polynucleotide encoding the binding molecule; (2) an expression vector or system comprising the polynucleotide; (3) a host cell comprising the expression system; (4) a pharmaceutical composition comprising the binding molecule and a carrier or diluent; and (5) treating diseases associated with nerve repair. The binding molecule has neuroprotective activity, and can be used in gene therapy. The binding molecule is useful in preparing a composition for treating central nervous system (CNS) injury or neurodegenerative disorders. The present sequence represents human NogoA, which is used in the exemplification of the present invention.  
 CC  
 XX  
 SQ Sequence 1192 AA;

Query Match 100.0%; Score 931; DB 8; Length 1192;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-92;  
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRD1KKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
 Db 1004 SVVDLLYWRD1KKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1063  
 Qy 61 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNCITIKELRRLFLVDDVLSLKFAV 120  
 Db 1064 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNCITIKELRRLFLVDDVLSLKFAV 1123  
 Qy 121 LMWFTYVYGALFNGLTLLILALISLFSVPVIYERHQAIIDHYLGLANKNVKDMAKIOAK 180  
 Db 1124 LMWFTYVYGALFNGLTLLILALISLFSVPVIYERHQAIIDHYLGLANKNVKDMAKIOAK 1183  
 Qy 181 IPGLKRAE 189  
 Db 1184 IPGLKRAE 1192

RESULT 14  
 ADP67234  
 ID ADP67234 standard; protein; 1192 AA.  
 XX  
 AC ADP67234;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Human Nogo-A protein.  
 XX  
 KW human; Nogo-A; neurite outgrowth inhibitor; Nogo;  
 KW contactin-associated protein-1; Caspr; neuroprotective; gene therapy;  
 KW CNS; spinal cord injury; multiple sclerosis; epilepsy; stroke.  
 XX  
 OS Homo sapiens.  
 XX

PN WO2004052389-A2.  
 XX  
 PD 24-JUN-2004.  
 XX  
 PF 05-DEC-2003; 2003WO-GB005329.  
 XX  
 PR 06-DEC-2002; 2002US-0431549P.  
 PR 20-JUN-2003; 2003US-0480138P.  
 XX  
 PA (SIGE-) SINGAPORE GEN HOSPITAL PTE LTD.  
 PA (FORR/) FORREST G R.  
 XX  
 PI Xiao Z;  
 PI  
 XX WPI; 2004-468705/44.  
 DR  
 XX  
 XX New composition comprising Nogo and Caspr or a substance capable of promoting interaction between Nogo and Caspr useful for treating injury to or disease of the CNS, e.g., spinal cord injury, multiple sclerosis, epilepsy or stroke.  
 PT  
 PT  
 XX  
 PS Disclosure; Page 14; 202pp; English.  
 XX  
 CC The invention relates to a novel composition comprising neurite outgrowth inhibitor (Nogo) and contactin-associated protein-1 (Caspr) or its mimetics or a substance capable of promoting interaction between Nogo and Caspr, in combination with a carrier. A composition of the invention has neuroprotective activity, and may have a use in gene therapy. The composition is useful for treating injury to or disease of the CNS, e.g. spinal cord injury, multiple sclerosis, epilepsy or stroke. The present sequence represents human Nogo-A.  
 CC  
 XX  
 SQ Sequence 1192 AA;

Query Match 100.0%; Score 931; DB 8; Length 1192;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-92;  
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRD1KKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
 Db 1004 SVVDLLYWRD1KKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1063  
 Qy 61 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNCITIKELRRLFLVDDVLSLKFAV 120  
 Db 1064 IQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNCITIKELRRLFLVDDVLSLKFAV 1123  
 Qy 121 LMWFTYVYGALFNGLTLLILALISLFSVPVIYERHQAIIDHYLGLANKNVKDMAKIOAK 180  
 Db 1124 LMWFTYVYGALFNGLTLLILALISLFSVPVIYERHQAIIDHYLGLANKNVKDMAKIOAK 1183  
 Qy 181 IPGLKRAE 189  
 Db 1184 IPGLKRAE 1192

RESULT 15  
 ADR13966  
 ID ADR13966 standard; protein; 1192 AA.  
 XX  
 AC ADR13966;  
 XX  
 DT 23-SEP-2004 (first entry)  
 XX  
 DE Human Nogo-A.  
 XX  
 KW human; myelin-associated glycoprotein; MAG; neural growth;  
 KW neural regeneration; apoptosis; amyotrophic lateral sclerosis;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease;  
 KW multiple sclerosis; Creutzfeldt-Jacob disease; kuru;  
 KW multiple system atrophy; Lou Gehrig's disease;  
 KW progressive supranuclear palsy.  
 XX  
 OS Homo sapiens.  
 XX

XX	US2004121341-A1.
PN	
XX	
XX	
PD	24-JUN-2004.
XX	
PF	20-DEC-2002; 2002US-00327213.
XX	
PR	20-DEC-2002; 2002US-00327213.
XX	
PA	(FILB/) FILBIN M T.
PA	(DOME/) DOMENICONI M.
PA	(CAOZ/) CAO Z.
XX	
PI	Filbin MT, Domeniconi M, Cao Z;
XX	
DR	WPI; 2004-479666/45.
DR	N-PSDB; ADR13965.
XX	
PT	New myelin-associated glycoprotein (MAG) derivative comprises a mutation
PT	in or flanking MAG Ig-like domain 5 (Igds), excluding the MAG derivative
PT	MAG (dl-3)-Fc, useful promoting neural growth and regeneration.
XX	
PS	Disclosure; SEQ ID NO 9; slpp; English.
XX	
CC	The invention relates to a myelin-associated glycoprotein (MAG)
CC	derivative comprising a mutation in or flanking MAG Ig-like domain 5
CC	(Igds), excluding the MAG derivative MAG (dl-3)-Fc, where the mutation
CC	reduces or eliminates the ability of the derivative to regulate neurite
CC	outgrowth as compared to endogenous or soluble MAG without eliminating
CC	binding to neuronal surfaces. The inhibitors of MAG are useful for
CC	promoting neural growth and regeneration. They are also useful for
CC	treating neural degeneration associated with injuries, disorders, or
CC	diseases. The disorder, disease, or condition is associated with
CC	apoptosis or results from a demyelinating disease and includes
CC	amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease,
CC	Huntington's disease, multiple sclerosis, Creutzfeldt-Jacob disease,
CC	kuru, multiple system atrophy, amyotrophic lateral sclerosis (Lou
CC	Gehrig's disease), or progressive supranuclear palsy. The present
CC	sequence represents the amino acid sequence of human NQO-A.
XX	
SQ	Sequence 1192 AA;
	Query Match . 100.0%; Score 931; DB 8; Length 1192;
	Best Local Similarity 100.0%; Pred. No. 6.7e-92;
	Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 SVDDLKYRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTFRIYKVIOA 60
Dd	1004 SVDDLKYRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTFRIYKVIOA 1063
Qy	61 IQKSDEGHPFRAYLESEVAISEELVOKYSNSALGHVNCTIKELRRLFLVDLDVLSKFV 120
Dd	1064 IQKSDEGHPFRAYLESEVAISEELVOKYSNSALGHVNCTIKELRRLFLVDLDVLSKFV 1123
Qy	121 LMWFTTVYGALFNGLTLLILIALISLFSVPVIYERHQAIIDHYLGANKNVKDAMAKIQAK 180
Dd	1124 LMWFTTVYGALFNGLTLLILIALISLFSVPVIYERHQAIIDHYLGANKNVKDAMAKIQAK 1183
Qy	181 IGPLKRKAE 189
Dd	1184 IGPLKRKAE 1192

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:19:00 ; Search time 7.13706 Seconds  
(without alignments)  
1976.818 Million cell updates/sec

Title: US-09-830-972-29\_COPY\_990\_1178

Perfect score: 931

Sequence: 1 SWDLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAE 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA.\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.psp.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.psp.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.psp.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.psp.\*  
5: /cgn2\_6/ptodata/1/iaa/PTCUS\_COMB.psp.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.psp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	927	99.6	199	2	US-08-700-607-1
2	927	99.6	201	4	US-09-949-016-9124
3	682	73.3	208	2	US-08-700-607-7
4	682	73.3	356	2	US-08-700-607-6
5	682	73.3	439	4	US-09-949-016-9180
6	682	73.3	776	2	US-08-700-607-5
7	682	73.3	776	4	US-09-949-016-6998
8	665	71.4	267	2	US-08-700-607-8
9	627.5	67.4	192	4	US-09-949-016-8859
10	541.5	58.2	168	4	US-09-149-476-563
11	518	55.6	219	4	US-09-270-767-45132
12	512	55.0	241	2	US-08-700-607-3
13	473.5	50.9	588	4	US-09-949-016-7290
14	285	30.6	92	4	US-09-149-476-411
15	246	26.4	114	4	US-09-513-999C-7861
16	144	15.5	374	4	US-09-248-796A-16008
17	100	10.7	480	3	US-08-905-223-411
18	89	9.6	468	4	US-08-487-536-8
19	89	9.6	468	4	US-08-660-451A-8
20	88.5	9.5	1278	4	US-09-462-136-2
21	88.5	9.5	1318	4	US-09-949-016-10152
22	88	9.5	382	4	US-09-949-016-11596
23	87.5	9.4	592	4	US-09-134-000C-5477
24	87.5	9.4	1051	3	US-09-134-001C-5005
25	85	9.1	414	4	US-08-956-171E-5246
26	85	9.1	414	4	US-08-781-986A-5246
27	83	8.9	744	4	US-09-785-381-1

Sequence 3, Appli  
Sequence 27968, A  
Sequence 53, Appl  
Sequence 7, Appli  
Sequence 6175, Ap  
Sequence 4866, Ap  
Sequence 4880, Ap  
Sequence 4818, Ap  
Sequence 302, App  
Sequence 9438, Ap  
Sequence 30, Appl  
Sequence 6579, Ap  
Sequence 12212, A  
Sequence 973, App  
Sequence 902, App  
Sequence 14833, A  
Sequence 5, Appli  
Sequence 7510, Ap

#### ALIGNMENTS

##### RESULT 1

US-08-700-607-1  
; Sequence 1, Application US/08700607  
; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/700,607

; FILING DATE: Filed Herewith

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0114 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 199 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; IMMEDIATE SOURCE:

; LIBRARY:

; CLONE: Consensus

US-08-700-607-1

Query Match 99.6%; Score 927; DB 2; Length 199;  
Best Local Similarity 100.0%; Pred. No. 7.9e-93;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 VVDLYWRDIKKTGVVFGASIFLLLSLTVPFSIVSVTAVALALLSVTISFRIYKGVQAI 61

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Db 12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 71
QY 62 QKSDEGHPPRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLDVSLKFAVL 121
Db 72 QKSDEGHPPRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLDVSLKFAVL 131
QY 122 MVFTTVGALFNGLTLLILALISLFSVPVIYERHQADIDHYLGLANKNVKDMAKIOAKI 181
Db 132 MVFTTVGALFNGLTLLILALISLFSVPVIYERHQADIDHYLGLANKNVKDMAKIOAKI 191
QY 182 PGLKRAE 189
Db 192 PGLKRAE 199

RESULT 2
US-09-949-016-9124
; Sequence 9124, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9124
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9124

Query Match 99.6%; Score 927; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 8e-93; Indels 0; Gaps 0;
Matches 188; Conservative 0; Mismatches 0;

QY 2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61
Db 14 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 73
QY 62 QKSDEGHPPRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLDVSLKFAVL 121
Db 74 QKSDEGHPPRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLDVSLKFAVL 133
QY 122 MVFTTVGALFNGLTLLILALISLFSVPVIYERHQADIDHYLGLANKNVKDMAKIOAKI 181
Db 134 MVFTTVGALFNGLTLLILALISLFSVPVIYERHQADIDHYLGLANKNVKDMAKIOAKI 193
QY 182 PGLKRAE 189
Db 194 PGLKRAE 201

RESULT 3
US-08-700-607-7
; Sequence 7, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304

Db 12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 71
QY 62 QKSDEGHPPRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLDVSLKFAVL 121
Db 72 QKSDEGHPPRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLDVSLKFAVL 131
QY 122 MVFTTVGALFNGLTLLILALISLFSVPVIYERHQADIDHYLGLANKNVKDMAKIOAKI 181
Db 132 MVFTTVGALFNGLTLLILALISLFSVPVIYERHQADIDHYLGLANKNVKDMAKIOAKI 191
QY 182 PGLKRAE 189
Db 192 PGLKRAE 199

RESULT 4
US-08-700-607-6
; Sequence 6, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307311
US-08-700-607-7

Query Match 73.3%; Score 682; DB 2; Length 208;
Best Local Similarity 68.4%; Pred. No. 3.8e-66;
Matches 128; Conservative 31; Mismatches 28; Indels 0; Gaps 0;

QY 3 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQ 62
Db 22 IDLLYWRDIKQTGIVFGSFLLLSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ 81
QY 63 KSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLDVSLKFAVL 122
Db 82 KTDGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLDVSLKFAVL 141
QY 123 WYFTTVGALFNGLTLLILALISLFSVPVIYERHQADIDHYLGLANKNVKDMAKIOAKIP 182
Db 142 WLLTVGALFNGLTLLILALISLFSVPVIYERHQADIDHYLGLANKNVKDMAKIOAKIP 201
QY 183 GLKRAE 189
Db 202 GAKRAE 208

RESULT 4
US-08-700-607-6
; Sequence 6, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 356 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 307309
US-08-700-607-6

Query Match 73.3%; Score 682; DB 2; Length 356;
Best Local Similarity 68.4%; Pred. No. 8e-66;
Matches 128; Conservative 31; Mismatches 28; Indels 0; Gaps 0;

QY 3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFISVSTAYIALALLSVTISFRIYKGVIAIQ 62
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Db 170 IDLLYWRDIKQTGIVFGSFLLLSLTVFISVSTAYIALALLSVTISFRIYKSVLQAVQ 229
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 63 KSDGHPFRAYLSEVAISEELVQKYSNSALGHVNCCTIKELRRFLVDLVDLSLKFVLM 122
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 230 KTDEGHPFKAYLELITLSQEQIKYTDCLQFYVNSTLKELRRLFLVDLVDLSLKFVLM 289
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 123 WFTYVGALFNLGLTLLILALISLFSVPVIYERHQAIQIDHYGLANKNVKDMAKIQAKIP 182
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 290 WLLTYVGALFNLGLTLLILALISLFSVPVIYERHQAIQIDHYGLANKNVKDMAKIQAKIP 349
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 183 GLKRAE 189
:|||||
Db 350 GAKRAE 356
:|||||

RESULT 5
US-09-949-016-9180
; Sequence 9180, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows version 4.0
; SEQ ID NO 9180
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9180
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Query Match 73.3%; Score 682; DB 4; Length 439;
Best Local Similarity 68.4%; Pred. No. 1.1e-65;
Matches 128; Conservative 31; Mismatches 28; Indels 0; Gaps 0;

QY 3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFISVSTAYIALALLSVTISFRIYKGVIAIQ 62
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 253 IDLLYWRDIKQTGIVFGSFLLLSLTVFISVSTAYIALALLSVTISFRIYKSVLQAVQ 312
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 63 KSDGHPFRAYLSEVAISEELVQKYSNSALGHVNCCTIKELRRFLVDLVDLSLKFVLM 122
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 313 KTDEGHPFKAYLELITLSQEQIKYTDCLQFYVNSTLKELRRLFLVDLVDLSLKFVLM 372
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 123 WFTYVGALFNLGLTLLILALISLFSVPVIYERHQAIQIDHYGLANKNVKDMAKIQAKIP 182
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 373 WLLTYVGALFNLGLTLLILALISLFSVPVIYERHQAIQIDHYGLANKNVKDMAKIQAKIP 432
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 183 GLKRAE 189
:|||||
Db 433 GAKRAE 439
:|||||

RESULT 6
US-08-700-607-5
; Sequence 5, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq version 1.5
; CURRENT APPLICATION DATA: US/08/700,607
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 776 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307307
US-08-700-607-5

Query Match 73.3%; Score 682; DB 2; Length 776;
Best Local Similarity 68.4%; Pred. No. 2.4e-65;
Matches 128; Conservative 31; Mismatches 28; Indels 0; Gaps 0;

QY 3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFISVSTAYIALALLSVTISFRIYKGVIAIQ 62
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 590 IDLLYWRDIKQTGIVFGSFLLLSLTVFISVSTAYIALALLSVTISFRIYKSVLQAVQ 649
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
QY 63 KSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNCITIKELRRLFLVDDLVDSLKFVLM 122
DB 650 KTDGHPFRAYLELEITLSQEQIKYTDCLQFVNSTLKLRLFLVQDLVDSLKFVLM 709
QY 123 WFTVYVGFALFNGITLLILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDMAKIOAKIP 182
DB 710 WLLTYVGFALFNGITLLMAVSMFTLPVVYVVKHQAIQIDYLGVLVRTHINAVVAKIOAKIP 769
QY 183 GLKRAE 189
DB 770 GAKRAE 776

RESULT 7
US-09-949-016-6998
; Sequence 6998, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6998
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6998

Query Match 73.3%; Score 682; DB 4; Length 776;
Best Local Similarity 68.4%; Pred. No. 2.4e-65;
Matches 128; Conservative 31; Mismatches 28; Indels 0; Gaps 0;

QY 3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAIYALALLSVTISPRIYKGVIOAQ 62
DB 590 IDLLYWRDIKQTGIVFGSFLLLFSLTQFSVSVWAYLALAALSATISPRIYKSVLQAVQ 649
QY 63 KSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNCITIKELRRLFLVDDLVDSLKFVLM 122
DB 650 KTDGHPFRAYLELEITLSQEQIKYTDCLQFVNSTLKLRLFLVQDLVDSLKFVLM 709
QY 123 WFTVYVGFALFNGITLLILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDMAKIOAKIP 182
DB 710 WLLTYVGFALFNGITLLMAVSMFTLPVVYVVKHQAIQIDYLGVLVRTHINAVVAKIOAKIP 769
QY 183 GLKRAE 189
DB 770 GAKRAE 776

RESULT 8
US-08-700-607-8
; Sequence 8, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bardman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
```

```
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 281046
US-08-700-607-8

Query Match 71.4%; Score 665; DB 2; Length 267;
Best Local Similarity 67.2%; Pred. No. 3.8e-64;
Matches 123; Conservative 33; Mismatches 27; Indels 0; Gaps 0;

QY 3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAIYALALLSVTISPRIYKGVIOAQ 62
DB 13 IDLLYWRDIKQTGIVFGSFLLLFSLTQFSVSVWAYLALAALSATISPRIYKSVLQAVQ 72
QY 63 KSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNCITIKELRRLFLVDDLVDSLKFVLM 122
DB 73 KTDGHPFRAYLELEITLSQEQIKYTDCLQVNVNSTLKLRLFLVQDLVDSLKFVLM 132
QY 123 WFTVYVGFALFNGITLLILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDMAKIOAKIP 182
DB 133 WLLTYVGFALFNGITLLMAVSMFTLPVVYVVKHQAVDQYLGVLVRTHINTVVAKIOAKIP 192
QY 183 GLK 185
DB 193 GAR 195

RESULT 9
US-09-949-016-8859
; Sequence 8859, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8859
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; LENGTH: 192
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8859

Query Match      67.4%; Score 627.5; DB 4; Length 192;
Best Local Similarity 61.1%; Pred. No. 2.9e-60;
Matches 116; Conservative 38; Mismatches 35; Indels 1; Gaps 1;

QY 1 SVDDLIVRDIKKTGVFGASFLILLSLTVPSIVSVTAIYALISLTVTSIRIYKGVIOA 60
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 3 SVHDLIFWRDVKKTGFVFGTTLIMLLSLAASFVSISWYSLTALISLTVTSIRIYKSVIOA 62
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 IOKSDEGHPPFRAYLESEVAISELQKYSNGALGHVNCTIKELRFLVDDLVDSLKFAV 120
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 63 VQSEEGHPPFRAYLDVDTLSEAFHNTYNAWVHNRAKLIIRLFLVEDLVDSLKLA 122
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 121 LMWVTVYGALFNGTLILALISLFSVPVYERHQAQIDHYGLANKVKNVDAKIOAK 180
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 123 FMWLMTVYGAVFNGITLLILAEILLFSPVIVVEKYKTQIDHYVGIARDQTKSIVEKIOAK 182
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 181 IPGL-KRKA 189
   ||:||||:||||:
Db 183 LPGIACKKAE 192
   ||:||||:||||:

RESULT 10
US-09-149-476-563
; Sequence 563, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
```



APPLICANT: Goli, Surya K.  
APPLICANT: Hillman, Jennifer L.  
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/700,607  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0114 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: THPINOB01  
CLONE: 31870  
US-08-700-607-3

Query Match 55.0%; Score 512; DB 2; Length 241;  
Best Local Similarity 52.4%; Pred. No. 1.4e-47;  
Matches 98; Conservative 35; Mismatches 34; Indels 20; Gaps 1;  
QY 1 SVVDLLYWRDIKKTGWFGASLFLLLSLTVFSIVSVTAIALALLSVTISFRIYKGVIOA 60  
DB 47 AVHDLIXWRDVKTGFVGTGLMLLSLAASFVISVSVLLALLSVTISFRIYKSVIOA 106  
QY 61 IQKSDGHPFRAYLSEVAISELVQKYSNLSALGHVNCITKELRLFLVDDLVDSLKPAV 120  
DB 107 VQKSEGHPPKAYLDVDTLSSEAFHNYNMAAMVHNRALKLIIRLFLVEDLVDSLKLV 166  
QY 121 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHOAQIDHYGLANKNVKDMAKIOAK 180  
DB 167 FNLMTYTGAVFNGTLLILAEILIXSVPIVYXKY-----KVPESK 206  
QY 181 IPLKRX 187  
DB 207 TPWRQK 213

RESULT 13  
US-09-949-016-7290  
Sequence 7290, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7290  
LENGTH: 588  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-7290  
Query Match 50.9%; Score 473.5; DB 4; Length 588;  
Best Local Similarity 47.3%; Pred. No. 7.8e-43;  
Matches 95; Conservative 37; Mismatches 56; Indels 13; Gaps 1;  
QY 2 VVDLLYWRDIKKTGWFGASLFLLLSLTVFSIVSVTAIALALLSVTISFRIYKGVIOA 61  
DB 388 VADLLYWKDTRTSGVFTGLMVSLCLLHFSIVSVAHALLLGGTISLRVYKVLQAV 447  
QY 62 QKSDGHPFRAYLSEVAISELVQKYSNLSALGHVNCITKELRLFLVDDLVDSLKPAV 121  
DB 448 HRGDGANPFQAYLDVDTLTREOTERLSHOITSRVSAATQLRHFFLEDLVDSLKLALL 507  
QY 122 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHOAQIDHYGLANKNVKDMAKIOAK 181  
DB 508 FVILTFVGAIENGLTLLILGVLGTLFTLLYRQHQAOIDQVVGVLVTNQLSHIKAKIRAKI 567  
QY 182 PGL-----KKAE 189  
DB 568 PGTGALASAAAAAASGSKAE 588  
RESULT 14  
US-09-149-476-411  
Sequence 411, Application US/09149476  
Patent No. 6420526  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: PZ002P1  
CURRENT APPLICATION NUMBER: US/09/149,476  
CURRENT FILING DATE: 1998-09-08  
EARLIER APPLICATION NUMBER: PCT/US98/04493  
EARLIER FILING DATE: 1998-03-06  
EARLIER APPLICATION NUMBER: 60/040,162  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,333  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/038,621  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,626  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,334  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,336  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,163  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/047,600  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,615  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,597  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,502  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,633  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,583  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,617  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,618

[illegible]

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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match      30.6%; Score 285; DB 4; Length 92;
Best Local Similarity 57.1%; Pred. No. 1.9e-23;
Matches 52; Conservative 20; Mismatches 19; Indels 0; Gaps 0;

QY 90 NSALGHVNCITKELRRLFLVDDLVDLSLKFAVLMMVFTYVVGALFNGLTLLILALISLRSVP 149
   :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.:
DB 2 NAAMVHINRAKLIIRLFLVEDVDSLKLAVFMMWMTYVGAVFNGITLLILAELLIFSVP 61

QY 150 VIYERHQAQIDHYLGLANKNVKDMAKIOAK 180
   :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.:
DB 62 IVEYKYQTIDHYVGIARDQTKSIVEKIPSK 92

RESULT 15
US-09-513-999C-7861
; Sequence 7861, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO. 7861
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -48...-1
; OTHER INFORMATION: score 4.6
; OTHER INFORMATION: seq VFGSFLLLFSLT/QF
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 22
; OTHER INFORMATION: Xaa=Phe or Leu
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 41
; OTHER INFORMATION: Xaa= * or Gly or Arg
US-09-513-999C-7861

Query Match      26.4%; Score 246; DB 4; Length 114;
Best Local Similarity 69.6%; Pred. No. 4.4e-19;
Matches 48; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQ 62
   :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.:
DB 22 IDLLYWRDIKQTGIVFGSFLLLFSLTQFSVVSVVAYIALAALSATISXRIYKSVLQAVQ 81

Search completed: June 16, 2005, 12:33:40
Job time : 8.13706 secs,
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```
QY 63 KSDEGHPR 71
   :.: :.: :.: :.: :.:
DB 82 ITDEGHRXR 90
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 12:55:32 ; Search time 5.68322 Seconds  
(without alignments)  
3199.767 Million cell updates/sec

Title: US-09-830-972-29\_COPY\_990\_1178

Perfect score: 931

Sequence: 1 SWVDLLYWRDIKKTGWFGA.....VKDAMAKIQAKIPGLKRAE 189.

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	682	73.3	208	2 I60904	neuroendocrine-spe
2	682	73.3	776	2 A46583	neuroendocrine-spe
3	665	71.4	267	2 A60021	tropomyosin-relate
4	335	36.0	2484	2 T26216	hypothetical prote
5	335	36.0	2607	2 T26215	hypothetical prote
6	334	35.9	222	2 T26213	hypothetical prote
7	191	20.5	255	2 E84899	hypothetical prote
8	182	19.5	271	2 T13013	hypothetical prote
9	163	17.5	275	2 T05595	hypothetical prote
10	147	15.8	393	2 S67763	probable membrane
11	144.5	15.5	242	2 B85016	hypothetical prote
12	131	14.1	183	2 A84527	hypothetical prote
13	127.5	13.7	295	2 S59439	probable membrane
14	124	13.3	206	2 T01153	probable seed matu
15	109.5	11.8	264	2 T47948	hypothetical prote
16	104.5	11.2	203	2 T47571	hypothetical prote
17	95	10.2	288	2 B90043	conserved hypothet
18	94.5	10.2	458	2 A72258	hypothetical prote
19	93	10.0	160	2 C84422	hypothetical prote
20	92.5	9.9	527	2 A84645	probable cytochrom
21	88.5	9.5	405	2 H71692	hypothetical prote
22	88	9.5	224	2 D71915	hydrogenase, cytoc
23	87.5	9.4	296	2 S46018	probable membrane
24	85.5	9.2	442	2 C75057	hypothetical prote
25	85.5	9.2	823	2 H83724	hypothetical prote
26	85.5	9.2	1065	2 E69795	acriflavin resista
27	85	9.1	224	1 A64599	hydrogenase (BC 1.
28	85	9.1	459	2 G86264	F3F19 hypothetical
29	85	9.1	468	2 A38223	nicotinic acetylch

30	85	9.1	1055	2 H90023	hypothetical prote
31	84.5	9.1	151	2 G96705	unknown protein, 7
32	84.5	9.1	457	2 H85095	hypothetical prote
33	84.5	9.1	464	2 C70414	NAOH2 dehydrogenas
34	84.5	9.1	677	2 F95232	immunity protein,
35	84.5	9.1	680	2 H98096	conserved hypothet
36	84	9.0	299	2 B69155	hypothetical prote
37	82.5	8.9	570	2 S52765	secD protein - Str
38	82.5	8.9	955	2 T33040	hypothetical prote
39	82	8.8	589	2 F64201	transport ATP-bind
40	81.5	8.8	324	2 A81700	phospho-N-acetylm
41	81.5	8.8	369	2 H90587	hypothetical prote
42	81.5	8.8	598	2 T14886	leukotoxin express
43	81.5	8.8	822	2 T41622	probable ABC trans
44	81.5	8.8	937	2 T41400	probable peroxisom
45	81	8.7	537	2 G82873	conserved hypothet

#### ALIGNMENTS

##### RESULT 1

I60904

neuroendocrine-specific protein C - human

C:Species: Homo sapiens (man)

C>Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 09-Jul-2004

C:Accession: I60904

R:Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.;

J. Biol. Chem. 268, 13439-13447, 1993

A>Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spe

A:Reference number: A46583; MUID:93293865; PMID:7685762

A:Accession: I60904

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-208 <RES>

A:Cross-references: UNIPROT:Q16799; GB:L10335; NID:g307310; PID:AAAS9952.1; PID:g307311

C:Genetics:

A:Gene: GDB:RTN1; NSP

A:Cross-references: GDB:203968; OMIM:600865

A:Map position: 14q21-14q22

Query Match 73.3%; Score 682; DB 2; Length 208;

Best Local Similarity 68.4%; Pred. No. 2.8e-55;

Matches 128; Conservative 31; Mismatches 28; Indels 0; Gaps 0;

Qy	3	VDLLYWRDIKKTGVVFGASL	LLLSLTVFSTVSTAYTALALLSVTISFRIYKGVIOAIQ 62
Db	22	IDLLYWRDIKQTGIVFGSFL	LLLSLTQFSVSVVAYLALALASATISFRIYKSVLQAVQ 81
Qy	63	KSDEGHPPRAYLSEVAISE	LBVLQKYSNSALGHVNCTIKELRRLFLVDDVDSLKFAVLM 122
Db	82	KTDEGHPPKAYLELEITLS	EQIKYTDCLQFYVNSTLKELRRLFLVQDLVDSLKFAVLM 141
Qy	123	WVTVYVGFALFNGLLILAL	ISLFSVPVIYERHQAIIDHYIGLANKNVKDAMAKIQAKIP 182
Db	142	WLLTVYVGFALFNGLLTLL	MAVSMFTLPVVYVKHQAIQDYLGVLVTHINAVVAKIQAKIP 201
Qy	183	GLKRAE 189	
Db	202	GAKRAE 208	

##### RESULT 2

A46583

neuroendocrine-specific protein, splice form A - human

N:Contains: neuroendocrine-specific protein, splice form B

C:Species: Homo sapiens (man)

C>Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 09-Jul-2004

C:Accession: A46583; I60903

R:Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.;

J. Biol. Chem. 268, 13439-13447, 1993

A>Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spe

A:Reference number: A46583; MUID:93293865; PMID:7685762

```
RESULT 4
T26216
hypothetical protein W06A7.3c - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26216
R:Ainscough, R.
submitted to the EMBL Data Library, August 1996
A:Reference number: Z20173
A:Accession: T26216
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2484 <WIL>
A:Cross-references: UNIPROT:Q9U347; EMBL:Z78066; PIDN:CAB51467.1; GSPDB:GN00023; CESP:W06A7
A:Experimental source: clone W06A7
C:Genetics:
A:Gene: CESP:W06A7.3c
A:Map position: 5
A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2

Query Match 36.0%; Score 335; DB 2; Length 2484;
Best Local Similarity 33.7%; Pred. No. 3.6e-22;
Matches 62; Conservative 46; Mismatches 76; Indels 0; Gaps 0;

QY 2 VVDLLYWRDIKKTGVVFGASFLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQ 61
DB 590 IDLLYWRDIKQTGIVFGSFLFLLSLTQFSVSVWVAYLALAALSATISFRIYKSVLQAVQ 649

QY 63 KSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFAVLM 122
DB 650 KTDGEHPFRAYLELEITLSQEQIKYTDCLQFYVNSTLKELRRLFLVQDLVDSLKFAVLM 709

QY 123 WFTYTYGALFNGLTLLILALISLFSVPVIYERHQAOIDHYLGLANKNVKDMAKIOAKIP 182
DB 710 WLLTYTYGALFNGLTLLMAVSNFTLPVYVVKHQAOIDQYLGIVRTHINNAVAKIOAKIP 769

QY 183 GLKRAE 189
DB 770 GAKRAE 776

RESULT 5
T26215
hypothetical protein W06A7.3a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26215
R:Ainscough, R.
submitted to the EMBL Data Library, August 1996
A:Reference number: Z20173
A:Accession: T26215
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2607 <WIL>
A:Cross-references: UNIPROT:Q23187; EMBL:Z78066; PIDN:CAB01522.2; GSPDB:GN00023; CESP:W06A7
A:Experimental source: clone W06A7
C:Genetics:
A:Gene: CESP:W06A7.3a
A:Map position: 5
A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2; 2586/2

Query Match 36.0%; Score 335; DB 2; Length 2607;
Best Local Similarity 33.7%; Pred. No. 3.8e-22;
Matches 62; Conservative 46; Mismatches 76; Indels 0; Gaps 0;

QY 2 VVDLLYWRDIKKTGVVFGASFLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQ 61
DB 2412 VLDVYWRDAKSAIVLSLALIVFLVAKYPLTIVTYSLLALGAAAGFRVFKVYEQAI 2471

QY 62 OKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFAVLM 121
DB 2472 KNTDSEHPFPSEITLQDLTLPQEKVHAQADVFEHATCIANKLKLKLVFVESPLESIKFGLV 2531
```

```
RESULT 3
A60021
tropomyosin-related protein; neuronal - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Nov-1999
C:Accession: A60021
R:Wiczorek, D.F.; Hughes, S.R.
Brain Res. Mol. Brain Res. 10, 33-41, 1991
A:Title: Developmentally regulated cDNA expressed exclusively in neural tissue.
A:Reference number: A60021; MUID:91278684; PMID:1647480
A:Accession: A60021
A:Molecule type: mRNA
A:Residues: 1-267 <WIE>
A:Cross-references: EMBL:X52817; NID:g456549; PIDN:CAA37001.1; PID:g456550
C:Comment: This neuronal-specific mRNA was identified by hybridization to an alpha-tropo

Query Match 71.4%; Score 665; DB 2; Length 267;
Best Local Similarity 67.2%; Pred. No. 1.4e-53;
Matches 123; Conservative 33; Mismatches 27; Indels 0; Gaps 0;

QY 3 VDLLYWRDIKKTGVVFGASFLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQ 62
DB 13 IDLLYWRDIKQTGIVFGSFLFLLSLTQFSVSVWVAYLALAALSATISFRIYKSVLQAVQ 72

QY 63 KSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFAVLM 122
DB 73 KTDGEHPFRAYLELEITLSQEQIKYTDCLQLYVNSTLKELRRLFLVQDLVDSLKFAVLM 132

QY 123 WFTYTYGALFNGLTLLILALISLFSVPVIYERHQAOIDHYLGLANKNVKDMAKIOAKIP 182
DB 133 WLLTYTYGALFNGLTLLMAVSNFTLPVYVVKHQAOVDQYLGIVRTHINTVAVAKIOAKIP 192

QY 183 GLK 185
DB 193 GAR 195
```



RESULT 7  
E84899  
hypothetical protein At2g46170 [imported] - Arabidopsis thaliana  
C.Species: Arabidopsis thaliana (mouse-ear cress)  
C.Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C.Accession: E84899  
R.Yin, X.; Kaul, S.; Rounleay, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
Rabin, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
Euseus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A.Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A.Reference number: A84420; MUID:20083487; PMID:10617197  
A.Accession: E84899  
A.Status: preliminary  
A.Molecule type: DNA  
A.Residues: 1-255 <STO>  
A.Cross-references: UNIPROT:O82352; GB:AE002093; NID:g3702332; PIDN:AAC62889.1; GSPDB:GN  
C.Genetics:  
A.Gene: At2g46170  
A.Map position: 2  
Query Match 20.5%; Score 191; DB 2; Length 255;  
Best Local Similarity 27.9%; Pred. No. 4,3e-10;

```

Matches 55; Conservative 40; Mismatches 78; Indels 24; Gaps 6
QY 4 DLLYWRDIKKTGVFG--ASFLLLSLTVFSIVSVYAYIALALLSVTISFRIYKGVIOAI 61
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 70 DVLWRDKLGSAGLVGATAIIVWLFELVEYHLLSLCHLILALG--GLPLWSNAHTLI 126
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 62 QKSDGHPFRAYLESEVAISEELVKYNSALGHVNCITIKELRRFLVDDLDVSLKPAVL 121
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 127 NKTSPQIP-----EIHVPESAFLVWASSLRNELNQAFVILRSIALGRDLKKFLMVVVG 179
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 122 MVVFTVVGALFNGLLTLLILALISLFSVPVYVERHQAOIDHYLGLANKVKQADAM----- 174
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 180 LMIISVGVNWFLLTVYICFVLHITVPMLYEKHKDVKD---PLAKKAKELQKQYVVD 236
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 175 AKIQAKIP--GLKRAE 189
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 237 EKVLKIPIASLKAKAK 253
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 8
T13013
hypothetical protein F8L21.10 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T13013
R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft,
submitted to the Protein Sequence Database, July 1999
A:Reference number: Z17587
A:Accession: T13013
A:Molecule type: DNA
A:Residues: 1-271 <BEV>
A:Cross-references: UNIPROT:Q9SUT9; EMBL:AL036882; GSPDB:GN00062; ATSP:F8L21.10
A:Experimental source: cultivar Columbia; BAC clone F8L21
C:Genetics:
A:Gene: ATSP:F8L21.10
A:Map position: 4
A:Introns: 85/1; 145/2; 192/3; 216/1

Query Match 19.5%; Score 182; DB 2; Length 271;
Best Local Similarity 26.1%; Pred. No. 3, 1e-09;
Matches 47; Conservative 42; Mismatches 79; Indels 12; Gaps 3;

QY 4 DLLYWRDIKKTGVFGAS--LFLLLSLTVFSIVSVYAYIALALLSVTISFRIYKGVIOAI 61
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 87 DIFWPKDKKMGSGVFGGATVAVLWLFELMEYHLLTLLCHWIVAVLAVLF--LWSNATWFI 143
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 62 QKSDGHPFRAYLESEVAISEELVKYNSALGHVNCITIKELRRFLVDDLDVSLKPAVL 121
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 144 HKSPKIP-----EVHPEEPLQLASGLRIEINRGISISLRITASGRDIKKFLSATAG 196
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 122 MVVFTVVGALFNGLLTLLILALISLFSVPVYVERHQAOIDHYLGLANKVKQADAKIOAKI 181
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 197 LVLVSLGCGCYFLTLAYIALVLLFTVPEFDKYEDKVDSTGKRAWELKKQYAVLDKAV 256
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 9
T05595
hypothetical protein F9D16.100 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T05595
R:Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; May
submitted to the Protein Sequence Database, February 1999
A:Reference number: Z15419
A:Accession: T05595
A:Molecule type: DNA
A:Residues: 1-275 <BEV>
A:Cross-references: UNIPROT:Q9SUR3; EMBL:AL035394
A:Experimental source: cultivar Columbia; BAC clone F9D16
C:Genetics:
A:Map position: 4
A:Introns: 89/1; 149/2; 196/3; 220/1
A:Note: F9D16.100

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Query Match      13.3%; Score 124; DB 2; Length 206;
Best Local Similarity 24.4%; Pred. No. 0.00048;
Matches 48; Conservative 44; Mismatches 75; Indels 30; Gaps 8;

Qy      2  VDLLLYWRDILKK--TGVVFGASLELLLSLTVFSTVSVTAYIALALLSVTISFRIYKGVIQ 59
      |||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      16  VEDIVLWRRKKLAFSTLLVSTWILLSPFGFTTIVSWIGIAVSMIF---LWGSLLR 72

```

	Qy	60	AIQNSDEGHFFKRAILDSSEVA---	ISEELVUKIENSALGHRVNCU11---	KEURKFPVMDUTL	115
			:	:	:	:
			:	:	:	:
	Dd	73	LLSK-----	VPEUSGLEVSBEFVVTVYRS---	CRLMEEMVMWMPRVGAES	116
			:	:	:	:
	Qy	114	DSLKFA--VL-MWVFTVGALFNGLTLILAI	SLSFSVPVIYERHQAOIDHYLGCLANKNV	170	
			:	:	:	:
	Dd	117	EWVFARTVLGFWSILSRIGNLLDFHTCL	FGLVWGTLVTKLWEYGDOIQHIGSLKDKS	176	
			:	:	:	:
	Qy	171	KDAWKIOAQIPGLKRK	187		
			:	:	:	:
	Dd	177	KGAYNTTHEXILEMKNK	193		
			:	:	:	:

```

A;Reference number: 224980
A;Accession: T47948
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-264 <DEH>
A;Cross-references: UNIPROT:Q9M312; EMBL:AL132962
A;Experimental source: cultivar Columbia; BAC clone F2A19
C;Genetics:
A;Map position: 3
A;Introns: 68/1; 128/2; 164/1; 210/1
A;Note: F2A19.160

Query Match          11.8%; Score 109.5; DB 2; Length 264;
Best Local Similarity 25.8%; Pred. No. 0.014;
Matches 55; Conservative 37; Mismatches 69; Indels 57; Gaps 14;

Qy      4 D L L Y W R D I K K T G V V F G - A S L F L L L S I T V F S I V S V T A Y I - - - - - A L A L I S V T I S F R I Y K 55
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      70 D V F L W R D K K L S A S V L G V A I W F L F E L V E H F L S L V C H I L I F A L A L F L L S N A H A F - M N K 128

Qy      56 G V T Q - - - - - A I Q S D S G - - - - - H P P R A Y L E S E V A I S E L V Q K - Y S N - S A L G H V N C T I K E 102
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      129 G T P P Y D C F C T E K R A E P G C Y F K E H C H L R K G L E E - - - I S H E L I Q S T Y E T F S I M G F V T R - - - 182

Qy      103 L R L R L F V D D L V D S L K F A V L - - M W V F Y V G A L F N G - L T L L I L A L I S I F S V P V I Y E R H Q A Q 158
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      183 - - - - - S I Y I G S G F W A V D N L G C - - - G K L V Q L L D S C F V L H T V P M L Y E R H E D K 227

Qy      159 I D H Y L G L A N K N V K D A M - - - - - A K I O A K T I P G L K R K A E 189
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      228 V D - - - P V A E K T L K E L K H Y M V F D E K V L S K L P V A S L K A K 262

Search completed: June 16, 2005, 13:32:01
Job time : 6.68322 secs

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Search completed: June 16, 2005, 13:32:01  
Job time : 6.68322 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:33:51 ; Search time 25.6406 Seconds  
(without alignments)  
3774.604 Million cell updates/sec

Title: US-09-830-972-29\_COPY\_990\_1178

Perfect score: 931

Sequence: 1 SVVDLLYWRDIKTKGVVFGA.....VKDAMAKIQAKIPGLKRAE 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	931	100.0	986	2 Q81UA4	Q81ua4 homo sapien
2	931	100.0	1192	1 RTN4 HUMAN	Q9nqc3 homo sapien
3	928	99.7	392	2 Q96B16	Q96b16 homo sapien
4	927	99.6	199	2 Q7YRW9	Q7yrw9 bos taurus
5	927	99.6	343	2 Q6IPN0	Q6ipn0 homo sapien
6	923	99.1	199	2 Q6IM70	Q6im70 sus scrofa
7	919	98.7	187	2 Q6IG15	Q6ig15 sus scrofa
8	918	98.6	199	2 Q7PCJ7	Q7pcj7 macaca fasc
9	915	98.3	578	2 Q8OW95	Q8ow95 mus musculus
10	915	98.3	639	2 Q8K290	Q8k290 mus musculus
11	915	98.3	1046	2 Q8BGK7	Q8bgk7 mus musculus
12	915	98.3	1162	2 Q8BGM9	Q8bgm9 mus musculus
13	912	98.0	375	2 Q8BHF5	Q8bhf5 mus musculus
14	911	97.9	199	1 RTN4 MOUSE	Q99p72 mus musculus
15	911	97.9	356	2 Q8BH78	Q8bh78 mus musculus
16	908	97.5	1163	1 RTN4 RAT	Q9jk11 rattus norv
17	904.5	97.2	1163	2 Q8K3G8	Q8k3g8 mus musculus
18	900.5	96.7	357	2 Q8K3G7	Q8k3g7 mus musculus
19	889	95.5	658	2 Q8R5S8	Q8rs88 gallus gall
20	882	94.7	199	2 Q7T224	Q7t224 gallus gall
21	867	93.1	179	2 Q9GM33	Q9gm33 macaca fasc
22	790	84.9	193	2 Q61FY5	Q61fy5 xenopus tro
23	789	84.7	315	2 Q61FY4	Q61fy4 xenopus tro
24	781	83.9	1024	2 Q6JRV2	Q6jrv2 xenopus lae
25	781	83.9	1043	2 Q6JRV0	Q6jrv0 xenopus lae
26	781	83.9	1055	2 Q6JRV1	Q6jrv1 xenopus lae
27	778	83.6	193	2 Q6JRV6	Q6jrv6 xenopus lae
28	778	83.6	330	2 Q6JRV4	Q6jrv4 xenopus lae
29	777	83.5	199	2 Q6PB23	Q6pb23 xenopus lae
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33	752	80.8	1044	2 Q6JRV8	Q6jrv8 xenopus lae
34	750	80.6	214	2 Q7T222	Q7t222 carassius a
35	749	80.5	193	2 Q6JRW4	Q6jrw4 xenopus lae
36	749	80.5	323	2 Q6JRW1	Q6jrw1 xenopus lae
37	748	80.3	199	2 Q6JRW3	Q6jrw3 xenopus lae
38	748	80.3	304	2 Q6JRW0	Q6jrw0 xenopus lae
39	748	80.3	316	2 Q6JRW2	Q6jrw2 xenopus lae
40	729	78.3	196	2 Q6IEI6	Q6iei6 cyprinus ca
41	715	76.8	193	2 Q6IEJ4	Q6iej4 fugu rubrip
42	710	76.3	197	2 Q6EH23	Q6eh23 brachydania
43	696.5	74.8	209	2 Q6IEJ1	Q6iej1 oncorhynch
44	682	73.3	199	2 Q9BQ59	Q9bq59 homo sapien
45	682	73.3	776	1 RTN1_HUMAN	Q16799 homo sapien

ALIGNMENTS

RESULT 1  
Q81UA4  
ID Q81UA4 PRELIMINARY; PRT; 986 AA.  
AC Q81UA4;  
DT 01-MAR-2003 (Tremblrel. 23, Created)  
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE RTN4 (RTN4 isoform Ab) (RTN4 isoform D) (RTN4 isoform E) (RTN4 isoform F) (RTN4 isoform G) (RTN4 isoform Aa).  
DE P) (RTN4 isoform G) (RTN4 isoform Aa).  
GN Name=RTN4;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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RC TISSUE=Testis;  
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;  
RT "Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4";  
RT J. Mol. Biol. 325:299-323(2003).  
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RA Van der Putten H.;  
RN Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
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RA Oertle T., Schwab M.E.;  
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AC Q9NQC3; Q94962; Q9BXG5; Q9H313; Q9UQ42; Q9V293; Q9V2V7;  
AC Q9Y5U6;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)  
DE (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific  
DE protein C homolog) (RTN-X) (Reticulon 5) (My043 protein).  
GN Name=RTN4; Synonyms=ASY, KIAA0886, NOGO;  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RX MEDLINE=20129242; PubMed=10667780; DOI=10.1038/35000287;  
RA Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G.,  
RA Michalovich D., Simmons D.L., Walsh F.S.;  
RT "Inhibitor of neurite outgrowth in humans.";  
RL Nature 403:383-384(2000).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RC TISSUE=Brain;  
RX MEDLINE=20237542; PubMed=10773680;  
RA Yang J., Yu L., Bi A.D., Zhao S.-Y.;  
RT "Assignment of the human reticulon 4 gene (RTN4) to chromosome  
RT 2p14-->2p13 by radiation hybrid mapping.";  
RL Cytogenet. Cell Genet. 88:101-102(2000).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 4).  
RA Jin W.-L., Ju G.;  
RT "Developmentally-regulated alternative splicing in a novel Nogo-A.";  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).  
RC TISSUE=Placenta, and Skeletal muscle;  
RA Ito T., Schwartz S.M.;  
RT "Cloning of a member of the reticulon gene family in human.";  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE=Fibroblast;  
RA Yutsudo M.;  
RT "Isolation of a cell death-inducing gene.";  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A. (ISOFORM 3).  
RC TISSUE=Placenta;  
RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,  
RA Luo B., Hu R., Chen J.;  
RT "Human neuroendocrine-specific protein C (NSP) homolog gene.";  
RL Nature 403:439-444(2000).  
RL 10KDEGHFPFRAYLSEVAISELVQKYSNSALGHVNCITKELRLFLVDDLVSLKFAV 917  
121 LKMFVTVGALFNGLLTLLIALISLSPVIVYERHOAQIDHYLGLANKVNDAMAKIOAK 180  
918 LKMFVTVGALFNGLLTLLIALISLSPVIVYERHOAQIDHYLGLANKVNDAMAKIOAK 977  
181 IPGLKPKAE 189  
978 IPGLKPKAE 986  
RESULT 2  
RTN4\_HUMAN  
ID RTN4\_HUMAN STANDARD; PRT; 1192 AA.  
AC Q9NQC3; Q94962; Q9BXG5; Q9H313; Q9UQ42; Q9V293; Q9V2V7;  
AC Q9Y5U6;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)  
DE (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific  
DE protein C homolog) (RTN-X) (Reticulon 5) (My043 protein).  
GN Name=RTN4; Synonyms=ASY, KIAA0886, NOGO;  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RX MEDLINE=20129242; PubMed=10667780; DOI=10.1038/35000287;  
RA Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G.,  
RA Michalovich D., Simmons D.L., Walsh F.S.;  
RT "Inhibitor of neurite outgrowth in humans.";  
RL Nature 403:383-384(2000).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RC TISSUE=Brain;  
RX MEDLINE=20237542; PubMed=10773680;  
RA Yang J., Yu L., Bi A.D., Zhao S.-Y.;  
RT "Assignment of the human reticulon 4 gene (RTN4) to chromosome  
RT 2p14-->2p13 by radiation hybrid mapping.";  
RL Cytogenet. Cell Genet. 88:101-102(2000).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 4).  
RA Jin W.-L., Ju G.;  
RT "Developmentally-regulated alternative splicing in a novel Nogo-A.";  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).  
RC TISSUE=Placenta, and Skeletal muscle;  
RA Ito T., Schwartz S.M.;  
RT "Cloning of a member of the reticulon gene family in human.";  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE=Fibroblast;  
RA Yutsudo M.;  
RT "Isolation of a cell death-inducing gene.";  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A. (ISOFORM 3).  
RC TISSUE=Placenta;  
RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,  
RA Luo B., Hu R., Chen J.;  
RT "Human neuroendocrine-specific protein C (NSP) homolog gene.";  
RL Nature 403:439-444(2000).

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
RN [8]  
RP SEQUENCE FROM N.A. (ISOFORM 3).  
RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,  
RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,  
RA Yu J., Han L.H.;  
RT "Novel human cDNA clones with function of inhibiting cancer cell  
RT growth.";  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
RN [9]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Brain;  
RX MEDLINE=99156230; PubMed=10048485;  
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hiroseawa M.,  
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. XII.  
RT The complete sequences of 100 new cDNA clones from brain which code  
RT for large proteins in vitro.";  
RL DNA Res. 5:355-364(1998).  
RN [10]  
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).  
RC TISSUE=Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [11]  
RP SEQUENCE FROM N.A. (ISOFORM 3).  
RC TISSUE=Umbilical cord blood;  
RX MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200;  
RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,  
RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,  
RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;  
RT "Cloning and functional analysis of cDNAs with open reading frames for  
RT 300 previously undefined genes expressed in CD34+ hematopoietic  
RT stem/progenitor cells.";  
RL Genome Res. 10:1546-1560(2000).  
RN [12]  
RP SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).  
RC TISSUE=Brain;  
RA Mao Y.M., Xie Y., Zheng Z.H.;  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
RN [13]  
RP SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1).  
RC TISSUE=Testis;  
RA Sha J.H., Zhou Z.M., Li J.M.;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
RN [14]  
RP TOPOLOGY.  
RC TISSUE=Brain;  
RX MEDLINE=20129259; PubMed=10667797; DOI=10.1038/35000226;  
RA GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.;  
RT "Identification of the Nogo inhibitor of axon regeneration as a  
RT reticulon protein.";  
RL Nature 403:439-444(2000).  
RN [15]



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DR GO: 0005783; C: endoplasmic reticulum; IEA.
DR InterPro: IPR003388; Reticulon.
DR Pfam: PF02453; Reticulon; 1.
DR PROSITE: PS50845; RETICULON; 1.
SQ SEQUENCE 392 AA; 42274 MW; D7B2AA5E839E58AD CRC64;

Query Match          99.7%; Score 928; DB 2; Length 392;
Best Local Similarity 99.5%; Pred. No. 5.5e-71;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60
Db :|||||
QY 204 AVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 263
Db :|||||
QY 61 IKSDEGHPFRAYLSEVAISELVOKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFVAV 120
Db :|||||
QY 264 IKSDEGHPFRAYLSEVAISELVOKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFVAV 323
Db :|||||
QY 121 LMWFTYVGLFNGLTLLILALISLFSVPVYERHQAQIDHYLGLANKNVKDMAKIOAK 180
Db :|||||
QY 324 LMWFTYVGLFNGLTLLILALISLFSVPVYERHQAQIDHYLGLANKNVKDMAKIOAK 383
Db :|||||
QY 181 IFGLKRAE 189
Db :|||||
QY 384 IFGLKRAE 392
Db :|||||

RESULT 4
QYRW9 PRELIMINARY; PRT; 199 AA.
AC QYRW9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE RTN4-C.
GN Name=RTN4;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22715887; PubMed=12832288;
RA Certe T.; Klinger M.; Stuermer C.A.; Schwab M.E.;
RT "A reticular thapsody: phylogenetic evolution and nomenclature of the
RL FASEB J. 17:1238-1247(2003).
DR EMBL; AV164744; AAP47319.2; -.
DR GO: 0005783; C: endoplasmic reticulum; IEA.
DR InterPro: IPR003388; Reticulon.
DR Pfam: PF02453; Reticulon; 1.
DR PROSITE: PS50845; RETICULON; 1.
SQ SEQUENCE 199 AA; 22395 MW; C60161DF3FB34D80 CRC64;

Query Match          99.6%; Score 927; DB 2; Length 199;
Best Local Similarity 100.0%; Pred. No. 3.4e-71;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61
Db :|||||
QY 12 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 71
Db :|||||
QY 62 QKSDEGHPFRAYLSEVAISELVOKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFVAV 121
Db :|||||
QY 72 QKSDEGHPFRAYLSEVAISELVOKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFVAV 131
Db :|||||
QY 122 MVVFTYVGLFNGLTLLILALISLFSVPVYERHQAQIDHYLGLANKNVKDMAKIOAK 181
Db :|||||
QY 132 MVVFTYVGLFNGLTLLILALISLFSVPVYERHQAQIDHYLGLANKNVKDMAKIOAK 191
Db :|||||
QY 182 PGLKRAE 189
Db :|||||

DR GO: 0005783; C: endoplasmic reticulum; IEA.
DR InterPro: IPR003388; Reticulon.
DR Pfam: PF02453; Reticulon; 1.
DR PROSITE: PS50845; RETICULON; 1.
SQ SEQUENCE 392 AA; 42274 MW; D7B2AA5E839E58AD CRC64;

Query Match          99.7%; Score 928; DB 2; Length 392;
Best Local Similarity 99.5%; Pred. No. 5.5e-71;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60
Db :|||||
QY 204 AVVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 263
Db :|||||
QY 61 IKSDEGHPFRAYLSEVAISELVOKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFVAV 120
Db :|||||
QY 264 IKSDEGHPFRAYLSEVAISELVOKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFVAV 323
Db :|||||
QY 121 LMWFTYVGLFNGLTLLILALISLFSVPVYERHQAQIDHYLGLANKNVKDMAKIOAK 180
Db :|||||
QY 324 LMWFTYVGLFNGLTLLILALISLFSVPVYERHQAQIDHYLGLANKNVKDMAKIOAK 383
Db :|||||
QY 181 IFGLKRAE 189
Db :|||||
QY 384 IFGLKRAE 392
Db :|||||

RESULT 5
QYRW9 PRELIMINARY; PRT; 343 AA.
AC QYRW9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE RTN4 protein.
GN Name=RTN4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.B.; Feingold E.A.; Grouse L.H.; Derge J.G.;
RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;
RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;
RA Hopkins R.P.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;
RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
RA Brownstein M.J.; Udwin T.B.; Toshlyuk S.; Carninci P.; Prange C.;
RA Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.;
RA Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;
RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;
RA Villalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
RA Fahey J.; Helton E.; Kettman A.; Madan A.; Rodriguez S.; Sanchez A.;
RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;
RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.;
RA Krzywinski M.I.; Skalska U.; Smailus D.E.; Scherch A.; Schein J.E.;
RA Jones J.J.; Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Eye;
RA Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC071848; AAH71848.1; -.
DR GO: 0005783; C: endoplasmic reticulum; IEA.
DR InterPro: IPR003388; Reticulon.
DR Pfam: PF02453; Reticulon; 1.
DR PROSITE: PS50845; RETICULON; 1.
SQ SEQUENCE 343 AA; 36918 MW; 813207C29AB15BA4 CRC64;

Query Match          99.6%; Score 927; DB 2; Length 343;
Best Local Similarity 100.0%; Pred. No. 5.8e-71;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61
Db :|||||
QY 156 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 215
Db :|||||
QY 62 QKSDEGHPFRAYLSEVAISELVOKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFVAV 121
Db :|||||
QY 216 QKSDEGHPFRAYLSEVAISELVOKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFVAV 275
Db :|||||
QY 122 MVVFTYVGLFNGLTLLILALISLFSVPVYERHQAQIDHYLGLANKNVKDMAKIOAK 181
Db :|||||
QY 276 MVVFTYVGLFNGLTLLILALISLFSVPVYERHQAQIDHYLGLANKNVKDMAKIOAK 335
Db :|||||
QY 182 PGLKRAE 189
Db :|||||
QY 336 PGLKRAE 343
Db :|||||

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RESULT 6
Q6IM70
ID Q6IM70 PRELIMINARY; PRT; 199 AA.
AC Q6IM70;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
RTN4-C.
DE RTN4-C.
GN Sus scrofa (Pig).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22715887; PubMed=12832288;
RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT "A reticular rhapsody: phylogenetic evolution and nomenclature of the
RTN/Nogo gene family.";
RL FASEB J. 17:1238-1247(2003).
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BK001795; DAA01967.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 199 AA; 22425 MW; C61D11DF3FB34D80 CRC64;

Query Match 99.1%; Score 923; DB 2; Length 199;
Best Local Similarity 99.5%; Pred. No. 7.4e-71;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61
Db 12 VDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 71

Qy 62 QKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCCTIKELRLFLVDDLDVSLKPAVL 121
Db 72 QKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCCTIKELRLFLVDDLDVSLKPAVL 131

Qy 122 MWFTYVVGALFNGLTLLILALISLFSVPVYERHQAQIDHYLGLANKNVKDMAKIQAKI 181
Db 132 MWFTYVVGALFNGLTLLILALISLFSVPVYERHQAQIDHYLGLANKNVKDMAKIQAKI 191

Qy 182 PGLKRAE 189
Db 192 PGLKRAKTE 199

RESULT 7
Q6IG15
ID Q6IG15 PRELIMINARY; PRT; 187 AA.
AC Q6IG15;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
RTN4-Bw (Fragment).
DE RTN4-Bw (Fragment).
GN Sus scrofa (Pig).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22715887; PubMed=12832288;
RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT "A reticular rhapsody: phylogenetic evolution and nomenclature of the
RTN/Nogo gene family.";
RL FASEB J. 17:1238-1247(2003).
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BK003966; DAA01973.1; -.

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DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
FT NON_TER
SQ SEQUENCE 187 AA; 20967 MW; A17D87A143C4607C CRC64;

Query Match 98.7%; Score 919; DB 2; Length 187;
Best Local Similarity 99.5%; Pred. No. 1.5e-70;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 VDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 62
Db 1 VDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 60

Qy 63 KSDGHPFRAYLESEVAISELVQKYSNSALGHVNCCTIKELRLFLVDDLDVSLKPAVL 122
Db 61 KSDGHPFRAYLESEVAISELVQKYSNSALGHVNCCTIKELRLFLVDDLDVSLKPAVL 120

Qy 123 MWFTYVVGALFNGLTLLILALISLFSVPVYERHQAQIDHYLGLANKNVKDMAKIQAKI 182
Db 121 MWFTYVVGALFNGLTLLILALISLFSVPVYERHQAQIDHYLGLANKNVKDMAKIQAKI 180

Qy 183 GLKRAE 189
Db 181 GLKRAKTE 187

RESULT 8
Q7PCJ7
ID Q7PCJ7 PRELIMINARY; PRT; 199 AA.
AC Q7PCJ7;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE RTN4-C.
GN Name=RTN4;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22715887; PubMed=12832288;
RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT "A reticular rhapsody: phylogenetic evolution and nomenclature of the
RTN/Nogo gene family.";
RL FASEB J. 17:1238-1247(2003).
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BK001695; DAA01940.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 199 AA; 22469 MW; 761A5FDB6C1DEC3C CRC64;

Query Match 98.6%; Score 918; DB 2; Length 199;
Best Local Similarity 98.4%; Pred. No. 2e-70;
Matches 185; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 61
Db 12 VDLLYWRDMKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 71

Qy 62 QKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCCTIKELRLFLVDDLDVSLKPAVL 121
Db 72 QKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCCTIKELRLFLVDDLDVSLKPAVL 131

Qy 122 MWFTYVVGALFNGLTLLILALISLFSVPVYERHQAQIDHYLGLANKNVKDMAKIQAKI 181
Db 132 MWFTYVVGALFNGLTLLILALISLFSVPVYERHQAQIDHYLGLANKNVKDMAKIQAKI 191

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QY 182 PGLKRAE 189
Db 192 PGLKRAE 199

RESULT 9
Q80W95
ID Q80W95 PRELIMINARY; PRT; 578 AA.
AC Q80W95;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Nogo-A (Fragment).
GN Names=Nogo-A;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tozaki H., Hirata T.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073672; BAC75974.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
FT NON_TER
SQ SEQUENCE 578 AA; 63696 MW; 832670C171E4AC61 CRC64;

Query Match 98.3%; Score 915; DB 2; Length 578;
Best Local Similarity 98.4%; Pred. No. 1e-69;
Matches 186; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIA 60
Db 390 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIA 449
QY 61 IQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNCCTIKELRLFLVDLVDLSLKPAV 120
Db 450 IQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNCCTIKELRLFLVDLVDLSLKPAV 509
QY 121 LMMVFTYVGALENGLLTLLILALISLFSVPVYERHQAQIDHYGLANKNVKDMAKIOAK 180
Db 510 LMMVFTYVGALENGLLTLLILALISLFSVPVYERHQAQIDHYGLANKNVKDMAKIOAK 569
QY 181 IPGLKRAE 189
Db 570 IPGLKRAE 578

RESULT 10
Q8K290
ID Q8K290 PRELIMINARY; PRT; 639 AA.
AC Q8K290;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-WAR-2004 (TREMBlrel. 26, Last annotation update)
DE Rtn4 protein.
GN Name=Rtn4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

QY 182 PGLKRAE 189
Db 192 PGLKRAE 199

RESULT 11
Q8BGK7
ID Q8BGK7 PRELIMINARY; PRT; 1046 AA.
AC Q8BGK7;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Rtn4.
GN Name=Rtn4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=129/SvcJ7, and 129SvCJ7;
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT "Genomic structure and functional characterisation of the promoters of
human and mouse nogo/rtn4.";
RN J. Mol. Biol. 325:299-323 (2003).
RP SEQUENCE FROM N.A.

```

RC STRAIN=129/SvcJ7;  
RA Van der Putten H.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129SVCJ7;  
RA Van der Putten H., Mir A.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY102280; AAM73502.1; -;  
DR EMBL; AY102286; AAM73507.1; -;  
DR MGD; MGI:1915835; Rtn4.  
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0001525; P:angiogenesis; IMP.  
DR GO; GO:0007399; P:neurogenesis; IDA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
SQ SEQUENCE 1046 AA; 114221 MW; 8CE2E2238ED51222 CRC64;

Query Match 98.3%; Score 915; DB 2; Length 1046;  
Best Local Similarity 98.4%; Pred. No. 1.9e-69;  
Matches 186; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
Db 858 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 917  
  
Qy 61 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120  
Db 918 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 977  
  
Qy 121 LMWFTYVYGALFNGTLTLILALISLFSIPVIYERHQAIQIDHYGLANKVVKDAMAKIOAK 180  
Db 978 LMWFTYVYGALFNGTLTLILALISLFSIPVIYERHQAIQIDHYGLANKVVKDAMAKIOAK 1037  
  
Qy 181 IPGLKRKAE 189  
Db 1038 IPGLKRKAE 1046

RESULT 12  
Q8BGM9 PRELIMINARY; PRT; 1162 AA.  
AC Q8BGM9;  
DT 01-MAR-2003 (TReMBLrel. 23, Created)  
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
DE RTN4.  
GN Name=Rtn4;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7;  
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;  
RA Certle T., Huber C., van der Putten H., Schwab M.E.;  
RT "Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4";  
RL J. Mol. Biol. 325:299-323(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7;  
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;  
RA Certle T., Huber C., van der Putten H., Schwab M.E.;  
RT "Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4";  
RL J. Mol. Biol. 325:299-323(2003).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7;  
RA Van der Putten H.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129SVCJ7;  
RA Van der Putten H., Mir A.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY102284; AAM73506.1; -;

DR EMBL; AY102286; AAM73511.1; -;  
DR MGD; MGI:1915835; Rtn4.  
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0001525; P:angiogenesis; IMP.  
DR GO; GO:0007399; P:neurogenesis; IDA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
SQ SEQUENCE 1162 AA; 126612 MW; 855697PBEE11781F CRC64;

Query Match 98.3%; Score 915; DB 2; Length 1162;  
Best Local Similarity 98.4%; Pred. No. 2.1e-69;  
Matches 186; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 60  
Db 974 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1033  
  
Qy 61 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120  
Db 1034 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 1093  
  
Qy 121 LMWFTYVYGALFNGTLTLILALISLFSIPVIYERHQAIQIDHYGLANKVVKDAMAKIOAK 180  
Db 1094 LMWFTYVYGALFNGTLTLILALISLFSIPVIYERHQAIQIDHYGLANKVVKDAMAKIOAK 1153  
  
Qy 181 IPGLKRKAE 189  
Db 1154 IPGLKRKAE 1162

RESULT 13  
Q8BHF5 PRELIMINARY; PRT; 375 AA.  
AC Q8BHF5;  
DT 01-MAR-2003 (TReMBLrel. 23, Created)  
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
DE RTN4.  
GN Name=Rtn4;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7; and 129SVCJ7;  
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;  
RA Certle T., Huber C., van der Putten H., Schwab M.E.;  
RT "Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4";  
RL J. Mol. Biol. 325:299-323(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7;  
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;  
RA Van der Putten H.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129SVCJ7;  
RA Van der Putten H., Mir A.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY102282; AAM73504.1; -;  
DR EMBL; AY102286; AAM73509.1; -;  
DR MGD; MGI:1915835; Rtn4.  
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0001525; P:angiogenesis; IMP.  
DR GO; GO:0007399; P:neurogenesis; IDA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.

SQ SEQUENCE 375 AA; 40300 MW; 23D9EB19BE671AE6 CRC64;  
 Query Match 98.0%; Score 912; DB 2; Length 375;  
 Best Local Similarity 97.9%; Pred. No. 1.2e-69;  
 Matches 185; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFVSIVTAYIALALLSVTISFRIYKGVIOA 60  
 DB 187 AVVDLLYWRDIKKTGVVFGASLFLLLSLTVFVSIVTAYIALALLSVTISFRIYKGVIOA 246  
 QY 61 IQKSDGHPFRAYLESEVAISELVOKYSNLSALGHVNCITIKELRLFLVLDLVDLSLKFAV 120  
 DB 247 IQKSDGHPFRAYLESEVAISELVOKYSNLSALGHVNCITIKELRLFLVLDLVDLSLKFAV 306  
 QY 121 LKMWFTYVGCALFNGLLTLLILALISLSPVPIYERHQAQIDHYGLANKVVKDAMAKIOAK 180  
 DB 307 LKMWFTYVGCALFNGLLTLLILALISLSPVPIYERHQAQIDHYGLANKVVKDAMAKIOAK 366  
 QY 181 IGLKRAE 189  
 DB 367 IGLKRAE 375

## RESULT 14

RTN4 MOUSE STANDARD; PRT; 199 AA.  
 ID RTN4 MOUSE STANDARD; PRT; 199 AA.  
 AC Q99P72; Q9CTE3;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein).  
 GN Name:Rtn4; Synonyms:NOGO;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Theria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=313-L1; TISSUE=Adipocyte;  
 RA Coulson A.C., Criggs P.D., Morris N.J.;  
 RT "Mouse vp20/RTN4C CDNA";  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 170-199 FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Embryo;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Clothia C., Corbani L.E., Cousins S.,  
 RA Dalia E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Kongaya A., Kurochkin I.V., Lee Y., Lennard H., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,  
 RA Pavlovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravelet T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sakai D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573 (2002).  
 CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help  
 CC block the regeneration of the nervous central system in adults (By  
 CC similarity).  
 CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the  
 CC membrane of the endoplasmic reticulum through 2 putative  
 CC transmembrane domains (By similarity).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=1;  
 CC Comment=A number of isoforms may be produced;  
 CC Name=1;  
 CC IsoId=Q99P72-1; Sequence=Displayed;  
 CC -!- SIMILARITY: Contains 1 reticulon domain.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
 CC or send an email to license@sib-sib.ch).  
 CC  
 CC EMBL; AF326337; AAK08076.1; -;  
 CC EMBL; AK003859; -; NOT\_ANNOTATED\_CDS.  
 CC MGI; MGI:1915835; Rtn4.  
 CC GO; GO:0005783; C:endoplasmic reticulum; IDA.  
 CC GO; GO:0030176; C:integral to endoplasmic reticulum membrane; ISS.  
 CC GO; GO:0005635; C:nuclear membrane; ISS.  
 CC GO; GO:0005515; P:protein binding; ISS.  
 CC GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.  
 CC GO; GO:0030517; P:negative regulation of axon extension; ISS.  
 CC GO; GO:0007399; P:neurogenesis; IDA.  
 CC InterPro; IPR003388; Reticulon.  
 CC Pfam; PF02453; Reticulon; 1.  
 CC PROSITE; PS50845; RETICULON; 1.  
 CC Alternative splicing; Endoplasmic reticulum; Transmembrane.  
 CC DOMAIN 1 25 Cytoplasmic (Potential).  
 CC TRANSMEM 26 50 Potential.  
 CC DOMAIN 51 137 Lumenal (Potential).  
 CC TRANSMEM 138 162 Potential.  
 CC DOMAIN 163 199 Cytoplasmic (Potential).  
 CC DOMAIN 12 199 Reticulon.  
 CC SEQUENCE 199 AA; 22466 MW; 07BE5D580059ED9C CRC64;  
 Query Match 97.9%; Score 911; DB 1; Length 199;  
 Best Local Similarity 98.4%; Pred. No. 7.8e-70;  
 Matches 185; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFVSIVTAYIALALLSVTISFRIYKGVIOAI 61  
 DB 12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFVSIVTAYIALALLSVTISFRIYKGVIOAI 71  
 QY 62 QKSDGHPFRAYLESEVAISELVOKYSNLSALGHVNCITIKELRLFLVLDLVDLSLKFAVL 121  
 DB 72 QKSDGHPFRAYLESEVAISELVOKYSNLSALGHVNCITIKELRLFLVLDLVDLSLKFAVL 131  
 QY 122 MVVFTYVGCALFNGLLTLLILALISLSPVPIYERHQAQIDHYGLANKVVKDAMAKIOAKI 181  
 DB 132 MVVFTYVGCALFNGLLTLLILALISLSPVPIYERHQAQIDHYGLANKVVKDAMAKIOAKI 191  
 QY 182 PGLKRAE 189  
 DB 192 PGLKRAE 199  
 RESULT 15  
 Q8BH78 PRELIMINARY; PRT; 356 AA.  
 AC Q8BH78;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE RTN4.  
CN Name=Rtn4;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7, and 129SvscJ7;  
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;  
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;  
RT "Genomic structure and functional characterisation of the promoters of  
human and mouse nogo/rtn4.";  
RL J. Mol. Biol. 325:299-323(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7;  
RA Van der Putten H.;  
RN [3]  
RP Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129SvscJ7;  
RA Van der Putten H., Mir A.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY102281; AAM73503.1; -;  
DR EMBL; AY102286; AAM73508.1; -;  
DR MGD; MGI:1915835; Rtn4.  
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
DR GO; GO:0005515; P:protein binding; IPI.  
DR GO; GO:0001525; P:angiogenesis; IMP.  
DR GO; GO:0007399; P:neurogenesis; IDA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS0845; RETICULON; 1.  
SQ SEQUENCE 356 AA; 38403 MW; 4366C03BA9630B56 CRC64;

Query Match 97.9%; Score 911; DB 2; Length 356;  
Best Local Similarity 98.4%; Fred. No. 1.4e-69;  
Matches 185; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Qy 2 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTVAYIALALLSVTISFRIYKGVIOAI 61  
Db 169 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTVAYIALALLSVTISFRIYKGVIOAI 228  
Qy 62 QKSDEGHPFRAYLESEVAISEELVOKYSNSALGHVNTIKELRLFLVDDLVDSLKPAVL 121  
Db 229 QKSDEGHPFRAYLESEVAISEELVOKYSNSALGHVNTIKELRLFLVDDLVDSLKPAVL 288  
Qy 122 MWVFTYVCGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKI 181  
Db 289 MWVFTYVCGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKI 348  
Qy 182 PGLKRAE 189  
Db 349 PGLKRAE 356

Search completed: June 16, 2005, 13:17:43  
Job time : 26.6406 secs

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